

SEQUENCE LISTING

<110> Calmune Corporation
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Keogh, Elissa

<120> ANTI-HUMAN RESPIRATORY SYNCYTIAL VIRUS
ANTIBODIES (RSV) AND METHODS OF USE

<130> 33335.01161.W011/1161PC

<150> 61/399,310

<151> 2010-07-09

<150> 61/456,454

<151> 2010-11-05

<160> 487

<170> FastSEQ for windows Version 4.0

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<211> 228

<212> PRT

<213> Homo sapiens

<220>

<223> 58c5 Fab Heavy Chain

<400> 1

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Asn	Tyr	Tyr	Trp	Thr	Trp	Ile	Arg	Gln	Arg	Pro	Gly	Gly	Gly	Leu	Glu
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Trp	Ile	Gly	His	Ile	Ser	Tyr	Thr	Gly	Asn	Thr	Tyr	Thr	Thr	Pro	Ser
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Leu	Lys	Ser	Arg	Leu	Ser	Met	Ser	Leu	Glu	Thr	Ser	Gln	Ser	Gln	Phe
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Ser	Leu	Arg	Leu	Thr	Ser	Val	Thr	Ala	Ala	Asp	Ser	Ala	Val	Tyr	Phe
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Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser
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Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
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Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys
		195					200					205			
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Pro	Lys	Ser	Cys												
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<212> PRT
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<223> 58c5 VH CDR1

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

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<223> 58c5 VH CDR2

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<212> PRT
<213> Homo sapiens

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<211> 214
<212> PRT
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<220>
<223> 58c5 Light Chain

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

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
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Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205
Phe Asn Arg Gly Glu Cys
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<213> Homo sapiens

<220>
<223> 58c5 VL CDR1

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<212> PRT
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<220>
<223> 58c5 VL CDR2

<400> 7
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<212> PRT
<213> Homo sapiens

<220>
<223> 58c5 VL CDR3

<400> 8
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<212> PRT
<213> Homo sapiens

<220>
<223> sc5 Fab Heavy Chain

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35 40 45
Ile Gly Glu Ile Tyr Tyr Arg Gly Thr Thr Asn Tyr Lys Ser Ser Leu
50 55 60
Lys Gly Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80
Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
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Ala	Arg	Gly	Gly	Arg	Ser	Thr	Phe	Gly	Pro	Asp	Tyr	Tyr	Tyr	Tyr	Met
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Asp	Val	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr
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Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser
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Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
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Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
				165					170					175	
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
			180					185					190		
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys
		195					200					205			
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu
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Pro	Lys	Ser	Cys												
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<210> 10
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<220>
 <223> sc5 VH CDR1

<400> 10
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<210> 11
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <223> sc5 VH CDR2

<400> 11
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 1 5 10 15

<210> 12
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <223> sc5 VH CDR3

<400> 12
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<210> 13
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 <212> PRT
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<220>
 <223> sc5 Light Chain

<400> 13

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 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
 35 40 45
 Tyr Ala Ala Ser Thr 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 Ser Cys Gln Gln Ser Tyr Asn Asn Gln Leu
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 Thr Phe Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
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 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
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 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
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<210> 14
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<220>
 <223> sc5 VL CDR1

<400> 14
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 1 5 10

<210> 15
 <211> 7
 <212> PRT
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<220>
 <223> sc5 VL CDR2

<400> 15
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<210> 16
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<220>
 <223> sc5 VL CDR3

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 <211> 702
 <212> DNA
 <213> Homo sapiens

<220>
 <223> 58c5 Heavy Chain

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 cagcgcacag gggggggcct ggagtggatt ggccacatct cttacactgg gaacacctac 180
 tacaccccgt cactcaagag ccgactttcc atgtcactag agacatctca gagccaattc 240
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 ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac 660
 aagaaagttg agcccaaatc ttgtggtcgg ccaggccggc cg 702

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 <211> 645
 <212> DNA
 <213> Homo sapiens

<220>
 <223> 58c5 Light Chain

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 <212> DNA
 <213> Homo sapiens

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 <223> sc5 Heavy Chain

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<212> DNA
<213> Homo sapiens

<220>
<223> sc5 Light Chain

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<213> Artificial Sequence

<220>
<223> RSV A2 F protein

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<223> NheI Restriction Site

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<220>
<223> HindIII Restriction Site

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<210> 24
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<212> DNA
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cctctgagct	attccagaag	tagtgaggag	gctttttttg	aggcctaggc	ttttgcaaag	3300
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tccagcgcg	ggatctcatg	ctggagttct	tcgcccaccc	tagggggagg	ctaactgaaa	4320
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atcgatttttc	gttccacttt	gcgtcagacc	ccgtagaaaa	gatcaaagga	tcttcttgag	4740
gtcttttttt	tctgcgcgta	atctgctgct	cgaaacaaa	aaaaccaccg	ctaccagcgg	4800
tggtttgttt	gccggatcaa	gagctaccaa	ctctttttcc	gaaggtaact	ggcttcagca	4860
gagcgcagat	accaaatact	gtccttctag	tgtagccgta	gttaggccac	cacttcaaga	4920
actctgtagc	accgcctaca	tacctcgctc	tgctaattcct	gttaccagtg	gctgctgcca	4980

