

SEQUENCE LISTING

<110> BRISTOL-MYERS SQUIBB COMPANY

<120> ANTIBODIES AGAINST IL-7R ALPHA SUBUNIT AND USES THEREOF

<130> 4521.001PC02/C-K/DKC

<150> US 62/795,378

<151> 2019-01-22

<150> US 62/868,791

<151> 2019-06-28

<160> 265

<170> PatentIn version 3.5

<210> 1

<211> 298

<212> PRT

<213> Homo sapiens

<400> 1

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
1 5 10 15

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

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
100 105 110

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Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
130 135 140

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

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
225 230 235 240

Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu
245 250 255

Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val
260 265 270

Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys
275 280 285

Lys Pro Arg Lys Val Ser Val Phe Gly Ala
290 295

<210> 2

<211> 252

<212> PRT

<213> Homo sapiens

<400> 2

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
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Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
 20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
 35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
 50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
 65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
 85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
 100 105 110

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
 115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
 130 135 140

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

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
 165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
 180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
 195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Leu Ser Leu Ser
225 230 235 240

Tyr Gly Pro Val Ser Pro Ile Ile Arg Gln Glu Leu
245 250

<210> 3

<211> 298

<212> PRT

<213> Homo sapiens

<400> 3

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
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Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
100 105 110

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn

130 135 140

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

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
 165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
 180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
 195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
 210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp Pro
225 230 235 240

Ile Leu Leu Thr Ile Ser Ile Leu Ser Phe Phe Ser Val Ala Leu Leu
 245 250 255

Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val
 260 265 270

Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys
 275 280 285

Lys Pro Arg Lys Val Ser Val Phe Gly Ala
 290 295

<210> 4

<211> 261

<212> PRT

<213> Homo sapiens

<400> 4

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
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Val Val Ser Gly Glu Ser Gly Tyr Ala Gln Asn Gly Asp Leu Glu Asp
20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Asn Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
100 105 110

Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
130 135 140

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

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
165 170 175

Lys Trp Thr His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
180 185 190

Arg Lys Leu Gln Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Ser Gly Leu Ser Leu Ser
 225 230 235 240

Tyr Gly Pro Val Ser Pro Ile Ile Arg Arg Leu Trp Asn Ile Phe Val
 245 250 255

Arg Asn Gln Glu Lys
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<210> 5

<211> 4643

<212> DNA

<213> Homo sapiens

<400> 5

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 gaagatctct gatttaaccg tgtactatcc acatgcatta caaacatttc gcagagctgc 4560
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 agaacaaaaa aaaaaaaaaa aaa 4643

<210> 6
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 <212> PRT
 <213> Homo sapiens
 <400> 6

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

His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val Asn Thr Thr Asn
 35 40 45

Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val Lys Cys Leu Asn
 50 55 60

Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr Lys Lys Phe Leu
 65 70 75 80

Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly Glu Lys Ser Leu
 85 90 95

Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys Pro Glu Ala Pro
 100 105 110

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

Thr Phe Asn Thr Ser His Leu Gln Lys Lys Tyr Val Lys Val Leu Met
130 135 140

His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn Lys Trp Thr His
145 150 155 160

Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln Arg Lys Leu Gln
165 170 175

Pro Ala Ala Met Tyr Glu Ile Lys Val Arg Ser Ile Pro Asp His Tyr
180 185 190

Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr Tyr Phe Arg Thr
195 200 205

Pro Glu Ile Asn Asn Ser Ser Gly Glu Met Asp
210 215

<210> 7

<211> 459

<212> PRT

<213> Macaca fascicularis

<400> 7

Met Thr Ile Leu Gly Thr Thr Phe Gly Met Val Phe Ser Leu Leu Gln
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20 25 30

Ala Glu Leu Asp Asp Tyr Ser Phe Ser Cys Tyr Ser Gln Leu Glu Val
35 40 45

Asn Gly Ser Gln His Ser Leu Thr Cys Ala Phe Glu Asp Pro Asp Val
50 55 60

Asn Thr Thr Asn Leu Glu Phe Glu Ile Cys Gly Ala Leu Val Glu Val
65 70 75 80

Lys Cys Leu Ser Phe Arg Lys Leu Gln Glu Ile Tyr Phe Ile Glu Thr
 85 90 95

Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys Val Lys Val Gly
 100 105 110

Gly Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr Thr Ile Val Lys
 115 120 125

