

5407-0234_SL
SEQUENCE LISTING

<110> XBIOTECH, INC.

<120> COMPOSITIONS AND METHODS FOR TREATING AND PREVENTING
STAPHYLOCOCCUS AUREUS INFECTIONS

<130> 5407-0234

<140>

<141>

<150> 62/115,665

<151> 2015-02-13

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<160> 86

<170> PatentIn version 3.5

<210> 1

<211> 20

<212> PRT

<213> Staphylococcus aureus

<220>

<223> Antigenic Peptide #5

<400> 1

Lys Pro Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn
1 5 10 15

Lys Pro Gly Lys
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<210> 2

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<223> PA8-G3 Heavy Chain CDR1

<400> 2

Thr Tyr Gly Met Ser
1 5

<210> 3

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<223> PA8-G3 Heavy Chain CDR2

<400> 3

Ser Ile Thr Gly Ser Gly Arg Ser Thr Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 4
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Heavy Chain CDR3

<400> 4
 Ser Pro Ala Asp Ile Val Thr Gly Tyr Tyr Pro Trp Trp Phe Asp Leu
 1 5 10 15

<210> 5
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Heavy Chain Variable Domain

<400> 5
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Pro Ala Asp Ile Val Thr Gly Tyr Tyr Pro Trp Trp Phe
 100 105 110

Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120 125

<210> 6
 <211> 502
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Heavy Chain

<400> 6
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1

5

10

15

Ser Leu Arg Leu₂₀ Ser Cys Ala Ala Ser₂₅ Gly Phe Thr Phe Ser₃₀ Thr Tyr

Gly Met Ser₃₅ Trp Val Arg Gln Ala₄₀ Pro Gly Lys Gly₄₅ Leu Glu Trp Val

Ser Ser₅₀ Ile Thr Gly Ser₅₅ Gly Arg Ser Thr Phe Tyr₆₀ Ala Asp Ser Val

Lys₆₅ Gly Arg Phe Thr Ile₇₀ Ser Arg Asp Asn Ser₇₅ Thr Asn Thr Leu Ser₈₀

Leu Gln Met Asn₈₅ Ser Leu Arg Ala Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Arg Ser₁₀₀ Pro Ala Asp Ile Val Thr₁₀₅ Gly Tyr Tyr Pro₁₁₀ Trp Trp Phe

Asp Leu Trp₁₁₅ Gly Gln Gly Thr Leu₁₂₀ Val Thr Val Ser Ser₁₂₅ Ala Ser Thr

Lys Gly₁₃₀ Pro Ser Val Phe Pro₁₃₅ Leu Ala Pro Cys Ser₁₄₀ Arg Ser Thr Ser

Gly₁₄₅ Gly Thr Ala Ala Leu₁₅₀ Gly Cys Leu Val Lys₁₅₅ Asp Tyr Phe Pro Glu₁₆₀

Pro Val Thr Val Ser₁₆₅ Trp Asn Ser Gly Ala₁₇₀ Leu Thr Ser Gly Val₁₇₅ His

Thr Phe Pro₁₈₀ Ala Val Leu Gln Ser Ser₁₈₅ Gly Leu Tyr Ser Leu₁₉₀ Ser Ser

Val Val Thr₁₉₅ Val Pro Ser Ser₂₀₀ Leu Gly Thr Gln Thr₂₀₅ Tyr Thr Cys

Asn Val₂₁₀ Asn His Lys Pro Ser₂₁₅ Asn Thr Lys Val Asp₂₂₀ Lys Arg Val Glu

Leu₂₂₅ Lys Thr Pro Leu Gly₂₃₀ Asp Thr Thr His Thr₂₃₅ Cys Pro Arg Cys Pro₂₄₀

Glu Pro Lys Ser Cys₂₄₅ Asp Thr Pro Pro Pro₂₅₀ Cys Pro Arg Cys Pro₂₅₅ Glu

Pro Lys Ser Cys₂₆₀ Asp Thr Pro Pro Pro₂₆₅ Cys Pro Arg Cys Pro₂₇₀ Glu Pro

Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu

275

280

285

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320

Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly
 325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
 405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430

Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr
 435 440 445

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Lys
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<210> 7
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Light Chain CDR1

<400> 7

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 Arg Ala Ser Gln Ser Ile Asn Thr Tyr Leu Asn
 1 5 10

<210> 8
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Light Chain CDR2

<400> 8
 Gly Ala Ser Ser Leu Gln Ser
 1 5

<210> 9
 <211> 9
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Light Chain CDR3

<400> 9
 Gln Gln Ala Asn Ser Phe Pro Leu Thr
 1 5

<210> 10
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Light Chain Variable Domain

<400> 10
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Ala Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 100 105

<210> 11

<211> 214
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA8-G3 Light Chain

<400> 11
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Thr Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45
 Ala Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
 85 90 95
 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 12
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>

<223> PA4-G3 Heavy Chain CDR1

<400> 12

Ser Tyr Ala Met Ser
1 5

<210> 13

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<223> PA4-G3 Heavy Chain CDR2

<400> 13

Ala Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 14

<211> 8

<212> PRT

<213> Homo sapiens

<220>

<223> PA4-G3 Heavy Chain CDR3

<400> 14

Gly Asp Ile Thr Ser Gly Phe Gly
1 5

<210> 15

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<223> PA4-G3 Heavy Chain Variable Domain

<400> 15

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Asp Ile Thr Ser Gly Phe Gly Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 16
<211> 494
<212> PRT
<213> Homo sapiens

<220>
<223> PA4-G3 Heavy Chain

<400> 16
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Gly Asp Ile Thr Ser Gly Phe Gly Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

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

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

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Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr
 210 215 220
 Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro
 225 230 235 240
 Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro
 245 250 255
 Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 260 265 270
 Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 275 280 285
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 290 295 300
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 305 310 315 320
 Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 325 330 335
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val
 340 345 350
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 355 360 365
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 370 375 380
 Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 385 390 395 400
 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 405 410 415
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly
 420 425 430
 Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp
 435 440 445
 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 450 455 460

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Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His
465 470 475 480

Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
485 490

<210> 17
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> PA4-G3 Light Chain CDR1

<400> 17
Arg Ala Ser Gln Gly Ile Arg Asn Asp Leu Gly
1 5 10

<210> 18
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> PA4-G3 Light Chain CDR2

<400> 18
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 19
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> PA4-G3 Light Chain CDR3

<400> 19
Gln Gln Ser Tyr Ser Thr Pro Trp Thr
1 5

<210> 20
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<223> PA4-G3 Light Chain Variable Domain

<400> 20
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

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Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 21

<211> 214

<212> PRT

<213> Homo sapiens

<220>

<223> PA4-G3 Light Chain

<400> 21

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp
85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 22
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> PA7.2-G3 Heavy Chain CDR1

<400> 22
Asn Tyr Ala Met Ser
1 5

<210> 23
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> PA7.2-G3 Heavy Chain CDR2

<400> 23
Thr Ile Ser Gly Ser Asp Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 24
<211> 12
<212> PRT
<213> Homo sapiens

<220>
<223> PA7.2-G3 Heavy Chain CDR3

<400> 24
Val Gly Leu Ser Ala Pro Val Thr Phe Phe Asp Phe
1 5 10

<210> 25
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<223> PA7.2-G3 Heavy Chain Variable Domain

<400> 25
Glu Val Gln Leu Val Glu Ser Arg Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Gly Ser Asp Gly Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Gly Asn Thr Val Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Glu Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Val Gly Leu Ser Ala Pro Val Thr Phe Phe Asp Phe Trp Gly
100 105 110
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 26
<211> 498
<212> PRT
<213> Homo sapiens

<220>
<223> PA7.2-G3 Heavy Chain

<400> 26
Glu Val Gln Leu Val Glu Ser Arg Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Ser Asp Gly Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Glu Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser

115

120

125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro
 210 215 220
 Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys
 245 250 255
 Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp
 260 265 270
 Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly
 275 280 285
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 290 295 300
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 305 310 315 320
 Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His
 325 330 335
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg
 340 345 350
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 355 360 365
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 370 375 380
 Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

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<210> 30
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA7.2-G3 Light Chain Variable Domain

<400> 30
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Phe
 85 90 95

Ser Phe Gly Gln Gly Thr Asp Leu Asp Leu Lys Arg
 100 105

<210> 31
 <211> 214
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA7.2-G3 Light Chain

<400> 31
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Phe
85 90 95

Ser Phe Gly Gln Gly Thr Asp Leu Asp Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 32
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> PA15-G3 Heavy Chain CDR1

<400> 32
Thr Phe Ala Met Asn
1 5

<210> 33
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> PA15-G3 Heavy Chain CDR2

<400> 33
Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 34
<211> 11

<212> PRT
 <213> Homo sapiens

<220>
 <223> PA15-G3 Heavy Chain CDR3

<400> 34
 Asp Phe Asn Trp Asp Ser Gly Thr Met Asp Leu
 1 5 10

<210> 35
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA15-G3 Heavy Chain Variable Domain

<400> 35
 Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Arg Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Thr Phe
 20 25 30

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

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Phe Asn Trp Asp Ser Gly Thr Met Asp Leu Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Pro
 115 120

<210> 36
 <211> 497
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA15-G3 Heavy Chain

<400> 36
 Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Arg Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ser Thr Phe
 20 25 30

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

Ser Ser Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Phe Asn Trp Asp Ser Gly Thr Met Asp Leu Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Pro Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

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

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu
210 215 220

Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys
225 230 235 240

Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp
245 250 255

Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr
260 265 270

Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
275 280 285

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
290 295 300

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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
305 310 315 320

Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn
325 330 335

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val
340 345 350

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
355 360 365

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
370 375 380

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
385 390 395 400

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
420 425 430

Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys

<210> 37
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> PA15-G3 Light Chain CDR1

<400> 37
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 38
<211> 7

<212> PRT
 <213> Homo sapiens

<220>
 <223> PA15-G3 Light Chain CDR2

<400> 38
 Ala Ala Ser Ser Leu Gln Ser
 1 5

<210> 39
 <211> 9
 <212> PRT
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<220>
 <223> PA15-G3 Light Chain CDR3

<400> 39
 Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
 1 5

<210> 40
 <211> 108
 <212> PRT
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<220>
 <223> PA15-G3 Light Chain Variable Domain

<400> 40
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105

<210> 41
 <211> 214
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA15-G3 Light Chain

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<400> 41

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
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<210> 42

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<223> PA21-G3 Heavy Chain CDR1

<400> 42

Ser Tyr Gly Met His

1

5

<210> 43
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA21-G3 Heavy Chain CDR2

<400> 43
 Gly Ile Ser Gly Asp Ala Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 44
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA21-G3 Heavy Chain CDR3

<400> 44
 Val Met Asn Tyr Tyr Gly Pro Gly Ser Ala Phe Asp Tyr
 1 5 10

<210> 45
 <211> 122
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA21-G3 Heavy Chain Variable Domain

<400> 45
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
 1 5 10 15

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

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Gly Asp Ala Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Val Met Asn Tyr Tyr Gly Pro Gly Ser Ala Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 46
<211> 499
<212> PRT
<213> Homo sapiens

<220>
<223> PA21-G3 Heavy Chain

<400> 46
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

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

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Gly Asp Ala Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Met Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Met Asn Tyr Tyr Gly Pro Gly Ser Ala Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr
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Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys
225 230 235 240

Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser
245 250 255

Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys
260 265 270

Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly
275 280 285

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
305 310 315 320

Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val
325 330 335

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe
340 345 350

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
405 410 415

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
420 425 430

Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro
435 440 445

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
450 455 460

Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met
465 470 475 480

His Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser
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490

