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<150> EP 19166345.9

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<150> EP 19200931.4

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 <213> Homo sapiens

<400> 2

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Leu	Gln	Gly	Thr	Leu	Ala	Gln	Ser	Ile	Lys	Gly	Asn	His	Leu	Val	Lys
			20					25					30		

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

Glu Ala Lys Asn Ile Thr Trp Phe Lys Asp Gly Lys Met Ile Gly Phe
50 55 60

Leu Thr Glu Asp Lys Lys Lys Trp Asn Leu Gly Ser Asn Ala Lys Asp
65 70 75 80

Pro Arg Gly Met Tyr Gln Cys Lys Gly Ser Gln Asn Lys Ser Lys Pro
85 90 95

Leu Gln Val Tyr Tyr Arg Met Cys Gln Asn Cys Ile Glu Leu Asn Ala
100 105 110

Ala Thr Ile Ser Gly Phe Leu Phe Ala Glu Ile Val Ser Ile Phe Val
115 120 125

Leu Ala Val Gly Val Tyr Phe Ile Ala Gly Gln Asp Gly Val Arg Gln
130 135 140

Ser Arg Ala Ser Asp Lys Gln Thr Leu Leu Pro Asn Asp Gln Leu Tyr
145 150 155 160

Gln Pro Leu Lys Asp Arg Glu Asp Asp Gln Tyr Ser His Leu Gln Gly
165 170 175

Asn Gln Leu Arg Arg Asn
180

<210> 3
<211> 171
<212> PRT
<213> Homo sapiens

<400> 3

Met Glu His Ser Thr Phe Leu Ser Gly Leu Val Leu Ala Thr Leu Leu
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1003643556_1.txt

Ser Gln Val Ser Pro Phe Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg
20 25 30

Val Phe Val Asn Cys Asn Thr Ser Ile Thr Trp Val Glu Gly Thr Val
35 40 45

Gly Thr Leu Leu Ser Asp Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile
50 55 60

Leu Asp Pro Arg Gly Ile Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys
65 70 75 80

Asp Lys Glu Ser Thr Val Gln Val His Tyr Arg Met Cys Gln Ser Cys
85 90 95

Val Glu Leu Asp Pro Ala Thr Val Ala Gly Ile Ile Val Thr Asp Val
100 105 110

Ile Ala Thr Leu Leu Leu Ala Leu Gly Val Phe Cys Phe Ala Gly His
115 120 125

Glu Thr Gly Arg Leu Ser Gly Ala Ala Asp Thr Gln Ala Leu Leu Arg
130 135 140

Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala Gln Tyr
145 150 155 160

Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys
165 170

<210> 4
<211> 207
<212> PRT
<213> Homo sapiens

<400> 4

Met Gln Ser Gly Thr His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser
1 5 10 15

Val Gly Val Trp Gly Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr

20

25

30

Gln Thr Pro Tyr Lys Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr
 35 40 45

Cys Pro Gln Tyr Pro Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys
 50 55 60

Asn Ile Gly Gly Asp Glu Asp Asp Lys Asn Ile Gly Ser Asp Glu Asp
 65 70 75 80

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

Val Cys Tyr Pro Arg Gly Ser Lys Pro Glu Asp Ala Asn Phe Tyr Leu
 100 105 110

Tyr Leu Arg Ala Arg Val Cys Glu Asn Cys Met Glu Met Asp Val Met
 115 120 125

Ser Val Ala Thr Ile Val Ile Val Asp Ile Cys Ile Thr Gly Gly Leu
 130 135 140

Leu Leu Leu Val Tyr Tyr Trp Ser Lys Asn Arg Lys Ala Lys Ala Lys
 145 150 155 160

Pro Val Thr Arg Gly Ala Gly Ala Gly Gly Arg Gln Arg Gly Gln Asn
 165 170 175

Lys Glu Arg Pro Pro Pro Val Pro Asn Pro Asp Tyr Glu Pro Ile Arg
 180 185 190

Lys Gly Gln Arg Asp Leu Tyr Ser Gly Leu Asn Gln Arg Arg Ile
 195 200 205

<210> 5

<211> 164

<212> PRT

<213> Homo sapiens

<400> 5

Met Lys Trp Lys Ala Leu Phe Thr Ala Ala Ile Leu Gln Ala Gln Leu
 1 5 10 15

Pro Ile Thr Glu Ala Gln Ser Phe Gly Leu Leu Asp Pro Lys Leu Cys
 20 25 30

Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala
 35 40 45

Leu Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
 50 55 60

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
 65 70 75 80

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
 85 90 95

Gly Gly Lys Pro Gln Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 100 105 110

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 115 120 125

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 130 135 140

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 145 150 155 160

Leu Pro Pro Arg

<210> 6

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> is K or R

<400> 6

Ser Xaa Thr Phe Thr Ile Ser

1 5

<210> 7

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR2

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> is L or I

<400> 7

Gly Ile Ile Pro Xaa Phe Gly Thr Ile Thr Tyr Ala Gln Lys Phe Gln

1 5 10 15

Gly

<210> 8

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> is L or F

<400> 8

Arg Gly Asn Trp Asn Pro Xaa Asp Pro
1 5

<210> 9

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR1

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> is F or Y

<400> 9

Arg Xaa Trp Ile Gly
1 5

<210> 10

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> is H or N

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> is D or V

<220>

<221> MISC_FEATURE

<222> (15)..(15)

<223> is L or M

<400> 10

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Xaa	Ile	Arg	Tyr	Phe	Xaa	Trp	Ser	Glu	Asp	Tyr	His	Tyr	Tyr	Xaa	Asp
1				5					10					15	

Val

<210> 11
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR2

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> is S or G

<220>
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 <223> is S or T

<220>
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 <222> (9)..(9)
 <223> is I or T

<220>
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 <222> (10)..(10)
 <223> is G or Y

<400> 11

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

Gly

<210> 12
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CDR3

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> is R or M

<220>

<221> MISC_FEATURE

<222> (15)..(15)

<223> is H or Y

<400> 12

Asp	His	Xaa	Gly	Tyr	Gly	Asp	Tyr	Glu	Gly	Gly	Gly	Phe	Asp	Xaa
1				5					10					15

<210> 13

<211> 267

<212> PRT

<213> Homo sapiens

<400> 13

Met	Trp	Gly	Val	Phe	Leu	Leu	Tyr	Val	Ser	Met	Lys	Met	Gly	Gly	Thr
1				5					10					15	

Thr	Gly	Gln	Asn	Ile	Asp	Gln	Pro	Thr	Glu	Met	Thr	Ala	Thr	Glu	Gly
			20					25					30		

Ala	Ile	Val	Gln	Ile	Asn	Cys	Thr	Tyr	Gln	Thr	Ser	Gly	Phe	Asn	Gly
		35					40					45			