Pro Glu Ala Pro Phe Asp Leu Ser Val Ile Tyr Arg Glu Gly Ala Asn
 130 135 140

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

Lys Val Leu Met His Asp Val Ala Tyr Arg Gln Glu Lys Asp Glu Asn
 165 170 175

Lys Trp Met His Val Asn Leu Ser Ser Thr Lys Leu Thr Leu Leu Gln
 180 185 190

Arg Asn Leu Gln Pro Glu Ala Met Tyr Glu Ile Lys Val Arg Ser Ile
 195 200 205

Pro Asp His Tyr Phe Lys Gly Phe Trp Ser Glu Trp Ser Pro Ser Tyr
 210 215 220

Tyr Phe Arg Thr Pro Glu Ile Asn Asn Ser Pro Gly Glu Met Asp Pro
 225 230 235 240

Ile Leu Leu Thr Ile Ser Leu Leu Ser Phe Phe Ser Val Ala Leu Leu
 245 250 255

Val Ile Leu Ala Cys Val Leu Trp Lys Lys Arg Ile Lys Pro Ile Val
 260 265 270

Trp Pro Ser Leu Pro Asp His Lys Lys Thr Leu Glu His Leu Cys Lys
 275 280 285

Lys Pro Arg Lys Asn Leu Asn Val Ser Phe Asn Pro Glu Ser Phe Leu

290 295 300

Asp Cys Gln Ile His Arg Val Asp Asp Ile Gln Ala Arg Asp Glu Val
305 310 315 320

Glu Gly Phe Leu Gln Asp Thr Phe Pro Gln Gln Leu Glu Glu Ser Lys
 325 330 335

Lys Gln Arg Leu Gly Gly Asp Val Gln Ser Pro Ser Cys Pro Ser Glu
 340 345 350

Asp Val Val Ile Thr Pro Glu Ser Phe Glu Arg Asp Ser Ser Leu Arg
 355 360 365

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

Ser Arg Ser Leu Asp Cys Arg Glu Ser Gly Lys Asn Gly Pro His Val
385 390 395 400

Tyr Gln Asp Leu Leu Leu Ser Leu Gly Thr Thr Asn Ser Thr Leu Pro
 405 410 415

Pro Pro Phe Ser Leu Gln Ser Gly Ile Leu Thr Leu Asn Pro Val Ala
 420 425 430

Gln Gly Gln Pro Ile Leu Thr Ser Leu Gly Ser Asn Gln Glu Glu Ala
 435 440 445

Tyr Val Thr Met Ser Ser Phe Tyr Gln Asn Gln
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<210> 8

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<212> PRT

<213> Artificial Sequence

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<223> Epitope 1

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<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

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<223> Epitope 2

<400> 9

Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys Ser Asn Ile Cys
1 5 10 15

<210> 10
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope 3

<400> 10

Val Lys Val Gly Glu Lys Ser Leu Thr Cys Lys Lys Ile Asp Leu Thr
1 5 10 15

Thr

<210> 11
<211> 14
<212> PRT
<213> Artificial Sequence

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<223> Epitope 4

<400> 11

Gln Lys Lys Tyr Val Lys Val Leu Met His Asp Val Ala Tyr
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<210> 12
<211> 16
<212> PRT

<213> Artificial Sequence

<220>

<223> Epitope 5

<400> 12

Tyr Glu Ile Lys Val Arg Ser Ile Pro Asp His Tyr Phe Lys Gly Phe
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<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain CDR1

<400> 13

Asp His Ala Met His
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<210> 14

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain CDR2

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Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 15

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy Chain CDR3

<400> 15

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Val
 1 5 10

<210> 16
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light Chain CDR1

<400> 16

Arg Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 17
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light Chain CDR2

<400> 17

Asp Ala Ser Ser Leu Glu Ser
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<210> 18
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<220>
 <223> Light Chain CDR3

<400> 18

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile Thr
 1 5 10

<210> 19
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 <213> Artificial Sequence

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 <223> Heavy Chain Variable Region (VH)

<400> 19

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

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

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

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

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

Ala Lys Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 20

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<213> Artificial Sequence

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<223> Light Chain Variable region (VL)

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20 25 30

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

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

Trp Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
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<210> 21

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<212> PRT

<213> Artificial Sequence

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<223> Heavy Chain

<400> 21

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 20 25 30

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

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

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

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

Ala Lys Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Val Trp Gly
100 105 110

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

Val Phe Pro Leu Ala Pro Ser Ser Lys 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 Ile Cys Asn Val Asn His
195 200 205

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

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

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

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Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
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Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly
450

<210> 22
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Light Chain

<400> 22

Ala 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 Ser Ser Ala
20 25 30

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

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

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

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

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

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

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

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

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

Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 23

<211> 330

<212> PRT

<213> Homo sapiens

<400> 23

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

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

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

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

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 24
<211> 330
<212> PRT
<213> Homo sapiens

<400> 24

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

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

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

245 250 255

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

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 25

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> IgG1.1f Constant Region

<400> 25

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

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

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

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

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 26
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1.3f Constant Region

<400> 26

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45

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

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160

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

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

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

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

<210> 27

<211> 107

<212> PRT

<213> Homo sapiens

<400> 27

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

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

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 28

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> LSPGK (C-terminal end of heavy chain)

<400> 28

Leu Ser Pro Gly Lys
1 5

<210> 29

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> LSPG (C-terminal end of heavy chain)

<400> 29

Leu Ser Pro Gly

1

<210> 30

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 30

Pro Val Gly Val Val

1

5

<210> 31

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR1 (18B1)

<400> 31

Gly Phe Thr Phe Asp Asp His Ala Met His

1

5

10

<210> 32

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR1 (F27Y)

<400> 32

Gly Tyr Thr Phe Asp Asp His Ala Met His

1

5

10

<210> 33

<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28P)

<400> 33

Gly Phe Pro Phe Asp Asp His Ala Met His
1 5 10

<210> 34
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28A)

<400> 34

Gly Phe Ala Phe Asp Asp His Ala Met His
1 5 10

<210> 35
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28V)