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<210> 103
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VH chain

```

<400> 103
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1      5      10      15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20     25     30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35     40     45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50     55     60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65     70     75
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85     90     95
Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
100    105    110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115    120    125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130    135    140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145    150    155
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165    170    175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180    185    190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195    200    205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210    215    220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225    230    235
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245    250    255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260    265    270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275    280    285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290    295    300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305    310    315
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325    330    335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340    345    350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355    360    365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370    375    380

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Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 104
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VH domain

<400> 104
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 105
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VH CDR1

<400> 105
 Thr Ser Gly Met Ser Val Gly
 1 5

<210> 106
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VH CDR2

<400> 106
 Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

<210> 107
 <211> 10
 <212> PRT

<213> Artificial Sequence

<220>

<223> Synagis VH CDR3

<400> 107

Ser Met Ile Thr Asn Trp Tyr Phe Asp Val
1 5 10

<210> 108

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Synagis VL chain

<400> 108

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

<210> 109

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Synagis VL domain

<400> 109

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

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 110
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VL CDR1

<400> 110
 Lys Cys Gln Leu Ser Val Gly Tyr Met His
 1 5 10

<210> 111
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VL CDR2

<400> 111
 Asp Thr Ser Lys Leu Ala Ser
 1 5

<210> 112
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synagis VL CDR3

<400> 112
 Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 1 5

<210> 113
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF VH CHAIN

<400> 113
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 114
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF VH DOMAIN

<400> 114
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Ala

Gly Thr Thr Val Thr Val Ser Ser 100 105 110
115 120

<210> 115
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VH CDR1

<400> 115
Thr Ala Gly Met Ser Val Gly
1 5

<210> 116
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VH CDR3

<400> 116
Ser Met Ile Thr Asn Phe Tyr Phe Asp Val
1 5 10

<210> 117
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> AFFF VL CHAIN

<400> 117
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
35 40 45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Phe Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

<210> 118
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF VL DOMAIN

<400> 118
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Cys Phe Gln Phe Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 119
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF VL CDR1

<400> 119
 Ser Ala Ser Ser Ser Val Gly Tyr Met His
 1 5 10

<210> 120
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF VL CDR2

<400> 120
 Asp Thr Phe Lys Leu Ala Ser
 1 5

<210> 121
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF VL CDR3

<400> 121
 Phe Gln Phe Ser Gly Tyr Pro Phe Thr
 1 5

<210> 122
 <211> 450

<212> PRT
 <213> Artificial Sequence

<220>
 <223> P1212 VH CHAIN

<400> 122
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 80 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 123

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

<220>
 <223> P1212 VH DOMAIN

<400> 123
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 124
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P1212 VH CDR1

<400> 124
 Thr Pro Gly Met Ser Val Gly
 1 5

<210> 125
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P1212 VH CDR2

<400> 125
 Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser Leu Lys Asp
 1 5 10 15

<210> 126
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P1212 VH CDR3

<400> 126
 Asp Met Ile Phe Asn Phe Tyr Phe Asp Val
 1 5 10

<210> 127
 <211> 213
 <212> PRT

<213> Artificial Sequence

<220>

<223> P1212 VL CHAIN

<400> 127

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1      5      10
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
 20     25     30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35     40     45
Asp Thr Phe Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50     55     60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65     70     75     80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85     90     95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100    105    110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115    120    125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130    135    140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145    150    155    160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165    170    175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180    185    190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195    200    205
Asn Arg Gly Glu Cys
210
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<210> 128

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> P1212 VL DOMAIN

<400> 128

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Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1      5      10
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
 20     25     30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35     40     45
Asp Thr Phe Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50     55     60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65     70     75     80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85     90     95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100    105
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<210> 129

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> P1212 VL CDR1

<400> 129
 Ser Leu Ser Ser Arg Val Gly Tyr Met His
 1 5 10

<210> 130
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P1212 VL CDR2

<400> 130
 Asp Thr Phe Tyr Leu Ser Ser
 1 5

<210> 131
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P12f4 VH CHAIN

<400> 131
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

<400> 134
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Arg Gly Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

<210> 135
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P12f4 VL DOMAIN

<400> 135
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Arg Gly Leu Pro Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 136
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P12f4 VL CDR2

<400> 136
 Asp Thr Arg Gly Leu Pro Ser
 1 5

<210> 137

<211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P11d4 VH CHAIN

<400> 137

Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln
1				5					10					15	
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Pro
			20					25					30		
Gly	Met	Ser	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
		35					40					45			
Trp	Leu	Ala	Asp	Ile	Trp	Trp	Asp	Gly	Lys	Lys	His	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Asp	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val
65					70					75				80	
Val	Leu	Lys	Val	Thr	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Asp	Met	Ile	Phe	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185						190	
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
225					230					235					240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
				245					250					255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			260					265					270		
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
		275					280					285			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	290					295					300				
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
305					310					315					320
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
				325					330					335	
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
			340					345					350		
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu
		355					360					365			
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	370					375					380				
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
385					390					395					400
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
				405					410					415	
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
			420					425					430		
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
		435					440					445			
Gly	Lys														
	450														

<210> 138
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P11d4 VH DOMAIN

<400> 138
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Pro
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 139
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P11d4 VH CDR3

<400> 139
 Asp Met Ile Phe Asn Trp Tyr Phe Asp Val
 1 5 10

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

<220>
 <223> P11d4 VL CHAIN

<400> 140
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Met Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu

145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 141
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P11d4 VL DOMAIN

<400> 141
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Met Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 142
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P11d4 VL CDR1

<400> 142
 Ser Pro Ser Ser Arg Val Gly Tyr Met His
 1 5 10

<210> 143
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P11d4 VL CDR2

<400> 143
 Asp Thr Met Arg Leu Ala Ser
 1 5

<210> 144
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>

<223> A1e9 VH CHAIN

<400> 144

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
50 55 60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 145

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> A1e9 VH DOMAIN

<400> 145

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

<210> 146

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> A1e9 VL CHAIN

<400> 146

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1      5      10      15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
20      25      30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
35      40      45
Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50      55      60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65      70      75      80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85      90      95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100      105      110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115      120      125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130      135      140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145      150      155      160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165      170      175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180      185      190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195      200      205
Asn Arg Gly Glu Cys
210
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<210> 147

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> A1e9 VL DOMAIN

<400> 147
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 148
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A1e9 VL CDR2

<400> 148
 Asp Thr Phe Lys Leu Ser Ser
 1 5

<210> 149
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A12a6 VH CHAIN

<400> 149
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220

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

<210> 150
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A12a6 VH DOMAIN

<400> 150
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 151
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A12a6 VH CDR2

<400> 151

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

<210> 152
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A12a6 VL CHAIN

<400> 152
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 153
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A12a6 VL DOMAIN

<400> 153
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 154
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A12a6 VL CDR1

<400> 154
 Ser Ala Ser Ser Arg Val Gly Tyr Met His
 1 5 10

<210> 155
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13c4 VH CHAIN

<400> 155
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 156
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13c4 VH DOMAIN

<400> 156
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 157
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13c4 VH CDR2

<400> 157
 Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser Leu Lys Asp
 1 5 10 15

<210> 158
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13c4 VL CHAIN

<400> 158
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr

```

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

```

<210> 159
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13c4 VL DOMAIN

```

<400> 159
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
  1      5      10      15
Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Arg Val Gly Tyr Met
      20      25      30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
      35      40      45
Asp Thr Met Tyr Gln Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
  50      55      60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
  65      70      75      80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
      85      90      95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
  100      105

```

<210> 160
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13c4 VL CDR2

```

<400> 160
Asp Thr Met Tyr Gln Ser Ser
  1      5

```

<210> 161
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>

<223> A17d4 VH CHAIN

<400> 161

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys Ser Tyr Asn Pro Ser
50 55 60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 162

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> A17d4 VH DOMAIN

<400> 162

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

<210> 163

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> A17d4 VH CDR2

<400> 163

```
Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser Leu Lys Asp
 1          5          10          15
```

<210> 164

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> A17d4 VL CHAIN

<400> 164

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1          5          10          15
Asp Arg Val Thr Ile Thr Cys Leu Pro Ser Ser Arg Val Gly Tyr Met
 20          25          30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35          40          45
Asp Thr Met Tyr Gln Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50          55          60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65          70          75
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85          90          95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100          105          110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115          120          125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130          135          140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145          150          155
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165          170          175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
```

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 180 185 190
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 165
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17d4 VL DOMAIN

<400> 165
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Leu Pro Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Met Tyr Gln Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Cys Phe Gln Phe Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 166
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17d4 VL CDR1

<400> 166
 Leu Pro Ser Ser Arg Val Gly Tyr Met His
 1 5 10

<210> 167
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4 VH CHAIN

<400> 167
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 168
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4 VH DOMAIN

<400> 168
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln

Gly Thr Thr Val Thr Val Ser Ser 100 105 110
115 120

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

<220>
<223> A4B4 VL CHAIN

<400> 169
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
35 40 45
Asp Thr Phe Phe Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

<210> 170
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A4B4 VL DOMAIN

<400> 170
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
35 40 45
Asp Thr Phe Phe Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 171
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4 VL CDR2