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

Tyr	Asn	Val	Leu	Asp	Gly	Leu	Glu	Glu	Lys	Gly	Arg	Phe	Ser	Ser	Phe
65					70					75					80

Leu	Ser	Arg	Ser	Lys	Gly	Tyr	Ser	Tyr	Leu	Leu	Leu	Lys	Glu	Leu	Gln
				85					90					95	

Met	Lys	Asp	Ser	Ala	Ser	Tyr	Leu	Cys	Ala	Val	Met	Asp	Ser	Asn	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Gln Leu Ile Trp Gly Ala Gly Thr Lys Leu Ile Ile Lys Pro Asp Ile
 115 120 125

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser
 130 135 140

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

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

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser
 180 185 190

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile
 195 200 205

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys
 210 215 220

Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn
 225 230 235 240

Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe
 245 250 255

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser
 260 265

<210> 14

<211> 310

<212> PRT

<213> Homo sapiens

<400> 14

Met Arg Ile Arg Leu Leu Cys Cys Val Ala Phe Ser Leu Leu Trp Ala
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Gly Pro Val Ile Ala Gly Ile Thr Gln Ala Pro Thr Ser Gln Ile Leu
20 25 30

Ala Ala Gly Arg Arg Met Thr Leu Arg Cys Thr Gln Asp Met Arg His
35 40 45

Asn Ala Met Tyr Trp Tyr Arg Gln Asp Leu Gly Leu Gly Leu Arg Leu
50 55 60

Ile His Tyr Ser Asn Thr Ala Gly Thr Thr Gly Lys Gly Glu Val Pro
65 70 75 80

Asp Gly Tyr Ser Val Ser Arg Ala Asn Thr Asp Asp Phe Pro Leu Thr
85 90 95

Leu Ala Ser Ala Val Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
100 105 110

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

Arg Leu Thr Val Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu Val
130 135 140

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
195 200 205

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
210 215 220

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
 225 230 235 240

Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
 245 250 255

Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln
 260 265 270

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

Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
 290 295 300

Val Lys Arg Lys Asp Phe
 305 310

<210> 15
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IGKV1-39/jk1

<220>
 <221> CDS
 <222> (1)..(321)

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

gac aga gtc acc atc act tgc cgg gca agt cag agc att agc agc tac 96
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctc ctg atc 144
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

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tat gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc	192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly	
50 55 60	

agt gga tct ggg aca gat ttc act ctc acc atc agc agt ctg caa cct	240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro	
65 70 75 80	

gaa gat ttt gca act tac tac tgt caa cag agt tac agt acc cct cca	288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro	
85 90 95	

acg ttc ggc caa ggg acc aag gtg gag atc aaa	321
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
100 105	

<210> 16
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 16

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 Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

100

<210> 17
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> IGKV1-39/jk5

<220>
<221> CDS
<222> (1)..(321)

<400> 17
cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 48
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 96
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 144
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45
tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 192
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60
acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 240
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80
aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 288
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95
ccc gtc aca aag agc ttc aac agg gga gag tgt tag 324
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 18
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

<400> 18

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> 19

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> IGKV1-39/jk5 common light chain variable domain translation

<400> 19

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 Pro
85 90 95

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

<210> 20
<211> 95
<212> PRT
<213> Artificial Sequence

<220>
<223> V-region IGKV1-39A

<400> 20

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
85 90 95

<210> 21
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR1 common light chain

<400> 21

Gln Ser Ile Ser Ser Tyr
 1 5

<210> 22
 <211> 3
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR2 common light chain

<400> 22

Ala Ala Ser
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<210> 23
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3 common light chain

<400> 23

Gln Gln Ser Tyr Ser Thr Pro
 1 5

<210> 24
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG heavy chain CH1 region

<220>

1003643556_1.txt

<221> CDS

<222> (1)..(294)

<400> 24

gct	agc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	aag	48
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	
1				5					10				15			

agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	96
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	
			20					25					30			

ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	agc	144
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	
		35					40					45				

ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	192
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	
	50					55					60					

ctc	agc	agc	gtc	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	acc	240
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	
65					70				75					80		

tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	aag	288
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	
			85					90					95			

aga	gtt															294
Arg	Val															

<210> 25

<211> 98

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Construct

<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

<210> 26
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG heavy chain hinge region

<220>
 <221> CDS
 <222> (1)..(45)

<400> 26
 gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca 45
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

<210> 27
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 27
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

<210> 28
 <211> 330
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG heavy chain CH2 region

<220>
 <221> CDS
 <222> (1)..(330)

<400> 28
 gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa 48
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 1 5 10 15
 ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg 96
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 20 25 30
 gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac 144
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 35 40 45
 gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag 192
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60
 cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac 240
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80
 cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 288
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 85 90 95
 gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa 330
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 100 105 110

<210> 29
 <211> 110
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 29

1003643556_1.txt

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 30
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG heavy chain CH2 domain containing L235G and G236R silencing
substitutions

<220>
<221> CDS
<222> (1)..(330)

<400> 30
gca cct gaa ctc ggc agg gga ccg tca gtc ttc ctc ttc ccc cca aaa 48
Ala Pro Glu Leu Gly Arg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
1 5 10 15

ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg 96
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

1003643556_1.txt

gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac 144
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag 192
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac 240
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 288
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
85 90 95

gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa 330
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
100 105 110

<210> 31
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 31

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

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
20 25 30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
35 40 45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
50 55 60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
65 70 75 80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
 100 105 110

<210> 32

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> IgG heavy chain CH3 domain containing substitutions L351K and T366K (KK)

<220>

<221> CDS

<222> (1)..(318)

<400> 32

ggg cag ccc cga gaa cca cag gtg tac acc aag ccc cca tcc cgg gag 48
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Lys Pro Pro Ser Arg Glu
 1 5 10 15

gag atg acc aag aac cag gtc agc ctg aag tgc ctg gtc aaa ggc ttc 96
 Glu Met Thr Lys Asn Gln Val Ser Leu Lys Cys Leu Val Lys Gly Phe
 20 25 30

tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag 144
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45

aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc 192
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60

ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg 240
 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80

aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac 288
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95

acg cag aag agc ctc tcc ctg tct ccg ggt tga 321
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 100 105

<210> 33

<211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 33

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Lys Pro Pro Ser Arg Glu
 1 5 10 15

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 100 105

<210> 34
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> IgG heavy chain CH3 region containing substitutions L351D and
 L368E (DE)

<220>
 <221> CDS
 <222> (1)..(318)

<400> 34

1003643556_1.txt

ggg cag ccc cga gaa cca cag gtg tac acc gac ccc cca tcc cgg gag 48
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Glu
1 5 10 15

gag atg acc aag aac cag gtc agc ctg acc tgc gag gtc aaa ggc ttc 96
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Glu Val Lys Gly Phe
20 25 30

tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag 144
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc 192
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60

ttc ctc tat agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg 240
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80

aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac 288
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95

acg cag aag agc ctc tcc ctg tct ccg ggt tga 321
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
100 105