<400> 35

Gly Phe Val Phe Asp Asp His Ala Met His
1 5 10

<210> 36
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28L)

<400> 36

Gly Phe Leu Phe Asp Asp His Ala Met His
1 5 10

<210> 37
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR1 (T28I)

<400> 37

Gly Phe Ile Phe Asp Asp His Ala Met His
 1 5 10

<210> 38
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR1 (T28M)

<400> 38

Gly Phe Met Phe Asp Asp His Ala Met His
 1 5 10

<210> 39
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR1 (T28H)

<400> 39

Gly Phe His Phe Asp Asp His Ala Met His
 1 5 10

<210> 40
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR1 (T28F)

<400> 40

Gly Phe Phe Phe Asp Asp His Ala Met His
1 5 10

<210> 41
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28Y)

<400> 41

Gly Phe Tyr Phe Asp Asp His Ala Met His
1 5 10

<210> 42
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28N)

<400> 42

Gly Phe Asn Phe Asp Asp His Ala Met His
1 5 10

<210> 43
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28D)

<400> 43

Gly Phe Asp Phe Asp Asp His Ala Met His
1 5 10

<210> 44
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR1 (T28E)

<400> 44

Gly Phe Glu Phe Asp Asp His Ala Met His
1 5 10

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR1 (T28Q)

<400> 45

Gly Phe Gln Phe Asp Asp His Ala Met His
1 5 10

<210> 46

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR1 (M34L)

<400> 46

Gly Phe Thr Phe Asp Asp His Ala Leu His
1 5 10

<210> 47

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (S52T)

<400> 47

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

Gly

<210> 48
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (N53H)

<400> 48

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

Gly

<210> 49
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (I57V)

<400> 49

Gly Ile Ser Trp Asn Ser Arg Gly Val Gly Tyr Ala Asp Ser Val Lys
 1 5 10 15

Gly

<210> 50
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60G)

<400> 50

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Gly Asp Ser Val Lys
 1 5 10 15

Gly

<210> 51
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60S)

<400> 51

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ser Asp Ser Val Lys
 1 5 10 15

Gly

<210> 52
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60T)

<400> 52

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Thr Asp Ser Val Lys
 1 5 10 15

Gly

<210> 53
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60V)

<400> 53

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Val Asp Ser Val Lys
 1 5 10 15

Gly

<210> 54
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60L)

<400> 54

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

Gly

<210> 55
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60I)

<400> 55

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ile Asp Ser Val Lys
 1 5 10 15

Gly

<210> 56
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60R)

<400> 56

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Arg Asp Ser Val Lys
 1 5 10 15

Gly

<210> 57
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60H)

<400> 57

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr His Asp Ser Val Lys
 1 5 10 15

Gly

<210> 58
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (A60N)

<400> 58

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Asn Asp Ser Val Lys
 1 5 10 15

Gly

<210> 59
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61P)

<400> 59

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Pro Ser Val Lys
 1 5 10 15

Gly

<210> 60
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61T)

<400> 60

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Thr Ser Val Lys
 1 5 10 15

Gly

<210> 61
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61N)

<400> 61

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asn Ser Val Lys
 1 5 10 15

Gly

<210> 62
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61E)

<400> 62

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Glu Ser Val Lys
 1 5 10 15

Gly

<210> 63
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61Q)

<400> 63

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Gln Ser Val Lys
 1 5 10 15

Gly

<210> 64
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61S)

<400> 64

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Ser Ser Val Lys
 1 5 10 15

Gly

<210> 65
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (D61H)

<400> 65

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala His Ser Val Lys
 1 5 10 15

Gly

<210> 66
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (S62P)

<400> 66

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Pro Val Lys
 1 5 10 15

Gly

<210> 67
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (S62G)

<400> 67

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Gly Val Lys
 1 5 10 15

Gly

<210> 68
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2 (S62A)

<400> 68

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ala Val Lys

1 5 10 15

Gly

<210> 69
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62T)

<400> 69

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

Gly

<210> 70
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62V)

<400> 70

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Val Val Lys
1 5 10 15

Gly

<210> 71
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62R)

<400> 71

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Arg Val Lys
1 5 10 15

Gly

<210> 72
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62H)

<400> 72

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp His Val Lys
1 5 10 15

Gly

<210> 73
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62F)

<400> 73

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

Gly

<210> 74
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62Y)

<400> 74

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Tyr Val Lys
1 5 10 15

Gly

<210> 75
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62N)

<400> 75

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Asn Val Lys
1 5 10 15

Gly

<210> 76
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62D)

<400> 76

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Asp Val Lys
1 5 10 15

Gly

<210> 77
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HC CDR2 (S62E)

<400> 77

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Glu Val Lys
1 5 10 15

Gly

<210> 78

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (V63I)

<400> 78

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Ile Lys
1 5 10 15

Gly

<210> 79

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64A)

<400> 79

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Ala
1 5 10 15

Gly

<210> 80

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64S)

<400> 80

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Ser
1 5 10 15

Gly

<210> 81

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64T)

<400> 81

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Thr
1 5 10 15

Gly

<210> 82

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64V)

<400> 82

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Val
1 5 10 15

Gly

<210> 83

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64L)

<400> 83

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Leu
1 5 10 15

Gly

<210> 84

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64I)