495

Pro Gly Lys

<210> 47
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA21-G3 Light Chain CDR1

<400> 47
 Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 1 5 10

<210> 48
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA21-G3 Light Chain CDR2

<400> 48
 Ala Ala Ser Ser Leu Gln Ser
 1 5

<210> 49
 <211> 9
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA21-G3 Light Chain CDR3

<400> 49
 Gln Gln Ser Tyr Ser Thr Pro Ile Thr
 1 5

<210> 50
 <211> 108
 <212> PRT
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<220>
 <223> PA21-G3 Light Chain Variable Domain

<400> 50
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
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50

55

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 51
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<223> PA21-G3 Light Chain

<400> 51
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 52
 <211> 5
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA27-G3 Heavy Chain CDR1

<400> 52
 Lys Tyr Gly Met Ser
 1 5

<210> 53
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA27-G3 Heavy Chain CDR2

<400> 53
 Thr Ile Ser Gly Ser Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 54
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA27-G3 Heavy Chain CDR3

<400> 54
 Asp Gly Trp Asp Tyr Glu Asp Phe Phe Gly Ser
 1 5 10

<210> 55
 <211> 120
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA27-G3 Heavy Chain Variable Domain

<400> 55
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Ser Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Trp Asp Tyr Glu Asp Phe Phe Gly Ser Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 56

<211> 497

<212> PRT

<213> Homo sapiens

<220>

<223> PA27-G3 Heavy Chain

<400> 56

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Gly Ser Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Gly Trp Asp Tyr Glu Asp Phe Phe Gly Ser Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

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Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu
 210 215 220
 Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys
 225 230 235 240
 Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp
 245 250 255
 Thr Pro Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr
 260 265 270
 Pro Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 275 280 285
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 290 295 300
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 305 310 315 320
 Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn
 325 330 335
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val
 340 345 350
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 355 360 365
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 370 375 380
 Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 385 390 395 400

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Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
405 410 415

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
420 425 430

Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu
435 440 445

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
450 455 460

Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu
465 470 475 480

Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
485 490 495

Lys

<210> 57
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<223> PA27-G3 Light Chain CDR1

<400> 57
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 58
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<223> PA27-G3 Light Chain CDR2

<400> 58
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 59
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> PA27-G3 Light Chain CDR3

<400> 59
Gln Gln Ser Tyr Ala Phe Pro Tyr Thr
1 5

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<210> 60
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA27-G3 Light Chain Variable Domain

<400> 60
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Thr Asn Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Ser Tyr Ala Phe Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
 100 105

<210> 61
 <211> 214
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA27-G3 Light Chain

<400> 61
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Thr Asn Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Ser Tyr Ala Phe Pro Tyr
 85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 62
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<223> PA32-G3 Heavy Chain CDR1

<400> 62
Asp Tyr Tyr Met Asp
1 5

<210> 63
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> PA32-G3 Heavy Chain CDR2

<400> 63
Ser Ile Lys Ala Asp Gly Ser Glu Thr His Tyr Val Asp Ser Val Lys
1 5 10 15

Gly

<210> 64
<211> 8
<212> PRT
<213> Homo sapiens

<220>

<223> PA32-G3 Heavy Chain CDR3

<400> 64

Asp Pro Gly Arg Arg Phe Asp Tyr
1 5

<210> 65

<211> 117

<212> PRT

<213> Homo sapiens

<220>

<223> PA32-G3 Heavy Chain Variable Domain

<400> 65

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ala Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Asp Tyr
20 25 30

Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
35 40 45

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

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

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Arg Asp Pro Gly Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 66

<211> 494

<212> PRT

<213> Homo sapiens

<220>

<223> PA32-G3 Heavy Chain

<400> 66

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ala Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Asp Tyr
20 25 30

Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val

35

40

45

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

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

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Arg Asp Pro Gly Arg Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