<210> 35
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Asp Pro Pro Ser Arg Glu
1 5 10 15

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

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe

50

55

60

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 100 105

<210> 36
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CH# sequence

<400> 36

Asp Glu Lys Lys
 1

<210> 37
 <211> 373
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF8057

<400> 37
 ggcccagccg gccatggccg aggtgcagct ggtgcagtct ggagctgagg tgaagaagcc 60
 tgggtcctcg gtgaaggtct cctgcaaggc ttctggaggc accttccgca gctttggtat 120
 cagttgggtg cgacaggccc ctggacaagg acttgagtgg atgggaggat tcatccctgt 180
 ccttggtaca gcaaactacg cacagaaatt ccagggcaga gtgacgatta tcgcggacaa 240
 atccacgaac acagcctaca tggagctgag cagcctgaga tctgaggaca cggccgtgta 300
 ttactgtgcg cgaaggggta actggaaccc gttcgacccc tggggccagg gaaccctggt 360
 caccgtctcg agt 373

<210> 38
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8057 FW1

<400> 38

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg
 20 25 30

<210> 39
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8057 FW2

<400> 39

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 1 5 10

<210> 40
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8057 FW3 -1AA in FW4

<400> 40

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

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 41

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

<220>
 <223> MF8057 FW4

<400> 41

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 42
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8057 CDR1

<400> 42

Ser Phe Gly Ile Ser
 1 5

<210> 43
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8057 CDR2

<400> 43

Gly Phe Ile Pro Val Leu Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 44
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8057 CDR3

<400> 44

Arg Gly Asn Trp Asn Pro Phe Asp Pro
1 5

<210> 45

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8057 VH

<400> 45

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Ser Phe
20 25 30

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

Gly Gly Phe Ile Pro Val Leu Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Arg Gly Asn Trp Asn Pro Phe Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 46

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> MF8058

<400> 46

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ggcccagccg gccatggccc aggtgcagct ggtgcagtct ggggctgagg tgaagaagcc      60
tgggtcctcg gtgaaggtct cctgcaaggc ttctggagac gccttcaaaa gcaaaacctt    120
tactatcagc tgggtgcgac aggcccctgg acaggggctt gagtggctgg gggggatcat    180
ccctcttttt ggtacaatta cctacgcaca gaagttccag ggcagagtca cgattaccgc    240
ggacaaatcc acgaacactg ccttcatgga actgagcagc ctgagatctg aggacacggc    300
catgtattat tgtacgcgac ggggggaactg gaacccttc gaccctggg gccagggaac    360
cctggtcacc gtctcgagt                                     379

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<210> 47

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8058 FW2

<400> 47

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Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu Gly
1           5           10

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<210> 48

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8058 FW1

<400> 48

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

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

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<210> 49
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8058 FW3

<400> 49

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

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys Thr Arg
 20 25 30

<210> 50
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8058 FW4

<400> 50

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 51
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8058 CDR1

<400> 51

Ser Lys Thr Phe Thr Ile Ser
 1 5

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

<220>

<223> MF8058 CDR2

<400> 52

Gly Ile Ile Pro Leu Phe Gly Thr Ile Thr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 53

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8058 CDR3

<400> 53

Arg Gly Asn Trp Asn Pro Phe Asp Pro
1 5

<210> 54

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8058 VH

<400> 54

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

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

Thr Phe Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
35 40 45

Trp Leu Gly Gly Ile Ile Pro Leu Phe Gly Thr Ile Thr Tyr Ala Gln
50 55 60

1003643556_1.txt

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

Ala Phe Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr
85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 55
<211> 379
<212> DNA
<213> Artificial Sequence

<220>
<223> MF8078

<400> 55
ggcccagccg gccatggccg aggtgcagct ggtgcagtct gggctctgagt tgaagaagcc 60
tgggtcctcg gtgaaggctt cctgcaaggc ttctggagtc accttcaaca gcagaacctt 120
tactatcagt tgggtgcgac agggccctgg acaagggtctt gagggtctgg ggagtatcat 180
ccctatTTTT ggtacaataa cctacgcaca gaagttccag ggcagagtca cgattaccgc 240
ggacaaatcc acgagcactg cttcatgga actgaccagc ctgagatctg aggacacggc 300
catatattat tgtacgagac gggggaactg gaacccttc gaccctggg gccagggcac 360
cctggtcacc gtctcgagt 379

<210> 56
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> MF8078 FW1

<400> 56

Glu Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ser

1 5 10 15

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

<210> 57
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MF8078 FW2

<400> 57

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu Gly
1 5 10

<210> 58
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> MF8078 FW3

<400> 58

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

Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys Thr Arg
20 25 30

<210> 59
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MF8078 FW4

<400> 59

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 60
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8078 CDR1

<400> 60

Ser Arg Thr Phe Thr Ile Ser
 1 5

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

<220>
 <223> MF8078 CDR2

<400> 61

Ser Ile Ile Pro Ile Phe Gly Thr Ile Thr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 62
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8078 CDR3

<400> 62

Arg Gly Asn Trp Asn Pro Phe Asp Pro
 1 5

<210> 63
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>

<223> MF8078 VH

<400> 63

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

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

Thr Phe Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 35 40 45

Trp Leu Gly Ser Ile Ile Pro Ile Phe Gly Thr Ile Thr Tyr Ala Gln
 50 55 60

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

Ala Phe Met Glu Leu Thr Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr
 85 90 95

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

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 64

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1

<400> 64

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg

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25

30

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<400> 65

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Gly
 1 5 10

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 <211> 32
 <212> PRT
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<220>
 <223> FW3

<400> 66

Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Thr Thr Ala Tyr Met Glu
 1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
 20 25 30

<210> 67
 <211> 11
 <212> PRT
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<220>
 <223> FW4

<400> 67

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 68
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<220>

<223> CDR1

<400> 68

Gly Ser Gly Ile Ser
1 5

<210> 69

<211> 17

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<223> CDR2

<400> 69

Gly Phe Ile Pro Phe Phe Gly Ser Ala Asn Tyr Ala Gln Lys Phe Arg
1 5 10 15

Asp

<210> 70

<211> 9

<212> PRT

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<400> 70

Arg Gly Asn Trp Asn Pro Leu Asp Pro
1 5

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<211> 118

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<223> VH

<400> 71

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Gly Ser
20 25 30

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

Gly Gly Phe Ile Pro Phe Phe Gly Ser Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Lys Arg Gly Asn Trp Asn Pro Leu Asp Pro Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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tcctgcaagg cttctggagg caccttcaga 90

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<211> 42
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<223> FW2