<400> 84

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Ile
1 5 10 15

Gly

<210> 85

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64M)

<400> 85

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Met
1 5 10 15

Gly

<210> 86

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64R)

<400> 86

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Arg
1 5 10 15

Gly

<210> 87

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64H)

<400> 87

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val His
1 5 10 15

Gly

<210> 88

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64F)

<400> 88

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Phe
1 5 10 15

Gly

<210> 89

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR2 (K64Y)

<400> 89

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Tyr
1 5 10 15

Gly

<210> 90

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<223> HC CDR2 (K64N)

<400> 90

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Asn
1 5 10 15

Gly

<210> 91

<211> 17

<212> PRT

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<223> HC CDR2 (K64D)

<400> 91

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Asp
1 5 10 15

Gly

<210> 92

<211> 17

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<223> HC CDR2 (K64E)

<400> 92

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Glu
1 5 10 15

Gly

<210> 93

<211> 17

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<223> HC CDR2 (K64Q)

<400> 93

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Gln
1 5 10 15

Gly

<210> 94

<211> 17

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<223> HC CDR2 (G65H)

<400> 94

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

His

<210> 95

<211> 17

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<400> 95

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Lys
1 5 10 15

Asp

<210> 96

<211> 17

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<223> HC CDR2 (G65Q)

<400> 96

Gly Ile Ser Trp Asn Ser Arg Gly Ile Gly Tyr Ala Asp Ser Val Lys
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Gln

<210> 97

<211> 12

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<220>

<223> HC CDR3 (S98T)

<400> 97

Asp Glu Tyr Thr Arg Gly Tyr Tyr Val Leu Asp Val
1 5 10

<210> 98

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<400> 98

Asp Glu Tyr Asn Arg Gly Tyr Tyr Val Leu Asp Val
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Asp Glu Tyr Asp Arg Gly Tyr Tyr Val Leu Asp Val
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Asp Glu Tyr Glu Arg Gly Tyr Tyr Val Leu Asp Val
1 5 10

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<223> HC CDR3 (R99L)

<400> 101

Asp Glu Tyr Ser Leu Gly Tyr Tyr Val Leu Asp Val
1 5 10

<210> 102

<211> 12

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<223> HC CDR3 (R99M)

<400> 102

Asp Glu Tyr Ser Met Gly Tyr Tyr Val Leu Asp Val
1 5 10

<210> 103

<211> 12

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<220>

<223> HC CDR3 (R99S)

<400> 103

Asp Glu Tyr Ser Ser Gly Tyr Tyr Val Leu Asp Val
1 5 10

<210> 104

<211> 12

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<223> HC CDR3 (V100cG)

<400> 104

Asp Glu Tyr Ser Arg Gly Tyr Tyr Gly Leu Asp Val
1 5 10

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<223> HC CDR3 (V100cA)

<400> 105

Asp Glu Tyr Ser Arg Gly Tyr Tyr Ala Leu Asp Val
1 5 10

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<400> 106

Asp Glu Tyr Ser Arg Gly Tyr Tyr Ser Leu Asp Val
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<400> 107

Asp Glu Tyr Ser Arg Gly Tyr Tyr Thr Leu Asp Val
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<210> 108
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<400> 108

Asp Glu Tyr Ser Arg Gly Tyr Tyr Met Leu Asp Val
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<400> 109

Asp Glu Tyr Ser Arg Gly Tyr Tyr Asn Leu Asp Val
1 5 10

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<400> 110

Asp Glu Tyr Ser Arg Gly Tyr Tyr Glu Leu Asp Val
1 5 10

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<400> 111

Asp Glu Tyr Ser Arg Gly Tyr Tyr Gln Leu Asp Val
1 5 10

<210> 112
<211> 12
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<220>
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<400> 112

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Ala
1 5 10

<210> 113
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<400> 113

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Ser
1 5 10

<210> 114

<211> 12

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<220>

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<400> 114

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Thr
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<210> 115

<211> 12

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<220>

<223> HC CDR3 (V102R)

<400> 115

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Arg
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<213> Artificial Sequence

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<223> HC CDR3 (V102H)

<400> 116

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp His
1 5 10

<210> 117

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<223> HC CDR3 (V102Y)

<400> 117

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Tyr
1 5 10

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<211> 12

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<223> HC CDR3 (V102W)

<400> 118

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Trp
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<400> 119

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Asn
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<211> 12

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<223> HC CDR3 (V102E)

<400> 120

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Glu
1 5 10

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<211> 12
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<400> 121

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Gln
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<400> 122

Asp Glu Tyr Ser Arg Gly Tyr Tyr Val Leu Asp Met
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<210> 123
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<400> 123

Ser Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 124
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<400> 124

Thr Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
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<210> 125
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<400> 125

Val Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
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<400> 126

Lys Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
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<400> 127

His Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
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<400> 128

Tyr Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
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<400> 129

Ile Ala Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 130

Arg Ser Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 131

Arg Thr Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 132

Arg Val Ser Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 133

<211> 11

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<223> LC CDR1 (S26P)

<400> 133

Arg Ala Pro Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<211> 11

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<223> LC CDR1 (S26G)

<400> 134

Arg Ala Gly Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 135

<211> 11

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<220>

<223> LC CDR1 (S26A)