<400> 171
 Asp Thr Phe Phe Leu Asp Ser
 1 5

<210> 172
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A8c7 VH CHAIN

<400> 172
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu


```
<210> 175
<211> 106
<212> PRT
<213> Artificial Sequence
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<220>
<223> A8c7 VL DOMAIN

<400>	175														
Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Arg	Val	Gly	Tyr	Met
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
		35					40					45			
Asp	Thr	Arg	Tyr	Gln	Ser	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp
65					70					75					80
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Phe	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
			100					105							

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<210> 176
<211> 451
<212> PRT
<213> Artificial Sequence
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<220>
<223> IX-493L1FR VH CHAIN

<400>	176														
Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln
1				5					10					15	
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		
Gly	Met	Ser	Val	Gly	Tyr	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu
		35					40					45			
Glu	Trp	Leu	Ala	Asp	Ile	Trp	Trp	Asp	Asp	Lys	Lys	Asp	Tyr	Asn	Pro
	50					55					60				
Ser	Leu	Lys	Ser	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln
65					70					75				80	
Val	Val	Leu	Lys	Val	Thr	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr
				85					90					95	
Tyr	Cys	Ala	Arg	Ser	Met	Ile	Thr	Asn	Trp	Tyr	Phe	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

Val	Leu	Gln	Ser	165	Ser	Gly	Leu	Tyr	Ser	170	Leu	Ser	Ser	Val	Val	175	Thr	Val
Pro	Ser	Ser	180	Ser	Leu	Gly	Thr	Gln	185	Thr	Tyr	Ile	Cys	Asn	190	Val	Asn	His
Lys	Pro	Ser	195	Asn	Thr	Lys	Val	Asp	200	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	
Asp	Lys	Thr	His	Thr	Cys	215	Pro	Pro	Cys	Pro	Ala	220	Pro	Glu	Leu	Leu	Gly	
Gly	Pro	Ser	Val	Phe	Leu	230	Phe	Pro	Pro	Lys	235	Lys	Asp	Thr	Leu	Met		
Ile	Ser	Arg	Thr	245	Pro	Glu	Val	Thr	Cys	250	Val	Val	Val	Asp	Val	Ser	His	
Glu	Asp	Pro	260	Glu	Val	Lys	Phe	Asn	265	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
His	Asn	Ala	Lys	Thr	Lys	Pro	280	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr		
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	300	Asp	Trp	Leu	Asn	Gly		
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	315	Leu	Pro	Ala	Pro	Ile		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val			
Tyr	Thr	Leu	340	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser		
Leu	Thr	Cys	Leu	Val	Lys	Gly	360	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu		
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	380	Lys	Thr	Thr	Pro	Pro		
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val			
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser			
Pro	Gly	Lys	435				440					445						
			450															

<210> 177
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IX-493L1FR VL CHAIN

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly			
1				5					10					15				
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Ala	25	Ser	Ser	Ser	Val	Gly	Tyr	Met		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr			
Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser			
50						55					60							
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp			
65					70					75					80			
Asp	Phe	Ala	Thr	Tyr	Cys	Phe	Gln	Gly	90	Ser	Gly	Tyr	Pro	Phe	Thr			
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro			
			100					105					110					
Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr			
			115				120					125						
Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys			
130						135					140							
Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu			
145					150					155					160			

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 Asn Arg Gly Glu Cys
 210

<210> 178
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IX-493L1FR VL DOMAIN

<400> 178
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 179
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M3H9 VH CHAIN

<400> 179
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

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

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

<220>
 <223> M3H9 VL CHAIN

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

180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 181
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M3H9 VL DOMAIN

<400> 181
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Tyr Lys Gln Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 182
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Y10H6 VH CHAIN

<400> 182
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp

Asn Arg Gly Glu Cys
210

<210> 184
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Y10H6 VL DOMAIN

<400> 184
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
35 40 45
Asp Thr Arg Tyr Leu Ser Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 185
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Y10H6 VL CDR2

<400> 185
Asp Thr Arg Tyr Leu Ser Ser
1 5

<210> 186
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> DG VH CHAIN

<400> 186
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala

130	Leu	Gly	Cys	Leu	Val	Lys	135	Asp	Tyr	Phe	Pro	Glu	140	Pro	Val	Thr	Val	Ser
145	Trp	Asn	Ser	Gly	Ala	150	Leu	Thr	Ser	Gly	Val	155	Thr	Phe	Pro	Ala	160	Val
				165	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	175	Pro
	Ser	Ser	Ser	180	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	190
	Pro	Ser	Asn	195	Thr	Lys	Val	Asp	200	Lys	Arg	Val	Glu	Pro	205	Lys	Ser	Cys
	Lys	Thr	His	Thr	Cys	Pro	215	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	220
225	Pro	Ser	Val	Phe	Leu	230	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	235
	Ser	Arg	Thr	Pro	Glu	245	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	250
	Asp	Pro	Glu	260	Val	Lys	Phe	Asn	Trp	265	Val	Asp	Gly	Val	Glu	Val	His	270
	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	285	300
	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	315	320
305	Glu	Tyr	Lys	Cys	Lys	310	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	330
	Lys	Thr	Ile	Ser	Lys	325	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	335
	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	345	350
	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	365	370
	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	380	385
	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	395	400
	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	410	415
	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	425	430
	Gly	Lys						440						445				450

<210> 187
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DG VH DOMAIN

<400> 187
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 188
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DG VH CDR3

<400> 188
 Asp Met Ile Thr Asn Phe Tyr Phe Asp Val
 1 5 10

<210> 189
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> DG VL CHAIN

<400> 189
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 190
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF(1) VH CHAIN

<400> 190
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu

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

<210> 192
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF(1) VL DOMAIN

<400> 192
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Phe Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 193
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AFFF(1) VL CDR3

<400> 193
 Phe Gln Gly Ser Phe Tyr Pro Phe Thr
 1 5

<210> 194
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 6H8 VH CHAIN

<400> 194

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
260 265 270
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285
Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr Tyr Arg
290 295 300
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
325 330 335
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350
Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 395 400
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
405 410 415
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445
Gly Lys
450

<210> 195

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> 6H8 VL CHAIN

<400> 195

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

<210> 196

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> 6H8 VL DOMAIN

<400> 196

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

<210> 197

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 6H8 VL CDR2

<400> 197
 Asp Thr Phe Lys Leu Thr Ser
 1 5

<210> 198
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> L1-7E5 VH CHAIN

<400> 198
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

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

<220>
 <223> L1-7E5 VL CHAIN

<400> 199
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 200
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> L1-7E5 VL DOMAIN

<400> 200
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

<210> 201
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> L2-15B10 VH CHAIN

<400> 201
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 80 85 90 95
 Cys Ala Arg Asp Met Ile Thr Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
450

<210> 202
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> L2-15B10 VL CHAIN

<400> 202
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
35 40 45
Asp Thr Phe Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

<210> 203
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> L2-15B10 VL DOMAIN

<400> 203
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45