<400> 73

tgggtgacgac aggccctgg acaagggtt gagggtgg gc

42

<210> 74

<211> 96

<212> DNA

<213> Artificial Sequence

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<223> FW3

<400> 74

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60

agatctgagg acacggccat atattactgt gcgaaa

96

<210> 75

<211> 33

<212> DNA

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<223> FW4

<400> 75

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33

<210> 76

<211> 15

<212> DNA

<213> Artificial Sequence

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<400> 76

ggttctggta tcagc

15

<210> 77

<211> 51

<212> DNA

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<400> 77
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<210> 78
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<210> 79
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<400> 79
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cctggacaag ggcttgagt ggtgggcggg ttcattccctt tctttggttc agcaaactac 180
gcacagaagt tccgggacag agtcacgatt accgcggaca aatccgacgac cacagcctac 240
atggaactga gcagcctgag atctgaggac acggccatat attactgtgc gaaaagagga 300
aattggaacc cgctcgaccc ctggggccag ggcaccctgg tcaccgtctc gagt 354

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<211> 30
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<220>
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<400> 80

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Val Thr Phe Lys
20 25 30

<210> 81
<211> 14
<212> PRT
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<400> 81

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Leu Gly
1 5 10

<210> 82
<211> 32
<212> PRT
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<220>
<223> FW3

<400> 82

Arg Val Ser Ile Thr Ala Asp Lys Ser Thr Asn Thr Ala Tyr Leu Glu
1 5 10 15

Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Arg
20 25 30

<210> 83
<211> 11
<212> PRT
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<220>
<223> FW4

<400> 83

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 84

<211> 7
 <212> PRT
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<220>
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<400> 84

Ser Lys Thr Leu Thr Ile Ser
 1 5

<210> 85
 <211> 17
 <212> PRT
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<220>
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<400> 85

Gly Ile Ile Pro Ile Phe Gly Ser Ile Thr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Asp

<210> 86
 <211> 9
 <212> PRT
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<220>
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<400> 86

Arg Gly Asn Trp Asn Pro Phe Asp Pro
 1 5

<210> 87
 <211> 120
 <212> PRT
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<220>
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<400> 87

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Val Thr Phe Lys Ser Lys
 20 25 30

Thr Leu Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
 35 40 45

Trp Leu Gly Gly Ile Ile Pro Ile Phe Gly Ser Ile Thr Tyr Ala Gln
 50 55 60

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

Ala Tyr Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr
 85 90 95

Tyr Cys Ala Arg Arg Gly Asn Trp Asn Pro Phe Asp Pro Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 88

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1

<400> 88

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tcctgcaagg cttctggagt caccttcaaa 90

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<212> DNA

<213> Artificial Sequence

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<223> FW2

<400> 89

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42

<210> 90

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> FW3

<400> 90

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60

aggtctgagg acacggccat ttattattgt gcgaga

96

<210> 91

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> FW4

<400> 91

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33

<210> 92

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> CDR1

<400> 92

agcaaaacct taactatcag c

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<400> 95

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tcctgcaagg cttctggagt caccttcaaa agcaaacct taactatcag ctgggtgcga

120

caggcccctg gacaagggtc tgagtggctg ggagggatca tccctatTTT tggttcaata

180

acctacgcac agaagttcca ggacagagtc tcgattaccg cggacaaatc cacgaacaca

240

gcctacttgg aactgaacag cctgaggtct gaggacacgg ccatttatta ttgtgcgaga

300

cgggggaact ggaaccctt cgaccctgg ggccagggca ccctgggtcac cgtctcgagt

360

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<220>

<223> FW1

<400> 96

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

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg
20 25 30

<210> 97
<211> 14
<212> PRT
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<220>
<223> FW2

<400> 97

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val Gly
1 5 10

<210> 98
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> FW3

<400> 98

Arg Val Thr Ile Thr Ala Asp Lys Ser Ala Thr Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
20 25 30

<210> 99
<211> 11
<212> PRT
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<220>
<223> FW4

<400> 99

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 100
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR1

<400> 100

Gly Ser Gly Ile Ser
 1 5

<210> 101
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR2

<400> 101

Gly Phe Ile Pro Phe Phe Gly Ser Ala Asn Tyr Ala Gln Lys Phe Arg
 1 5 10 15

Asp

<210> 102
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3

<400> 102

Arg Gly Asn Trp Asn Pro Phe Asp Pro
 1 5

<210> 103
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>

<223> VH

<400> 103

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Gly Ser
 20 25 30

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

Gly Gly Phe Ile Pro Phe Phe Gly Ser Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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

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

Ala Lys Arg Gly Asn Trp Asn Pro Phe Asp Pro Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 104

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1

<400> 104

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tcctgcaagg cttctggagg caccttcaga 90

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<211> 42
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 <213> Artificial Sequence

 <220>
 <223> FW2

 <400> 105
 tgggtgacgac aggccctgg acaagggtt gagggtgg gc 42

 <210> 106
 <211> 96
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> FW3

 <400> 106
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 agatctgagg acacggccat atattactgt gcgaaa 96

 <210> 107
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> FW4

 <400> 107
 tggggccagg gcaccctggt caccgtctcg agt 33

 <210> 108
 <211> 15
 <212> DNA
 <213> Artificial Sequence

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 <223> CDR1

 <400> 108
 ggttctggta tcagc 15

 <210> 109
 <211> 51
 <212> DNA

<213> Artificial Sequence

<220>

<223> CDR2

<400> 109

gggttcatcc ctttctttgg ttcagcaaac tacgcacaga agttccggga c

51

<210> 110

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> CDR3

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agaggaaatt ggaacccgtt cgacccc

27

<210> 111

<211> 354

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tcctgcaagg cttctggagg caccttcaga ggttctggta tcagctgggt gcgacaggcc

120

cctggacaag ggcttgagtg ggtgggcggg ttcattcctt tctttggttc agcaaactac

180

gcacagaagt tccgggacag agtcacgatt accgcggaca aatccgcgac cacagcctac

240

atggaactga gcagcctgag atctgaggac acggccatat attactgtgc gaaaagagga

300

aattggaacc cgttcgaccc ctggggccag ggcaccctgg tcaccgtctc gagt

354

<210> 112

<211> 379

<212> DNA

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<223> MF8397

<400> 112

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ccaggggaagg gactggagtg ggtctcaggt attagtggta gtggctgcac cacatggtat 180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagacggt 300
ggatacagct atggccctta ctggtacttc gatctctggg gccgtggaac cctggtcacc 360
cctggtcacc gtctccagt 379

<210> 113
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
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<400> 113

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

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

<210> 114
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MF8397 FW2

<400> 114

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 115
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> MF8397 FW3

<400> 115

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 116

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8397 FW4

<400> 116

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 117

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8397 CDR1

<400> 117

Ser Tyr Ala Leu Ser
1 5

<210> 118

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8397 CDR2

<400> 118

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

1 5 10 15

Gly

<210> 119
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8397 CDR3

<400> 119

Asp Gly Gly Tyr Ser Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu
 1 5 10

<210> 120
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8397 VH

<400> 120

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

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

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

Ser Gly Ile Ser Gly Ser Gly Arg Thr Thr Trp 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