<400> 135

Arg Ala Ala Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 136

<211> 11

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<220>

<223> LC CDR1 (S26T)

<400> 136

Arg Ala Thr Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 137

<211> 11

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<213> Artificial Sequence

<220>

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<400> 137

Arg Ala Val Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 138

<211> 11

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<220>

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<400> 138

Arg Ala Leu Gln Gly Ile Ser Ser Ala Leu Ala
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<210> 139

<211> 11

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Arg Ala Ile Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 140

Arg Ala Met Gln Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 141
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<400> 141

Arg Ala Lys Gln Gly Ile Ser Ser Ala Leu Ala
 1 5 10

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Arg Ala Arg Gln Gly Ile Ser Ser Ala Leu Ala
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<400> 143

Arg Ala His Gln Gly Ile Ser Ser Ala Leu Ala

1 5 10

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1 5 10

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Arg Ala Glu Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 146

Arg Ala Gln Gln Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 147

Arg Ala Ser Pro Gly Ile Ser Ser Ala Leu Ala
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<210> 148

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<400> 148

Arg Ala Ser Gly Gly Ile Ser Ser Ala Leu Ala
1 5 10

<210> 149

<211> 11

<212> PRT

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<400> 149

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<210> 150

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<400> 151

Arg Ala Ser Thr Gly Ile Ser Ser Ala Leu Ala

1 5 10

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<400> 152

Arg Ala Ser Val Gly Ile Ser Ser Ala Leu Ala

1 5 10

<210> 153

<211> 11

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<223> LC CDR1 (Q27L)

<400> 153

Arg Ala Ser Leu Gly Ile Ser Ser Ala Leu Ala

1 5 10

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<211> 11

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<400> 154

Arg Ala Ser Ile Gly Ile Ser Ser Ala Leu Ala

1 5 10

<210> 155

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<400> 155

Arg Ala Ser Met Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 156

Arg Ala Ser His Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 157

Arg Ala Ser Phe Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<220>
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<400> 158

Arg Ala Ser Tyr Gly Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 159

Arg Ala Ser Asn Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 160
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Arg Ala Ser Asp Gly Ile Ser Ser Ala Leu Ala
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<400> 161

Arg Ala Ser Glu Gly Ile Ser Ser Ala Leu Ala
 1 5 10

<210> 162
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<400> 162

Arg Ala Ser Gln Pro Ile Ser Ser Ala Leu Ala
1 5 10

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<400> 163

Arg Ala Ser Gln Ala Ile Ser Ser Ala Leu Ala
1 5 10

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Arg Ala Ser Gln Ser Ile Ser Ser Ala Leu Ala
1 5 10

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

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<400> 166

Arg Ala Ser Gln His Ile Ser Ser Ala Leu Ala
1 5 10

<210> 167

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<400> 167

Arg Ala Ser Gln Glu Ile Ser Ser Ala Leu Ala
1 5 10

<210> 168

<211> 11

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<220>

<223> LC CDR1 (G28Q)

<400> 168

Arg Ala Ser Gln Gln Ile Ser Ser Ala Leu Ala
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<210> 169

<211> 11

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<220>

<223> LC CDR1 (G28M)

<400> 169

Arg Ala Ser Gln Met Ile Ser Ser Ala Leu Ala
1 5 10

<210> 170

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<220>

<223> LC CDR1 (G28N)

<400> 170

Arg Ala Ser Gln Asn Ile Ser Ser Ala Leu Ala
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<210> 171

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<400> 171

Arg Ala Ser Gln Asp Ile Ser Ser Ala Leu Ala
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<210> 172

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<223> LC CDR1 (I29P)

<400> 172

Arg Ala Ser Gln Gly Pro Ser Ser Ala Leu Ala
1 5 10

<210> 173

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<220>

<223> LC CDR1 (I29G)

<400> 173

Arg Ala Ser Gln Gly Gly Ser Ser Ala Leu Ala
1 5 10

<210> 174

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<220>
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<400> 174

Arg Ala Ser Gln Gly Ala Ser Ser Ala Leu Ala
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<210> 175
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Arg Ala Ser Gln Gly Ser Ser Ser Ala Leu Ala
 1 5 10

<210> 176
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<400> 176

Arg Ala Ser Gln Gly Thr Ser Ser Ala Leu Ala
 1 5 10

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<400> 177

Arg Ala Ser Gln Gly Val Ser Ser Ala Leu Ala
 1 5 10

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<400> 178

Arg Ala Ser Gln Gly Leu Ser Ser Ala Leu Ala
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<400> 179

Arg Ala Ser Gln Gly Asn Ser Ser Ala Leu Ala
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<210> 180
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Arg Ala Ser Gln Gly Ile Thr Ser Ala Leu Ala
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<210> 181
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<400> 181

Arg Ala Ser Gln Gly Ile Val Ser Ala Leu Ala
1 5 10

<210> 182
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<400> 182

Arg Ala Ser Gln Gly Ile Leu Ser Ala Leu Ala
1 5 10

<210> 183
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<400> 183

Arg Ala Ser Gln Gly Ile Ile Ser Ala Leu Ala
1 5 10

<210> 184
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<400> 184

Arg Ala Ser Gln Gly Ile Met Ser Ala Leu Ala
1 5 10

<210> 185
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<223> LC CDR1 (S30M)