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

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr
 210 215 220

Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro
 225 230 235 240

Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro
 245 250 255

Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
 260 265 270

Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 275 280 285

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 290 295 300

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val

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305				310				315				320			
Gln	Phe	Lys	Trp	Tyr 325	Val	Asp	Gly	Val	Glu 330	Val	His	Asn	Ala	Lys 335	Thr
Lys	Pro	Arg	Glu 340	Glu	Gln	Tyr	Asn	Ser 345	Thr	Phe	Arg	Val	Val 350	Ser	Val
Leu	Thr	Val 355	Leu	His	Gln	Asp	Trp 360	Leu	Asn	Gly	Lys	Glu 365	Tyr	Lys	Cys
Lys	Val 370	Ser	Asn	Lys	Ala	Leu 375	Pro	Ala	Pro	Ile	Glu 380	Lys	Thr	Ile	Ser
Lys 385	Thr	Lys	Gly	Gln	Pro 390	Arg	Glu	Pro	Gln	Val 395	Tyr	Thr	Leu	Pro	Pro 400
Ser	Arg	Glu	Glu	Met 405	Thr	Lys	Asn	Gln	Val 410	Ser	Leu	Thr	Cys	Leu 415	Val
Lys	Gly	Phe	Tyr 420	Pro	Ser	Asp	Ile	Ala 425	Val	Glu	Trp	Glu	Ser 430	Ser	Gly
Gln	Pro	Glu 435	Asn	Asn	Tyr	Asn	Thr 440	Thr	Pro	Pro	Met	Leu 445	Asp	Ser	Asp
Gly	Ser 450	Phe	Phe	Leu	Tyr	Ser 455	Lys	Leu	Thr	Val	Asp 460	Lys	Ser	Arg	Trp
Gln 465	Gln	Gly	Asn	Ile	Phe 470	Ser	Cys	Ser	Val	Met 475	His	Glu	Ala	Leu	His 480
Asn	Arg	Phe	Thr	Gln 485	Lys	Ser	Leu	Ser	Leu 490	Ser	Pro	Gly	Lys		

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<210> 67
<211> 11
<212> PRT
<213> Homo sapiens
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<400> 67
Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<220>
<223> PA32-G3 Light Chain CDR2

<400> 68

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 69

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> PA32-G3 Light Chain CDR3

<400> 69

Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
1 5

<210> 70

<211> 108

<212> PRT

<213> Homo sapiens

<220>

<223> PA32-G3 Light Chain Variable Domain

<400> 70

Ala Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
85 90 95Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 71

<211> 214

<212> PRT

<213> Homo sapiens

<220>

<223> PA32-G3 Light Chain

<400> 71

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

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 72

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<223> PA37-G3 Heavy Chain CDR1

<400> 72

Ser Tyr Ala Met Asn
1 5

<210> 73

<211> 17

<212> PRT

<213> Homo sapiens

<220>

<223> PA37-G3 Heavy Chain CDR2

<400> 73

Ala Ile Ser Gly Ser Gly Asp Ile Thr His Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 74

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> PA37-G3 Heavy Chain CDR3

<400> 74

Gly Pro Trp Leu Ala Pro Gly Gly Trp Phe Asp Pro
 1 5 10

<210> 75

<211> 121

<212> PRT

<213> Homo sapiens

<220>

<223> PA37-G3 Heavy Chain Variable Domain

<400> 75

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

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

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Pro Trp Leu Ala Pro Gly Gly Trp Phe Asp Pro Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 76

<211> 498

<212> PRT

<213> Homo sapiens

<220>

<223> PA37-G3 Heavy Chain

<400> 76

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

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

Leu Gln Met Asn Ser Leu Arg Gly Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Pro Trp Leu Ala Pro Gly Gly Trp Phe Asp Pro Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro
 210 215 220

Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser
 225 230 235 240

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Cys Asp Thr Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys
 245 250 255
 Asp Thr Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp
 260 265 270
 Thr Pro Pro Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly
 275 280 285
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 290 295 300
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 305 310 315 320
 Asp Pro Glu Val Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His
 325 330 335
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg
 340 345 350
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 355 360 365
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 370 375 380
 Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 385 390 395 400
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 405 410 415
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 420 425 430
 Glu Ser Ser Gly Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met
 435 440 445
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 450 455 460
 Lys Ser Arg Trp Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His
 465 470 475 480
 Glu Ala Leu His Asn Arg Phe Thr Gln Lys Ser Leu Ser Leu Ser Pro
 485 490 495
 Gly Lys

<210> 77
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA37-G3 Light Chain CDR1

<400> 77
 Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 1 5 10

<210> 78
 <211> 7
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA37-G3 Light Chain CDR2

<400> 78
 Ala Ala Ser Ser Leu Gln Ser
 1 5

<210> 79
 <211> 9
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA37-G3 Light Chain CDR3

<400> 79
 Gln Gln Ser Tyr Ser Thr Pro Tyr Thr
 1 5

<210> 80
 <211> 108
 <212> PRT
 <213> Homo sapiens

<220>
 <223> PA37-G3 Light Chain Variable Domain

<400> 80
 Ala Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 81
<211> 214
<212> PRT
<213> Homo sapiens

<220>
<223> PA37-G3 Light Chain

<400> 81
Ala Ile Arg Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 82
<211> 21
<212> PRT
<213> Staphylococcus aureus

<220>
<223> Antigenic Peptide #1

<400> 82
Gly Glu Ala Lys Lys Leu Asn Glu Ser Gln Ala Pro Lys Ala Asp Asn
1 5 10 15

Asn Phe Asn Lys Glu
20

<210> 83
<211> 16
<212> PRT
<213> Staphylococcus aureus

<220>
<223> Antigenic Peptide #2

<400> 83
Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys
1 5 10 15

<210> 84
<211> 21
<212> PRT
<213> Staphylococcus aureus

<220>
<223> Antigenic Peptide #3

<400> 84
Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn
1 5 10 15

Lys Phe Asn Lys Glu
20

<210> 85
<211> 20
<212> PRT
<213> Staphylococcus aureus

<220>
<223> Antigenic Peptide #4

<400> 85
Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
1 5 10 15

Lys Glu Glu Asp
20

<210> 86
 <211> 520
 <212> PRT
 <213> Staphylococcus aureus

<220>
 <223> Protein A

<400> 86
 Met Met Thr Leu Gln Ile His Thr Gly Gly Ile Asn Leu Lys Lys Lys
 1 5 10 15

Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile Ala Ser Val Thr
 20 25 30

Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro Ala Ala Asn Ala
 35 40 45

Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn
 50 55 60

Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu
 65 70 75 80

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

Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Asn Phe
 100 105 110

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

Leu Asn Glu Ala Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp
 130 135 140

Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu
 145 150 155 160

Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn
 165 170 175

Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg
 180 185 190

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

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

Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu
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225 230 235 240
 His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser
 245 250 255
 Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys
 260 265 270
 Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala Asp Asn Lys Phe Asn Lys
 275 280 285
 Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Thr
 290 295 300
 Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser
 305 310 315 320
 Val Ser Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln
 325 330 335
 Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Asn Asn
 340 345 350
 Lys Pro Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Asn Asn
 355 360 365
 Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys
 370 375 380
 Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Asn Lys
 385 390 395 400
 Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn
 405 410 415
 Lys Pro Gly Lys Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly
 420 425 430
 Asp Thr Val Asn Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys
 435 440 445
 Ile Ala Ala Asp Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly
 450 455 460
 Gln Glu Leu Val Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala
 465 470 475 480
 Asn Lys Ala Gln Ala Leu Pro Glu Thr Gly Glu Glu Asn Pro Phe Ile
 485 490 495
 Gly Thr Thr Val Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu
 500 505 510 515 520

500

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505

510

Leu Ala Gly Arg Arg Arg Glu Leu
515 520