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

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 121
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW1

<400> 121

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 Thr Ser Gly Phe Thr Phe Ile
 20 25 30

<210> 122
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW2

<400> 122

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1 5 10

<210> 123
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW3

<400> 123

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Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 124
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> FW4

<400> 124

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 125
<211> 5
<212> PRT
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<220>
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<400> 125

Ser Tyr Ala Leu Ser
1 5

<210> 126
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 126

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

Gly

<210> 127
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3

<400> 127

Asp Gly Gly Tyr Thr Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu
 1 5 10

<210> 128
 <211> 123
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 128

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 Thr Ser Gly Phe Thr Phe Ile Ser Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 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 Gly Gly Tyr Thr Tyr Gly Pro Tyr Trp Tyr Phe Asp Leu

100

105

110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 129
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FW1

<400> 129
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 tcctgtgcaa cctctggatt cacctttatc 90

<210> 130
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FW2

<400> 130
 tgggtccgcc aggctccagg gaaggggctg gaatgggtct ca 42

<210> 131
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FW3

<400> 131
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 agagccgagg acacggccgt atattactgt gcgaga 96

<210> 132
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> FW4

<400> 132

tggggccgtg gcaccctggg caccgtctcg agt

33

<210> 133

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> CDR1

<400> 133

agctatgccc tgagc

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<210> 134

<211> 51

<212> DNA

<213> Artificial Sequence

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<223> CDR2

<400> 134

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51

<210> 135

<211> 42

<212> DNA

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42

<210> 136

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> VH

<400> 136

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 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cagctgtttt 240
 ctgcaaatga acagcctgag agccgaggac acggccgtat attactgtgc gagagacggt 300
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 gtctcgagt 369

<210> 137
 <211> 391
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF8508

<400> 137
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 gcactgggtc cggcaagctc cagggaaggg cctggagtgg gtctcagata ttagttggag 180
 tagtggtagc ataggctatg cggactctgt gaagggccga ttcaccatct ccagagacaa 240
 cgccaagaac tccctgtggc tgcaaatgaa cagtctgaga actgaggaca cggccttgta 300
 tttctgtgca aaagatcata ggggggtacg tgactacgag ggtggtggct ttgactactg 360
 gggccaggga accctggtca ccgtctccag t 391

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 <211> 30
 <212> PRT
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<220>
 <223> MF8508 FW1

<400> 138

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

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

<210> 139
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8508 FW2

<400> 139

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1 5 10

<210> 140
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8508 FW3

<400> 140

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Trp Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Phe Cys Ala Lys
 20 25 30

<210> 141
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8508 FW4

<400> 141

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 142

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

<220>
 <223> MF8508 CDR1

<400> 142

Asp Tyr Thr Met His
 1 5

<210> 143
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8508 CDR2

<400> 143

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

Gly

<210> 144
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8508 CDR3

<400> 144

Asp His Arg Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp Tyr
 1 5 10 15

<210> 145
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8508 VH

<400> 145

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

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

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

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

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

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

Ala Lys Asp His Arg Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp
 100 105 110

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

<210> 146

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1

<400> 146

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

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

<210> 147
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW2

<400> 147

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1 5 10

<210> 148
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW3

<400> 148

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Phe Cys Ala Lys
 20 25 30

<210> 149
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW4

<400> 149

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 150
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> CDR1

<400> 150

Asp Tyr Thr Met His
1 5

<210> 151

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3

<400> 151

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

Gly

<210> 152

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR3

<400> 152

Asp His Arg Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp His
1 5 10 15

<210> 153

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> VH

<400> 153

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg

1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Asp Ile Ser Trp Ser Ser Gly Ser Ile Gly Tyr Ala 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 Ala Glu Asp Thr Ala Leu Tyr Phe Cys
 85 90 95
 Ala Lys Asp His Arg Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp
 100 105 110
 His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 154
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FW1

<400> 154
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 tcctgtgcaa cctctggatt cacctttgat 90

<210> 155
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> FW2

<400> 155
tgggtccggc aagctccagg gaagggcctg gagggtct ca 42

<210> 156
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> FW3

<400> 156
cgattcacca tctccagaga caacgccaag aactccctgt atctgcaa at gaacagtctg 60
agagctgagg acacggcctt gtatttctgt gcaaaa 96

<210> 157
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> FW4

<400> 157
tggggccagg gaaccctggt caccgtctcc agt 33

<210> 158
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> CDR1

<400> 158
gattatacca tgcac 15

<210> 159
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> CDR2

<400> 159

gatattagtt ggagtagtgg tagcataggc tatgcggact ctgtgaaggg c 51

<210> 160
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF8998_16

<400> 160
 gatcataggg ggtacggtga ctacgagggt ggtggctttg accac 45

<210> 161
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH

<400> 161
 gaggtgcagc tggtaggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcaa cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
 ccaggaagg gcctggagt ggtctcagat attagttgga gtagtggtag cataggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt atttctgtgc aaaagatcat 300
 aggggggtacg gtgactacga gggtaggtggc tttgaccact ggggccaggg aaccctggtc 360
 accgtctcca gt 372

<210> 162
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW1

<400> 162

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

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

<210> 163
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW2

<400> 163

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 1 5 10

<210> 164
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW3

<400> 164

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Lys
 20 25 30

<210> 165
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FW4

<400> 165

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 166

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

<220>
 <223> CDR1

<400> 166

Asp Tyr Thr Met His
 1 5

<210> 167
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR2

<400> 167

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

Gly

<210> 168
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CDR3

<400> 168

Asp His Arg Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp Tyr
 1 5 10 15

<210> 169
 <211> 124
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VH

<400> 169

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

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

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

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

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

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

Ala Lys Asp His Arg Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp
 100 105 110

Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 170

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1

<400> 170

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agctgcgccg ccagcggctt caccttcgac 90

<210> 171

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> FW2

<400> 171

tgggtgagac aggcccccg caagggcctg gagggggtga gc

42

<210> 172

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> FW3

<400> 172

agattcacca tcagcagaga caacagcaag aacagcctgt acctgcagat gaacagcctg

60

agaaccgagg acaccgccct gtactactgc gccaaag

96

<210> 173

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> FW4

<400> 173

tggggcagag gcaccctggt caccgtctcg agc

33

<210> 174

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> CDR1

<400> 174

gactacacca tgcac

15

<210> 175

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> CDR2

<400> 175

gacatcagct ggagcggcgg cagcatctac tacgccgaca gcgtgaaggg c 51

<210> 176

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> CDR3

<400> 176

gaccacagag gctacggcga ctacgagggc ggcggcttcg actac 45

<210> 177

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> VH

<400> 177

gaggtgcagc tggtggagag cggcggcgtg gtggtgcagc ccggcggcag cctgagactg 60

agctgcgccg ccagcggcctt caccttcgac gactacacca tgcactgggt gagacaggcc 120

cccggcaagg gcctggagtg ggtgagcgac atcagctgga gcggcggcag catctactac 180

gccgacagcg tgaagggcag attcaccatc agcagagaca acagcaagaa cagcctgtac 240

ctgcagatga acagcctgag aaccgaggac accgccctgt actactgcgc caaggaccac 300

agaggctacg gcgactacga gggcggcggc ttcgactact ggggcagagg caccctggtc 360

accgtctcga gc 372

<210> 178

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> FW1

<400> 178

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

Ser Leu Arg Leu Ser Cys Val Thr Ser Gly Phe Thr Phe Asp
20 25 30

<210> 179
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> FW2

<400> 179

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 180
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> FW3