<400> 185

Arg Ala Ser Gln Gly Ile His Ser Ala Leu Ala
1 5 10

<210> 186

<211> 11

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<223> LC CDR1 (S30F)

<400> 186

Arg Ala Ser Gln Gly Ile Phe Ser Ala Leu Ala
1 5 10

<210> 187

<211> 11

<212> PRT

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<223> LC CDR1 (S30Y)

<400> 187

Arg Ala Ser Gln Gly Ile Tyr Ser Ala Leu Ala
1 5 10

<210> 188

<211> 11

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<213> Artificial Sequence

<220>

<223> LC CDR1 (S30N)

<400> 188

Arg Ala Ser Gln Gly Ile Asn Ser Ala Leu Ala
1 5 10

<210> 189

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR1 (S30D)

<400> 189

Arg Ala Ser Gln Gly Ile Asp Ser Ala Leu Ala
1 5 10

<210> 190

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR1 (S30E)

<400> 190

Arg Ala Ser Gln Gly Ile Glu Ser Ala Leu Ala
1 5 10

<210> 191

<211> 11

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<213> Artificial Sequence

<220>

<223> LC CDR1 (S30Q)

<400> 191

Arg Ala Ser Gln Gly Ile Gln Ser Ala Leu Ala
1 5 10

<210> 192

<211> 11

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<223> LC CDR1 (A32P)

<400> 192

Arg Ala Ser Gln Gly Ile Ser Ser Pro Leu Ala
1 5 10

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<400> 193

Arg Ala Ser Gln Gly Ile Ser Ser Ala Ala Ala
 1 5 10

<210> 194
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<220>
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<400> 194

Arg Ala Ser Gln Gly Ile Ser Ser Ala Val Ala
 1 5 10

<210> 195
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<220>
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<400> 195

Asp Gly Ser Ser Leu Glu Ser
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<220>
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<400> 196

Asp Ser Ser Ser Leu Glu Ser

1 5

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<212> PRT
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<400> 197

Asp Met Ser Ser Leu Glu Ser
1 5

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<220>
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<400> 198

Asp His Ser Ser Leu Glu Ser
1 5

<210> 199
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<220>
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<400> 199

Asp Asn Ser Ser Leu Glu Ser
1 5

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<220>
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<400> 200

Asp Asp Ser Ser Leu Glu Ser
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<210> 201

<211> 7

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<220>

<223> LC CDR2 (A51E)

<400> 201

Asp Glu Ser Ser Leu Glu Ser
1 5

<210> 202

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (A51Q)

<400> 202

Asp Gln Ser Ser Leu Glu Ser
1 5

<210> 203

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S52G)

<400> 203

Asp Ala Gly Ser Leu Glu Ser
1 5

<210> 204

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S52A)

<400> 204

Asp Ala Ala Ser Leu Glu Ser

1 5

<210> 205

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S52T)

<400> 205

Asp Ala Thr Ser Leu Glu Ser

1 5

<210> 206

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> LC CDR2 (S52V)

<400> 206

Asp Ala Val Ser Leu Glu Ser

1 5

<210> 207

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S52M)

<400> 207

Asp Ala Met Ser Leu Glu Ser

1 5

<210> 208

<211> 7

<212> PRT
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<220>
<223> LC CDR2 (S52H)

<400> 208

Asp Ala His Ser Leu Glu Ser
1 5

<210> 209
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S52F)

<400> 209

Asp Ala Phe Ser Leu Glu Ser
1 5

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

<220>
<223> LC CDR2 (S52Y)

<400> 210

Asp Ala Tyr Ser Leu Glu Ser
1 5

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

<220>
<223> LC CDR2 (S52N)

<400> 211

Asp Ala Asn Ser Leu Glu Ser
1 5

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

<220>
 <223> LC CDR2 (S52D)

<400> 212

Asp Ala Asp Ser Leu Glu Ser
 1 5

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

<220>
 <223> LC CDR2 (S52E)

<400> 213

Asp Ala Glu Ser Leu Glu Ser
 1 5

<210> 214
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR2 (S52Q)

<400> 214

Asp Ala Gln Ser Leu Glu Ser
 1 5

<210> 215
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR2 (S53A)

<400> 215

Asp Ala Ser Ala Leu Glu Ser
1 5

<210> 216
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S53F)

<400> 216

Asp Ala Ser Phe Leu Glu Ser
1 5

<210> 217
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S53Y)

<400> 217

Asp Ala Ser Tyr Leu Glu Ser
1 5

<210> 218
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S53W)

<400> 218

Asp Ala Ser Trp Leu Glu Ser
1 5

<210> 219
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S53N)

<400> 219

Asp Ala Ser Asn Leu Glu Ser
1 5

<210> 220

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S53D)

<400> 220

Asp Ala Ser Asp Leu Glu Ser
1 5

<210> 221

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S53E)

<400> 221

Asp Ala Ser Glu Leu Glu Ser
1 5

<210> 222

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (S53L)

<400> 222

Asp Ala Ser Leu Leu Glu Ser
1 5

<210> 223

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (L54P)

<400> 223

Asp Ala Ser Ser Pro Glu Ser
1 5

<210> 224

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (L54S)