Asp Thr Phe Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 204
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> L2-15B10 VL CDR2

<400> 204
 Asp Thr Phe Arg Leu Ala Ser
 1 5

<210> 205
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13a11 VH CHAIN

<400> 205
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	370					375					380				
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
385					390					395					400
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
				405					410					415	
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
			420					425					430		
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
		435					440					445			
Gly	Lys														
	450														

<210> 206
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13a11 VH DOMAIN

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

<210> 207
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13a11 VL CHAIN

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Pro	Ser	Ser	Arg	Val	Gly	Tyr	Met
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
		35					40					45			
Asp	Thr	Tyr	Arg	His	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80
Asp	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Phe
				85					90					95	
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala
			100					105					110		
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly
		115					120					125			
Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala
	130					135					140				

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 208
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A13a11 VL DOMAIN

<400> 208
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Tyr Arg His Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

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

<220>
 <223> A13a11 VL CDR2

<400> 209
 Asp Thr Tyr Arg His Ser Ser
 1 5

<210> 210
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A1h5 VH CHAIN

<400> 210
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Gly Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val

65	Val	Leu	Lys	Val	Thr	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Tyr	80
				85						90					95		
Cys	Ala	Arg	Asp	Met	Ile	Phe	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln		
			100					105					110				
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val		
		115					120					125					
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala		
	130					135					140						
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser		
145					150					155					160		
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val		
				165				170						175			
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro		
			180					185					190				
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys		
		195					200					205					
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp		
	210					215					220						
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly		
225					230					235					240		
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile		
				245				250						255			
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu		
			260					265					270				
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His		
		275					280					285					
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg			
	290					295				300							
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys		
305				310						315					320		
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu		
				325					330					335			
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr		
			340					345					350				
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu		
		355					360					365					
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp		
	370					375					380						
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val		
385					390					395					400		
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp		
				405				410						415			
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His		
		420						425					430				
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro		
		435					440					445					
Gly	Lys																
	450																

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

<220>
 <223> A1h5 VL CHAIN

<400> 211
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Phe His Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

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

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

<220>
 <223> A1h5 VL DOMAIN

<400> 212
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Leu Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Phe Phe His Arg Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

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

<220>
 <223> A1h5 VL CDR1

<400> 213
 Ser Leu Ser Ser Ser Val Gly Tyr Met His
 1 5 10

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

<220>
 <223> A1h5 VL CDR2

<400> 214
 Asp Thr Phe Phe His Arg Ser
 1 5

<210> 215
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4(1) VH CHAIN

<400> 215
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 80 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

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

<220>
 <223> A4B4(1) VL CHAIN

<400> 216
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Leu Leu Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 217
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4(1) VL DOMAIN

<400> 217
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Leu Leu Leu Asp Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

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

<220>
 <223> A4B4(1) VL CDR2

<400> 218
 Asp Thr Leu Leu Leu Asp Ser
 1 5

<210> 219
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4L1 VH CHAIN

<400> 219
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Phe Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

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

<220>
 <223> A4B4L1 VL CHAIN

<400> 220
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 221
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4L1 VL DOMAIN

<400> 221
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Arg Val Gly Tyr Met
 20 25 30

His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
		35					40					45			
Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp
65				70					75						80
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Phe	Thr
			85						90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
			100					105							

<210> 222
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A4B4-F25S VH CHAIN

<400>	222															
Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln	
1				5					10					15		
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ala	
			20					25					30			
Gly	Met	Ser	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu	
		35					40					45				
Trp	Leu	Ala	Asp	Ile	Trp	Trp	Asp	Asp	Lys	Lys	His	Tyr	Asn	Pro	Ser	
	50					55					60					
Leu	Lys	Asp	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	
65					70					75					80	
Val	Leu	Lys	Val	Thr	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Tyr	
				85					90					95		
Cys	Ala	Arg	Asp	Met	Ile	Phe	Asn	Phe	Tyr	Phe	Asp	Val	Trp	Gly	Gln	
			100					105					110			
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
		115					120					125				
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
	130					135					140					
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
145					150					155					160	
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
				165					170					175		
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			180					185					190			
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
		195					200					205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	
	210					215					220					
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
225					230					235					240	
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
				245					250					255		
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
			260					265					270			
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
		275					280					285				
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	
	290					295					300					
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
305					310					315					320	
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
				325					330					335		
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
			340					345					350			
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	
		355					360					365				
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	


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

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<210> 229
<211> 106
<212> PRT
<213> Artificial Sequence

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<220>
<223> H3-3F4 VL DOMAIN

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<400> 229
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1      5      10      15
Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
      20      25      30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
      35      40      45
Asp Thr Phe Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
      50      55      60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
      65      70      75      80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
      85      90      95
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
      100      105

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

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<220>
<223> VL CDR2

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```

<400> 230
Asp Thr Arg Tyr Gln Ser Ser
1      5