<400> 180

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asp Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Lys
20 25 30

<210> 181
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> FW4

<400> 181

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

1

5

10

<210> 182
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR1

<400> 182

Asp Tyr Thr Met His
1 5

<210> 183
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR2

<400> 183

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

Gly

<210> 184
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR3

<400> 184

Asp His Met Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp Tyr
1 5 10 15

<210> 185
<211> 124
<212> PRT

<213> Artificial Sequence

<220>

<223> VH

<400> 185

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

Ser Leu Arg Leu Ser Cys Val Thr Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

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

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

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

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

Ala Lys Asp His Met Gly Tyr Gly Asp Tyr Glu Gly Gly Gly Phe Asp
100 105 110

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

<210> 186

<211> 90

<212> DNA

<213> Artificial Sequence

<220>

<223> FW1

<400> 186

gaagtgcagc tgggtggagtc tggggggaggc ttggtacagc ctggcaggtc cctgagactc 60

tcctgtgtaa cctctggatt cacctttgat 90

<210> 187
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> FW2

 <400> 187
 tgggtccggc aagctccggg gaagggcctg gagtgggtct ca 42

 <210> 188
 <211> 96
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> FW3

 <400> 188
 cgattcacca tctccagaga caatgccaag gactccctgt atctgcaaat gaacagtctg 60
 agaactgagg acacggcctt gtattactgt gcaaaa 96

 <210> 189
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> FW4

 <400> 189
 tggggccagg gaaccctggt caccgtctcg agc 33

 <210> 190
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> CDR1

 <400> 190
 gattatacca tgcac 15

 <210> 191

<211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CDR2

<400> 191
 gatattagtt ggagtagtgg caccactggc tatgcggact ctgtgaaggg c 51

<210> 192
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CDR3

<400> 192
 gatcatatgg ggtacggtga ctacgagggt ggtggctttg actac 45

<210> 193
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH

<400> 193
 gaagtgcagc tggtagtgc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgtaa cctctggatt cacctttgat gattatacca tgcactgggt ccggcaagct 120
 ccggggaagg gcctggagtg ggtctcagat attagttgga gtagtggcac cactggctat 180
 gcggactctg tgaagggccg attcaccatc tccagagaca atgccaagga ctccctgtat 240
 ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagatcat 300
 atgggggtacg gtgactacga gggtagtggtc tttgactact ggggccaggg aaccctggtc 360
 accgtctcga gc 372

<210> 194
 <211> 397
 <212> DNA
 <213> Artificial Sequence

<220>

<223> MF9249

<400> 194

ggcccagccg gccatggccg aggtgcagct ggtgcagtct ggagcagaag tgaaaaagcc 60

cggggagtct ctgaagatct cctgtaaggg ttctggatac agttttacta ggttttggat 120

cggctgggtg cgccagatgc ccgggaaagg cctggagtgg atggggatca tctatcctgg 180

tgactctgat accagataca gcccgtcctt ccaaggccag gtcaccatct cagccgacaa 240

gtccaccagt accgcctacc tgcagtggag cagcctgaag gcctcggaca ccggcatgta 300

ttattgtgtg agacatatac gatattttga ctggtcggaa gactaccact attacctgga 360

cgtctggggc aaagggacca cggtcacctg ctccagt 397

<210> 195

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9249 FW1

<400> 195

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

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

<210> 196

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9249 FW2

<400> 196

Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met	Gly
1				5					10				

<210> 197

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

<220>
 <223> MF9249 FW3

<400> 197

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

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

<210> 198
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9249 FW4

<400> 198

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 1 5 10

<210> 199
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9249 CDR1

<400> 199

Arg Phe Trp Ile Gly
 1 5

<210> 200
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9249 CDR2

<400> 200

Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe	Gln
1				5					10					15	

Gly

<210> 201

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9249 CDR3

<400> 201

His	Ile	Arg	Tyr	Phe	Asp	Trp	Ser	Glu	Asp	Tyr	His	Tyr	Tyr	Leu	Asp
1				5					10					15	

Val

<210> 202

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9249 VH

<400> 202

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

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

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

Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
 85 90 95

Val Arg His Ile Arg Tyr Phe Asp Trp Ser Glu Asp Tyr His Tyr Tyr
 100 105 110

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

<210> 203
 <211> 378
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF9267

<400> 203
 gaggtgcagc tggtggagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60
 tcctgtaagg gttctggata cagttttact aggtattgga tcggctgggt gcgccagatg 120
 cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180
 agcccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag tactgcctac 240
 ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attattgtgt gagaaatata 300
 cgatatatttg tctggtcggg ggactaccac tactacatgg acgtctgggg caaagggacc 360
 acggtcaccg tctccagt 378

<210> 204
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9267 FW1

<400> 204

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

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

<210> 205
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9267 FW2

<400> 205

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 206
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9267 FW3

<400> 206

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

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Val Arg
20 25 30

<210> 207
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9267 FW4

<400> 207

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser

1

5

10

<210> 208
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9267 CDR1

<400> 208

Arg Tyr Trp Ile Gly
 1 5

<210> 209
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9267 CDR2

<400> 209

Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
 1 5 10 15

Gly

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

<220>
 <223> MF9267 CDR3

<400> 210

Asn Ile Arg Tyr Phe Val Trp Ser Glu Asp Tyr His Tyr Tyr Met Asp
 1 5 10 15

Val

<210> 211
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9267 VH

<400> 211

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

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

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

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Val Arg Asn Ile Arg Tyr Phe Val Trp Ser Glu Asp Tyr His Tyr Tyr
 100 105 110

Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 115 120 125

<210> 212
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5377

<400> 212

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tcctgcaagg cttctggagg catcttcagc acctatgcta tcagctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggaggg atcatcccta tctttgatac accaaactac 180
gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
atggacctga gcagcctgag atctgaggac acggccgtat attactgtgc gaaaaacgtg 300
cgtggatata gtgcctacga ccttgactac tggggccagg gcaccctggt caccgtctcc 360
agt 363

<210> 213
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> MF5377 FW1

<400> 213

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ile Phe Ser
20 25 30

<210> 214
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MF5377 FW2

<400> 214

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 215
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> MF5377 FW3