<400> 224

Asp Ala Ser Ser Ser Glu Ser
1 5

<210> 225

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (L54T)

<400> 225

Asp Ala Ser Ser Thr Glu Ser
1 5

<210> 226

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2 (L54K)

<400> 226

Asp Ala Ser Ser Lys Glu Ser
1 5

<210> 227

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

<220>
 <223> LC CDR2 (L54H)

<400> 227

Asp Ala Ser Ser His Glu Ser
 1 5

<210> 228
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR2 (L54N)

<400> 228

Asp Ala Ser Ser Asn Glu Ser
 1 5

<210> 229
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR2 (E55D)

<400> 229

Asp Ala Ser Ser Leu Asp Ser
 1 5

<210> 230
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR2 (E55Q)

<400> 230

Asp Ala Ser Ser Leu Gln Ser
 1 5

<210> 231
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56G)

<400> 231

Asp Ala Ser Ser Leu Glu Gly
1 5

<210> 232
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56T)

<400> 232

Asp Ala Ser Ser Leu Glu Thr
1 5

<210> 233
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56N)

<400> 233

Asp Ala Ser Ser Leu Glu Asn
1 5

<210> 234
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56D)

<400> 234

Asp Ala Ser Ser Leu Glu Asp
1 5

<210> 235
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56Q)

<400> 235

Asp Ala Ser Ser Leu Glu Gln
1 5

<210> 236
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56P)

<400> 236

Asp Ala Ser Ser Leu Glu Pro
1 5

<210> 237
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR2 (S56E)

<400> 237

Asp Ala Ser Ser Leu Glu Glu
1 5

<210> 238
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> LC CDR3 (Q89M)

<400> 238

Met Gln Phe Asn Ser Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 239

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (Q90G)

<400> 239

Gln Gly Phe Asn Ser Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 240

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (Q90A)

<400> 240

Gln Ala Phe Asn Ser Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 241

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (Q90D)

<400> 241

Gln Asp Phe Asn Ser Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 242

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (Q90E)

<400> 242

Gln Glu Phe Asn Ser Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 243

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (N92E)

<400> 243

Gln Gln Phe Glu Ser Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 244

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (S93P)

<400> 244

Gln Gln Phe Asn Pro Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 245

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (S93A)

<400> 245

Gln Gln Phe Asn Ala Tyr Pro Leu Trp Ile Thr
1 5 10

<210> 246
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR3 (W95bT)

<400> 246

Gln Gln Phe Asn Ser Tyr Pro Leu Thr Ile Thr
 1 5 10

<210> 247
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR3 (W95bl)

<400> 247

Gln Gln Phe Asn Ser Tyr Pro Leu Ile Ile Thr
 1 5 10

<210> 248
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR3 (W95bM)

<400> 248

Gln Gln Phe Asn Ser Tyr Pro Leu Met Ile Thr
 1 5 10

<210> 249
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LC CDR3 (W95bK)

<400> 249

Gln Gln Phe Asn Ser Tyr Pro Leu Lys Ile Thr

1 5 10

<210> 250
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR3 (W95bN)

<400> 250

Gln Gln Phe Asn Ser Tyr Pro Leu Asn Ile Thr
1 5 10

<210> 251
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR3 (W95bE)

<400> 251

Gln Gln Phe Asn Ser Tyr Pro Leu Glu Ile Thr
1 5 10

<210> 252
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR3 (W95bQ)

<400> 252

Gln Gln Phe Asn Ser Tyr Pro Leu Gln Ile Thr
1 5 10

<210> 253
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LC CDR3 (I96L)

<400> 253

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Leu Thr
1 5 10

<210> 254

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (T97M)

<400> 254

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile Met
1 5 10

<210> 255

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (T97K)

<400> 255

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile Lys
1 5 10

<210> 256

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (T97H)

<400> 256

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile His
1 5 10

<210> 257

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (T97Y)

<400> 257

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile Tyr

1 5 10

<210> 258

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (T97E)

<400> 258

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile Glu

1 5 10

<210> 259

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3 (T97Q)

<400> 259

Gln Gln Phe Asn Ser Tyr Pro Leu Trp Ile Gln

1 5 10

<210> 260

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR1

<220>

<221> misc_feature

<222> (1)..(1)

<223> Wherein Xaa is Phe or Tyr

<220>

<221> misc_feature

<222> (2)..(2)
 <223> Wherein Xaa is Thr,
 Pro,Ala,Ser,Val,Leu,Ile,Met,His,Phe,Tyr,Asn,Asp,Glu, or Gln

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> Wherein Xaa is Leu, or Met

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> Xaa can be any naturally occurring amino acid

<400> 260

Gly Xaa Xaa Phe Asp Asp His Ala Xaa His
 1 5 10

<210> 261
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HC CDR2

<220>
 <221> misc_feature
 <222> (1)..(1)
 <223> Wherein Xaa is Ser or Thr

<220>
 <221> misc_feature
 <222> (2)..(2)
 <223> Wherein Xaa is His or Asn

<220>
 <221> misc_feature
 <222> (3)..(3)
 <223> Wherein Xaa is Ile or Val

<220>
 <221> misc_feature
 <222> (4)..(4)
 <223> Wherein Xaa is Gly, Ala, Ser, Thr, Val, Leu, Ile, Arg, His, or
 Asn