```

```

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

```

```

<220>
<223> M3H9 VL CDR2

```

```

<400> 231

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Asp Thr Tyr Lys Gln Thr Ser
1 5

<210> 232
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> IX-493L1FR VH domain

<400> 232
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 233
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A3e2 VH chain

<400> 233
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Asp Ile Trp Trp Gly Asp Lys Gly His Tyr Asn Pro Ser
50 55 60
Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80
Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
85 90 95
Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

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

<210> 234
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A3e2 VH domain

<400> 234
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Gly Asp Lys Gly His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 235
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A3e2 VH CDR2

<400> 235

Asp Ile Trp Trp Gly Asp Lys Gly His Tyr Asn Pro Ser Leu Lys Asp
 1 5 10 15

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

<220>
 <223> A3e2 VL chain

<400> 236
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Phe Tyr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 237
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A3e2 VL domain

<400> 237
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 35 40 45
 Asp Thr Phe Tyr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 238
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A3e2 VL CDR2

<400> 238
 Asp Thr Phe Tyr Leu His Ser
 1 5

<210> 239
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A14a4 VH chain

<400> 239
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 240
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A14a4 VH domain

<400> 240
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Ser Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 241
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A14a4 VH CDR3

<400> 241
 Asp Met Ile Thr Asn Trp Tyr Phe Asp Val
 1 5 10

<210> 242
 <211> 197
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A14a4 VL chain

<400> 242
 Asp Arg Val Thr Ile Thr Cys Leu Leu Ser Ser Arg Val Gly Tyr Met
 1 5 10 15
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 20 25 30
 Asp Thr Tyr Tyr Gln Thr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
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<400> 245
 Asp Thr Tyr Tyr Gln Thr Ser
 1 5

<210> 246
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A16b4 VH chain

<400> 246
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His

420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 247
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A16b4 VH domain

<400> 247
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys His Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 248
 <211> 197
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A16b4 VL chain

<400> 248
 Asp Arg Val Thr Ile Thr Cys Leu Leu Ser Ser Arg Val Gly Tyr Met
 1 5 10 15
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
 20 25 30
 Asp Thr Met Tyr Gln Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 35 40 45
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 50 55 60
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 65 70 75 80
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 85 90 95
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 100 105 110
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 115 120 125
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 130 135 140
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 145 150 155 160
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 165 170 175
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 180 185 190
 Asn Arg Gly Glu Cys

195

<210> 249
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL domain

<400> 249
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Leu Leu Ser Ser Arg Val Gly Tyr Met
20 25 30
His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
35 40 45
Asp Thr Met Tyr Gln Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
65 70 75 80
Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
85 90 95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 250
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL CDR1

<400> 250
Leu Leu Ser Ser Arg Val Gly Tyr Met His
1 5 10

<210> 251
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A16b4 VL CDR2

<400> 251
Asp Thr Met Tyr Gln Ala Ser
1 5

<210> 252
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> A17b5 VH chain

<400> 252
Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
20 25 30
Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu

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

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

<220>
 <223> A17b5 VL chain

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

<210> 255
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17b5 VL domain

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Ser	Leu	Ser	Ser	Arg	Val	Gly	Tyr	Met
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr
		35					40					45			

Asp	Thr	Tyr	Tyr	Leu	Pro	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Asp
65					70					75					80
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Phe	Gln	Gly	Ser	Gly	Tyr	Pro	Phe	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105							

<210> 256
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17b5 VLCDR2

<400> 256
 Asp Thr Tyr Tyr Leu Pro Ser
 1 5

<210> 257
 <211> 450
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17f5 VH chain

<400> 257

Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln
1				5					10					15	
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ala
			20					25					30		