<400> 215

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

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

<210> 216

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5377 FW4

<400> 216

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 217

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5377 CDR1

<400> 217

Thr Tyr Ala Ile Ser
1 5

<210> 218

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5377 CDR2

<400> 218

Gly Ile Ile Pro Ile Phe Asp Thr Pro Asn Tyr Ala Gln Lys Phe Gln

1 5 10 15

Gly

<210> 219
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5377 CDR3

<400> 219

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

<210> 220
 <211> 121
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5377 VH

<400> 220

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ile Phe Ser Thr Tyr
 20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Asp Thr Pro Asn Tyr Ala Gln Lys Phe
 50 55 60

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

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

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

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 221
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5444

<400> 221
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 cctggacaag ggcttgagtg gatgggatgg atcaacacca acactgggaa cccaacgtat 180
 gccagggct tcacaggacg gtttgtcttc tccttgga cctctgtcag cacggcatat 240
 ctgcagatca gcagcctaaa ggctgaggac actgccgtgt attactgtgc gagagatcac 300
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 agt 363

<210> 222
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5444 FW1

<400> 222

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 20 25 30

<210> 223
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5444 FW2

<400> 223

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 1 5 10

<210> 224
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5444 FW3

<400> 224

Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln
 1 5 10 15

Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 225
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5444 FW4

<400> 225

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 1 5 10

<210> 226
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> MF5444 CDR1

<400> 226

Ser Tyr Ser Met Asn

1 5

<210> 227

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5444 CDR2

<400> 227

Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe Thr

1 5 10 15

Gly

<210> 228

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5444 CDR3

<400> 228

Asp His Asp Phe Arg Thr Gly Arg Ala Phe Asp Ile

1 5 10

<210> 229

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5444 VH

<400> 229

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

1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Ser Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Asn Thr Gly Asn Pro Thr Tyr Ala Gln Gly Phe
 50 55 60
 Thr Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp His Asp Phe Arg Thr Gly Arg Ala Phe Asp Ile Trp Gly
 100 105 110
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 230
 <211> 372
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF5380

<400> 230
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 ccaggcaagg ggctggagtg ggtggcagtt atatcatatg atggaagtaa taaatactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca actccaagag cacgctgttt 240
 ctgcaaatga acagcctgag agctgaggac acggctgtgt atttctgtgt gagaggcctc 300
 cccataacta tggttcgggg agcgtactcc tttgactact ggggccaggg caccctggtc 360

accgtctcca gt

<210> 231
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5380 FW1

<400> 231

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

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

<210> 232
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5380 FW2

<400> 232

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
 1 5 10

<210> 233
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5380 FW3

<400> 233

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Phe Leu Gln
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Val Arg
 20 25 30

<210> 234
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5380 FW4

<400> 234

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 235
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5380 CDR1

<400> 235

Ser Tyr Gly Met His
 1 5

<210> 236
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF5380 CDR2

<400> 236

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

Gly

<210> 237
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> MF5380 CDR3

<400> 237

Gly Leu Pro Ile Thr Met Val Arg Gly Ala Tyr Ser Phe Asp Tyr
 1 5 10 15

<210> 238

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> MF5380 VH

<400> 238

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Val Val Gln Pro Gly Arg
 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

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

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

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

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

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

<210> 239

<211> 366
 <212> DNA
 <213> Artificial Sequence

<220>

<223> MF8233

<400> 239
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 gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
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 tccagt 366

<210> 240
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>

<223> MF8233 FW1

<400> 240

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 20 25 30

<210> 241
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>

<223> MF8233 FW2

<400> 241

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly

1

5

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<210> 242
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8233 FW3

<400> 242

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
 1 5 10 15

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

<210> 243
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8233 FW4

<400> 243

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1 5 10

<210> 244
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF8233 CDR1

<400> 244

Ser Tyr Gly Ile Ser
 1 5

<210> 245
 <211> 17
 <212> PRT

<213> Artificial Sequence

<220>

<223> MF8233 CDR2

<400> 245

Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 246

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8233 CDR3

<400> 246

Asp Arg His Trp His Trp Trp Leu Asp Ala Phe Asp Tyr
1 5 10

<210> 247

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> MF8233 VH

<400> 247

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu

50

55

60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Lys Asp Arg His Trp His Trp Trp Leu Asp Ala Phe Asp Tyr Trp
100 105 110

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

<210> 248
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> MF9891

<400> 248
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cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatgccaa cacaaactat 180
gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggctgtgt attactgtgc aaaagatctg 300
tacggtcatt ggtggctgga tgcctttgat tattggggcc aaggtaccct ggtcaccgtc 360
tccagt 366

<210> 249
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9891 FW1

<400> 249

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 250
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9891 FW2

<400> 250

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 251
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9891 FW3

<400> 251

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

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

<220>
<223> MF9891 FW4

<400> 252

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

1

5

10

<210> 253
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9891 CDR1

<400> 253

Ser Tyr Gly Ile Ser
1 5

<210> 254
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9891 CDR2

<400> 254

Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 255
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9891 CDR3

<400> 255

Asp Leu Tyr Gly His Trp Trp Leu Asp Ala Phe Asp Tyr
1 5 10

<210> 256
<211> 122
<212> PRT

<213> Artificial Sequence

<220>

<223> MF9891 VH

<400> 256

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Lys Asp Leu Tyr Gly His Trp Trp Leu Asp Ala Phe Asp Tyr Trp
100 105 110

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

<210> 257

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> MF9886

<400> 257

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tcctgcaagg cttctggtta cacctttacc agctatggta tcagctgggt gcgacaggcc 120

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cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatgccaa cacaaactat 180
gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
atggagctga ggagcctgag atctgacgac acggctgtgt attactgtgc aaaaggtcca 300
ggttctcatt ggtggctgga tgcctttgat tattggggcc aaggtaccct ggtcaccgtc 360
tccagt 366

<210> 258
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9886 FW1

<400> 258

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 259
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9886 FW2

<400> 259

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 260
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9886 FW3

<400> 260

1003643556_1.txt

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> 261
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9886 FW4

<400> 261

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 262
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9886 CDR1

<400> 262

Ser Tyr Gly Ile Ser
1 5

<210> 263
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9886 CDR2

<400> 263

Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 264
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9886 CDR3

<400> 264

Gly Pro Gly Ser His Trp Trp Leu Asp Ala Phe Asp Tyr
 1 5 10

<210> 265
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9886 VH

<400> 265

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

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

Gly Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Lys Gly Pro Gly Ser His Trp Trp Leu Asp Ala Phe Asp Tyr Trp

100

105

110

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

<210> 266
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF9873

<400> 266
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 cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatgccaa cacaaactat 180
 gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggagctga ggagcctgag atctgacgac acggctgtgt attactgtgc aaaagataga 300
 ggttggcatt ggtggctgga tgcctttgat tattggggcc aaggtaccct ggtcaccgtc 360
 tccagt 366