<220>
 <221> misc_feature
 <222> (5)..(5)

<223> Wherein Xaa is Pro, Thr, Asn, As, Glu, Gln, Ser, His, or Tyr

<220>

<221> misc_feature

<222> (6)..(6)

<223> Wherein Xaa is

Pro,Gly,Ala,Ser,Thr,Val,Arg,His,Phe,Tyr,Asn,Asp,Arg, or Glu

<220>

<221> misc_feature

<222> (7)..(7)

<223> Wherein Xaa is Val or Ile

<220>

<221> misc_feature

<222> (8)..(8)

<223> Wherein Xaa is Ala, Ser, Thr, Val,Leu, Ile,Met, Lys, Arg, His,
Phe, Tyr, Asn, Asp, Glu, Arg, or Gln

<220>

<221> misc_feature

<222> (9)..(9)

<223> Wherein Xaa is Gly, His, Asp, or Gln

<220>

<221> misc_feature

<222> (12)..(17)

<223> Xaa can be any naturally occurring amino acid

<400> 261

Gly	Ile	Xaa	Trp	Xaa	Ser	Arg	Gly	Xaa	Gly	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa
1		5			10		15								

Xaa

<210> 262

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> HC CDR3

<220>

<221> misc_feature

<222> (1)..(1)

<223> Wherein X is Ser,Thr, Asn, Asp, Glu

<220>

<221> misc_feature

<222> (2)..(2)

<223> Wherein X is Lys, Met, Arg, or Ser

<220>

<221> misc_feature

<222> (3)..(3)

<223> Wherein Xaa is Gly, Ala, Ser, Thr, Val, Met, Asn, Glu, or Gln

<220>

<221> misc_feature

<222> (4)..(4)

<223> Wherein X is Ala, Ser, Thr, Val, Arg, His, Tyr, Trp, Asn, Glu, or Met

<220>

<221> misc_feature

<222> (5)..(5)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (12)..(12)

<223> Xaa can be any naturally occurring amino acid

<400> 262

Asp Glu Tyr Xaa Xaa Gly Tyr Tyr Xaa Leu Asp Xaa

1 5 10

<210> 263

<211> 11

<212> PRT

<213> Macaca fascicularis

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Wherein Xaa is Ser, Thr, Val, Lys, Arg, His, Tyr or Ile

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Wherein Xaa is Ala, Ser, Thr, or Val

<220>
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 <222> (3)..(3)
 <223> Wherein Xaa is Pro, Gly, Ala, Ser, Thr, Val, Leu, Ile, Met, Lys,
 Arg, His, Asn, Glu

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> Wherein Xaa is Pro, Gly, Ala, Ser, Thr, Val, Leu, Ile, Met, His,
 Phe, Tyr, Asn, As, Glu

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> Wherein Xaa is Pro, Gly, Aal, Ser, Thr, His, Glu, Gln, Met, Asn,
 or Asp

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Wherein Xaa is Pro, Gly, Ala, Ser, Thr, Val, Leu, Ile, Asn

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> Wherein Xaa is Ser, Thr, Val, Leu, Ile, Met, His, Phe, Tyr, Asn,
 Asp, Glu, or Gln

<220>
 <221> MISC_FEATURE
 <222> (8)..(8)
 <223> Wherein Xaa is Pro or Ala

<220>
 <221> MISC_FEATURE
 <222> (9)..(9)
 <223> Wherein Xaa is Ala, Leu, or Val

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> Xaa can be any naturally occurring amino acid

<400> 263

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Ala
 1 5 10

<210> 264
 <211> 7
 <212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR2

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Wherein Xaa is Gly, Ala, Ser, Met, His, Asn, Asp, Glu, or Gln

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Wherein Xaa is
Gly,Ala,Ser,Thr,Val,Met,His,Phe,Tyr,Asn,Asp,Glu,Gln

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Wherein Ala,Ser,Phe,Tyr,Trp,Asn,Asp,Glu,Arg, Leu

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Wherein Xaa is Pro, Ser, Tyr, Leu, Lys, His, or Asn

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> Wherein Xaa is Asp, Glu, or Gln

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Wherein Xaa is Gly, Ser, Thr, Asn, Asp, Gln, Pro, Glu

<220>

<221> misc_feature

<222> (7)..(7)

<223> Xaa can be any naturally occurring amino acid

<400> 264

Asp Xaa Xaa Xaa Xaa Xaa Xaa

1 5

<210> 265

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LC CDR3

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> wherein Xaa is Met or Gln

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> wherein Xaa is Gly, Ala, Asp, Glu, or Gln

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> wherein Xaa is Asn or Glu

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> wherein Xaa is Pro, Ala, or Ser

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> wherein Xaa is Thr, Ile, Met, Lys, Trp, Asn, Glu

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> Wherein Xaa is Leu or Ile

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> Wherein Xaa is Thr, Met, Leu, His, Tyr, Glu or Gly

<220>

<221> misc_feature

<222> (9)..(11)

<223> Xaa can be any naturally occurring amino acid

<400> 265

Xaa Xaa Phe Xaa Xaa Tyr Pro Leu Xaa Xaa Xaa

1 5 10