Gly	Met	Ser	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
		35					40					45			
Trp	Leu	Ala	Asp	Ile	Trp	Trp	Asp	Asp	Lys	Lys	Asp	Tyr	Asn	Pro	Ser
	50					55					60				
Leu	Lys	Asp	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val
65					70					75					80
Val	Leu	Lys	Val	Thr	Asn	Met	Asp	Pro	Ala	Asp	Thr	Ala	Thr	Tyr	Tyr
				85					90					95	
Cys	Ala	Arg	Asp	Met	Ile	Phe	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln
			100				105						110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
		115					120					125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp
		210				215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
225					230					235					240
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
				245					250					255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			260					265					270		
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
		275					280					285			

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445
 Gly Lys
 450

<210> 258
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17f5 VH domain

<400> 258
 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ala
 20 25 30
 Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60
 Leu Lys Asp Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Asp Met Ile Phe Asn Trp Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 259
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17f5 VH CDR2

<400> 259
 Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser Leu Lys Asp
 1 5 10 15

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

<220>

<223> A17f5 VL chain

<400> 260

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

<210> 261

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> A17f5 VL domain

<400> 261

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

<210> 262

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> A17f5 VL CDR2

<400> 262
 Asp Thr Phe Arg His Thr Ser
 1 5

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

<220>
 <223> A17h4 VL chain

<400> 263
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Tyr Tyr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110
 Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125
 Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140
 Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160
 Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175
 Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190
 Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205
 Asn Arg Gly Glu Cys
 210

<210> 264
 <211> 106
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A17h4 VL domain

<400> 264
 Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Ser Pro Ser Ser Ser Val Gly Tyr Met
 20 25 30
 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Ile Tyr
 35 40 45
 Asp Thr Tyr Tyr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60
 Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80
 Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95
 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 265
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A17h4 VL CDR1

<400> 265
Ser Pro Ser Ser Ser Val Gly Tyr Met His
1 5 10

<210> 266
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> A17h4 VL CDR2

<400> 266
Asp Thr Tyr Tyr Leu Ala Ser
1 5

<210> 267
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 267
Gly Gly Ser Ser Arg Ser Ser Ser Ser Gly Gly Gly Gly Ser Gly Gly
1 5 10 15
Gly Gly

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 268
Gly Ser Gly Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 269
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 269
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr
1 5 10

<210> 270
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 270
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser Thr Gln
1 5 10 15

<210> 271
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 271
Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
1 5 10

<210> 272
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 272
Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
1 5 10

<210> 273
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 273
Lys Glu Ser Gly Ser Val Ser Ser Glu Gln Leu Ala Gln Phe Arg Ser
1 5 10 15
Leu Asp

<210> 274
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 274
Glu Ser Gly Ser Val Ser Ser Glu Glu Leu Ala Phe Arg Ser Leu Asp
1 5 10 15

<210> 275

<211> 298
 <212> PRT
 <213> Human respiratory syncytial virus

<400> 275
 Met Ser Lys Thr Lys Asp Gln Arg Thr Ala Lys Thr Leu Glu Arg Thr
 1 5 10 15
 Trp Asp Thr Leu Asn His Leu Leu Phe Ile Ser Ser Cys Leu Tyr Lys
 20 25 30
 Leu Asn Leu Lys Ser Ile Ala Gln Ile Thr Leu Ser Ile Leu Ala Met
 35 40 45
 Ile Ile Ser Thr Ser Leu Ile Ile Ala Ala Ile Ile Phe Ile Ala Ser
 50 55 60
 Ala Asn His Lys Val Thr Leu Thr Thr Ala Ile Ile Gln Asp Ala Thr
 65 70 75 80
 Asn Gln Ile Lys Asn Thr Thr Pro Thr Tyr Leu Thr Gln Asn Pro Gln
 85 90 95
 Leu Gly Ile Ser Phe Ser Asn Leu Ser Glu Thr Thr Ser Gln Pro Ile
 100 105 110
 Thr Ile Leu Ala Ser Thr Thr Pro Ser Ala Glu Ser Thr Pro Gln Ser
 115 120 125
 Thr Thr Val Lys Thr Lys Asn Thr Thr Thr Thr Gln Ile Gln Pro Ser
 130 135 140
 Lys Ser Thr Thr Lys Gln Arg Gln Asn Lys Pro Gln Asn Lys Pro Asn
 145 150 155 160
 Asn Asp Phe His Phe Glu Val Phe Asn Phe Val Pro Cys Ser Ile Cys
 165 170 175
 Ser Asn Asn Pro Thr Cys Trp Ala Ile Cys Lys Arg Ile Pro Asn Lys
 180 185 190
 Lys Pro Gly Lys Lys Thr Thr Thr Lys Pro Thr Lys Lys Pro Thr Ile
 195 200 205
 Lys Thr Thr Lys Lys Asp Leu Lys Pro Gln Thr Thr Lys Ser Lys Glu
 210 215 220
 Val Leu Thr Thr Lys Pro Thr Glu Lys Pro Thr Ile Asn Thr Thr Lys
 225 230 235 240
 Thr Asn Ile Arg Thr Thr Leu Leu Ile Ser Asn Thr Thr Gly Asn Pro
 245 250 255
 Glu His Thr Ser Gln Lys Glu Thr Leu His Ser Thr Thr Ser Glu Gly
 260 265 270
 Asn Pro Ser Pro Ser Gln Val Tyr Thr Thr Ser Glu Tyr Leu Ser Gln
 275 285
 Ser Leu Ser Pro Ser Asn Thr Tyr Tyr