<210> 267
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9873 FW1

<400> 267

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 20 25 30

<210> 268
 <211> 14
 <212> PRT

<213> Artificial Sequence

<220>

<223> MF9873 FW2

<400> 268

Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly
1				5					10				

<210> 269

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9873 FW3

<400> 269

Arg	Val	Thr	Met	Thr	Thr	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu
1				5					10					15	

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

<210> 270

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9873 FW4

<400> 270

Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 271

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9873 CDR1

<400> 271

Ser Tyr Gly Ile Ser
1 5

<210> 272
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9873 CDR2

<400> 272

Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 273
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9873 CDR3

<400> 273

Asp Arg Gly Trp His Trp Trp Leu Asp Ala Phe Asp Tyr
1 5 10

<210> 274
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9873 VH

<400> 274

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

20

25

30

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

Gly Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

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

Ala Lys Asp Arg Gly Trp His Trp Trp Leu Asp Ala Phe Asp Tyr Trp
 100 105 110

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

<210> 275
 <211> 375
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MF9988

<400> 275
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 cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatgccaa cacaaactat 180
 gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggagctga ggagcctgag atctgacgac acggctgtgt attactgtgc aaaagatcgt 300
 cattggcatt ggtggctgga cggctttgat tattggggcc aaggtaccct ggtcaccgtc 360
 tcgagtgtct ccagt 375

<210> 276

<211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9988 FW1

<400> 276

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
 20 25 30

<210> 277
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9988 FW2

<400> 277

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 1 5 10

<210> 278
 <211> 32
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF9988 FW3

<400> 278

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
 1 5 10 15

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

<210> 279
 <211> 11
 <212> PRT

<213> Artificial Sequence

<220>

<223> MF9988 FW4

<400> 279

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 280

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9988 CDR1

<400> 280

Ser Tyr Gly Ile Ser
1 5

<210> 281

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9988 CDR2

<400> 281

Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu Gln
1 5 10 15

Gly

<210> 282

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> MF9988 CDR3

<400> 282

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Asp Arg His Trp His Trp Trp Leu Asp Gly Phe Asp Tyr
1 5 10

<210> 283
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> MF9988 VH

<400> 283

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Ser Ala Tyr Asn Ala Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Lys Asp Arg His Trp His Trp Trp Leu Asp Gly Phe Asp Tyr Trp
100 105 110

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

<210> 284
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> MF6744 anti-CD127 antibody sequence

<400> 284

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gaggtgcagc tgggtgcagtc tggagcagag gtgaaaaagc ccggggagtc actgaaaatc      60
tcctgtaagg gttctggata cagctttacc agctactgga tcggctgggt gcgccagatg      120
cccgggaaag gcctggagtg gatggggatc atctttcctg atgactctga taccagatac      180
agtccgtcct tccaaggcca ggtcaccatc tcagccgaca agtccatcag taccgcctac      240
ctgcagtgga gcagcctgaa accctcggac accgccatgt attactgtgt gagacttggt      300
ggatatagtg gctacgctga ggattttgtt gacttctggg gccagggaac cctgggtcacc      360
gtctccagt                                     369

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<210> 285

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> MF6744 FW1

<400> 285

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

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

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<210> 286

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MF6744 FW2

<400> 286

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Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1           5           10

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<210> 287

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

<220>
 <223> MF6744 FW3

<400> 287

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

Trp	Ser	Ser	Leu	Lys	Pro	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Val	Arg
			20					25					30		

<210> 288
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF6744 FW4

<400> 288

Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 289
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF6744 CDR1

<400> 289

Ser	Tyr	Trp	Ile	Gly
1				5

<210> 290
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MF6744 CDR2

<400> 290

Ile Ile Phe Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 291

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MF6744 CDR3

<400> 291

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

<210> 292

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> MF6744 VH

<400> 292

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

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

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

Gly Ile Ile Phe Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr

Leu Val Thr Val Ser Ser
115

<210> 294
<211> 393
<212> DNA
<213> Artificial Sequence

<220>
<223> H1H7232B (1129) VH-MF6955 in combination with common light chain,
VH gene: IGHV3-9

<400> 294
gcggcccagc cggccatggc cgaggtgcag ctggtggagt cggggggagg cttggttcac 60
cctggcaggt ccctgagact ctcctgtgca gcctctggat tcacctttga tgattatacc 120
atgcactggg tccggcaagc tccaggggaag ggcctggaat gggcttcaga tattagttgg 180
aatagtggta gcagaggcta tgcggactct gtgaagggcc gattcaccat ctccagagat 240
aatgccgaga actccctgta cctgcaaata aacagtctga gagctgagga cacggccttg 300
tattactgtg caaaagataa aagtggctac ggccactact actactacgc tatggacgtc 360
tggggccaag ggaccacggt caccgtctcc tca 393

<210> 295
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> H1H7232B (1129) VH - MF6955 in combination with common light
chain

VH gene: IGHV3-9

<400> 295

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

Gly Leu Val His Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25 30

Gly Phe Thr Phe Asp Asp Tyr Thr Met His Trp Val Arg Gln Ala Pro

35

40

45

Gly Lys Gly Leu Glu Trp Val Ser Asp Ile Ser Trp Asn Ser Gly Ser
 50 55 60

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

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

Asp Thr Ala Leu Tyr Tyr Cys Ala Lys Asp Lys Ser Gly Tyr Gly His
 100 105 110

Tyr Tyr Tyr Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr
 115 120 125

Val Ser Ser
 130

<210> 296

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> H1H7241B (1145) VH - MF6964 in combination with common light chain

VH gene: IGHV3-9

<400> 296

gcggcccagc cggccatggc cgaggtgcag ctggtggagt ctgggggagg cttggttcag 60

cctggcaggt ccctgagact ctcctgtgca gcctctggat ttacctttgc tgactatacc 120

atgcactggg tccggcaagg tccaggggaag ggcctggagt gggtctcaga tattggttgg 180

aatagtaata ctataggcta tgcggactct gtgaagggcc gattcgccat ctccagagac 240

aacgccaaga actccctgta tcttcaaata aacagtctgc gacctgagga cacggcctta 300

tattactgtg taaaggataa aagtggttac gggaaattcc aatacggttt ggacgtctgg 360

ggccaaggga ccacggtcac cgtctcctca 390

<210> 297
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H1H7241B (1145) VH - MF6964 in combination with common light chain

VH gene: IGHV3-9

<400> 297

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

Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 20 25 30

Gly Phe Thr Phe Ala Asp Tyr Thr Met His Trp Val Arg Gln Gly Pro
 35 40 45

Gly Lys Gly Leu Glu Trp Val Ser Asp Ile Gly Trp Asn Ser Asn Thr
 50 55 60

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

Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Pro Glu
 85 90 95

Asp Thr Ala Leu Tyr Tyr Cys Val Lys Asp Lys Ser Gly Tyr Gly Lys
 100 105 110

Phe Gln Tyr Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
 115 120 125

Ser Ser
 130