 290 295

<210> 276
 <211> 2165
 <212> PRT
 <213> Human respiratory syncytial virus

<400> 276
 Met Asp Pro Ile Ile Asn Gly Asn Ser Ala Asn Val Tyr Leu Thr Asp
 1 5 10 15
 Ser Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Cys Asn Ala Leu Gly
 20 25 30
 Ser Tyr Ile Phe Asn Gly Pro Tyr Leu Lys Asn Asp Tyr Thr Asn Leu
 35 40 45
 Ile Ser Arg Gln Asn Pro Leu Ile Glu His Met Asn Leu Lys Lys Leu
 50 55 60
 Asn Ile Thr Gln Ser Leu Ile Ser Lys Tyr His Lys Gly Glu Ile Lys
 65 70 75 80
 Leu Glu Glu Pro Thr Tyr Phe Gln Ser Leu Leu Met Thr Tyr Lys Ser
 85 90 95
 Met Thr Ser Ser Glu Gln Ile Ala Thr Asn Leu Leu Lys Lys Ile
 100 105 110
 Ile Arg Arg Ala Ile Glu Ile Ser Asp Val Lys Val Tyr Ala Ile Leu
 115 120 125
 Asn Lys Leu Gly Leu Lys Glu Lys Asp Lys Ile Lys Ser Asn Asn Gly

1220 1225 1230
 Thr Thr Ser Thr Ile Ser Ser Gly Ile Ile Ile Glu Lys Tyr Asn Val
 1235 1240 1245
 Asn Ser Leu Thr Arg Gly Glu Arg Gly Pro Thr Lys Pro Trp Val Gly
 1250 1255 1260
 Ser Ser Thr Gln Glu Lys Lys Thr Met Pro Val Tyr Asn Arg Gln Val
 1265 1270 1275 1280
 Leu Thr Lys Lys Gln Arg Asp Gln Ile Asp Leu Leu Ala Lys Leu Asp
 1285 1290 1295
 Trp Val Tyr Ala Ser Ile Asp Asn Lys Asp Glu Phe Met Glu Glu Leu
 1300 1305 1310
 Ser Ile Gly Thr Leu Gly Leu Thr Tyr Glu Lys Ala Lys Lys Leu Phe
 1315 1320 1325
 Pro Gln Tyr Leu Ser Val Asn Tyr Leu His Arg Leu Thr Val Ser Ser
 1330 1335 1340
 Arg Pro Cys Glu Phe Pro Ala Ser Ile Pro Ala Tyr Arg Thr Thr Asn
 1345 1350 1355 1360
 Tyr His Phe Asp Thr Ser Pro Ile Asn Arg Ile Leu Thr Glu Lys Tyr
 1365 1370 1375
 Gly Asp Glu Asp Ile Asp Ile Val Phe Gln Asn Cys Ile Ser Phe Gly
 1380 1385 1390
 Leu Ser Leu Met Ser Val Val Glu Gln Phe Thr Asn Val Cys Pro Asn
 1395 1400 1405
 Arg Ile Ile Leu Ile Pro Lys Leu Asn Glu Ile His Leu Met Lys Pro
 1410 1415 1420
 Pro Ile Phe Thr Gly Asp Val Asp Ile His Lys Leu Lys Gln Val Ile
 1425 1430 1435 1440
 Gln Lys Gln His Met Phe Leu Pro Asp Lys Ile Ser Leu Thr Gln Tyr
 1445 1450 1455
 Val Glu Leu Phe Leu Ser Asn Lys Thr Leu Lys Ser Gly Ser His Val
 1460 1465 1470
 Asn Ser Asn Leu Ile Leu Ala His Lys Ile Ser Asp Tyr Phe His Asn
 1475 1480 1485
 Thr Tyr Ile Leu Ser Thr Asn Leu Ala Gly His Trp Ile Leu Ile Ile
 1490 1495 1500
 Gln Leu Met Lys Asp Ser Lys Gly Ile Phe Glu Lys Asp Trp Gly Glu
 1505 1510 1515 1520
 Gly Tyr Ile Thr Asp His Met Phe Ile Asn Leu Lys Val Phe Phe Asn
 1525 1530 1535
 Ala Tyr Lys Thr Tyr Leu Leu Cys Phe His Lys Gly Tyr Gly Lys Ala
 1540 1545 1550
 Lys Leu Glu Cys Asp Met Asn Thr Ser Asp Leu Leu Cys Val Leu Glu
 1555 1560 1565
 Leu Ile Asp Ser Ser Tyr Trp Lys Ser Met Ser Lys Val Phe Leu Glu
 1570 1575 1580
 Gln Lys Val Ile Lys Tyr Ile Leu Ser Gln Asp Ala Ser Leu His Arg
 1585 1590 1595 1600
 Val Lys Gly Cys His Ser Phe Lys Leu Trp Phe Leu Lys Arg Leu Asn
 1605 1610 1615
 Val Ala Glu Phe Thr Val Cys Pro Trp Val Val Asn Ile Asp Tyr His
 1620 1625 1630
 Pro Thr His Met Lys Ala Ile Leu Thr Tyr Ile Asp Leu Val Arg Met
 1635 1640 1645
 Gly Leu Ile Asn Ile Asp Arg Ile His Ile Lys Asn Lys His Lys Phe
 1650 1655 1660
 Asn Asp Glu Phe Tyr Thr Ser Asn Leu Phe Tyr Ile Asn Tyr Asn Phe
 1665 1670 1675 1680
 Ser Asp Asn Thr His Leu Leu Thr Lys His Ile Arg Ile Ala Asn Ser
 1685 1690 1695
 Glu Leu Glu Asn Asn Tyr Asn Lys Leu Tyr His Pro Thr Pro Glu Thr
 1700 1705 1710
 Leu Glu Asn Ile Leu Ala Asn Pro Ile Lys Ser Asn Asp Lys Lys Thr
 1715 1720 1725
 Leu Asn Asp Tyr Cys Ile Gly Lys Asn Val Asp Ser Ile Met Leu Pro
 1730 1735 1740
 Leu Leu Ser Asn Lys Lys Leu Ile Lys Ser Ser Ala Met Ile Arg Thr
 1745 1750 1755 1760
 Asn Tyr Ser Lys Gln Asp Leu Tyr Asn Leu Phe Pro Met Val Val Ile

1765 1770 1775
 Asp Arg Ile Ile Asp His Ser Gly Asn Thr Ala Lys Ser Asn Gln Leu
 Tyr Thr Thr 1780 Ser His Gln Ile Ser Leu Val His Asn Ser Thr Ser
 1795 1800 1805
 Leu Tyr Cys Met Leu Pro Trp His His Ile Asn Arg Phe Asn Phe Val
 1810 1815 1820
 Phe Ser Ser Thr Gly Cys Lys Ile Ser Ile Glu Tyr Ile Leu Lys Asp
 1825 1830 1835 1840
 Leu Lys Ile Lys Asp Pro Asn Cys Ile Ala Phe Ile Gly Glu Gly Ala
 1845 1850 1855
 Gly Asn Leu Leu Leu Arg Thr Val Val Glu Leu His Pro Asp Ile Arg
 1860 1865 1870
 Tyr Ile Tyr Arg Ser Leu Lys Asp Cys Asn Asp His Ser Leu Pro Ile
 1875 1880 1885
 Glu Phe Leu Arg Leu Tyr Asn Gly His Ile Asn Ile Asp Tyr Gly Glu
 1890 1895 1900
 Asn Leu Thr Ile Pro Ala Thr Asp Ala Thr Asn Asn Ile His Trp Ser
 1905 1910 1915 1920
 Tyr Leu His Ile Lys Phe Ala Glu Pro Ile Ser Leu Phe Val Cys Asp
 1925 1930 1935
 Ala Glu Leu Ser Val Thr Val Asn Trp Ser Lys Ile Ile Ile Glu Trp
 1940 1945 1950
 Ser Lys His Val Arg Lys Cys Lys Tyr Cys Ser Ser Val Asn Lys Cys
 1955 1960 1965
 Met Leu Ile Val Lys Tyr His Ala Gln Asp Asp Ile Asp Phe Lys Leu
 1970 1975 1980
 Asp Asn Ile Thr Ile Leu Lys Thr Tyr Val Cys Leu Gly Ser Lys Leu
 1985 1990 1995 2000
 Lys Gly Ser Glu Val Tyr Leu Val Leu Thr Ile Gly Pro Ala Asn Ile
 2005 2010 2015
 Phe Pro Val Phe Asn Val Val Gln Asn Ala Lys Leu Ile Leu Ser Arg
 2020 2025 2030
 Thr Lys Asn Phe Ile Met Pro Lys Lys Ala Asp Lys Glu Ser Ile Asp
 2035 2040 2045
 Ala Asn Ile Lys Ser Leu Ile Pro Phe Leu Cys Tyr Pro Ile Thr Lys
 2050 2055 2060
 Lys Gly Ile Asn Thr Ala Leu Ser Lys Leu Lys Ser Val Val Ser Gly
 2065 2070 2075 2080
 Asp Ile Leu Ser Tyr Ser Ile Ala Gly Arg Asn Glu Val Phe Ser Asn
 2085 2090 2095
 Lys Leu Ile Asn His Lys His Met Asn Ile Leu Lys Trp Phe Asn His
 2100 2105 2110
 Val Leu Asn Phe Arg Ser Thr Glu Leu Asn Tyr Asn His Leu Tyr Met
 2115 2120 2125
 Val Glu Ser Thr Tyr Pro Tyr Leu Ser Glu Leu Leu Asn Ser Leu Thr
 2130 2135 2140
 Thr Asn Glu Leu Lys Lys Leu Ile Lys Ile Thr Gly Ser Leu Leu Tyr
 2145 2150 2155 2160
 Asn Phe His Asn Glu
 2165

<210> 277
 <211> 391
 <212> PRT
 <213> Human respiratory syncytial virus

<400> 277
 Met Ala Leu Ser Lys Val Lys Leu Asn Asp Thr Leu Asn Lys Asp Gln
 1 5 10 15
 Leu Leu Ser Ser Ser Lys Tyr Thr Ile Gln Arg Ser Thr Gly Asp Asn
 20 25 30
 Ile Asp Thr Pro Asn Tyr Asp Val Gln Lys His Leu Asn Lys Leu Cys
 35 40 45
 Gly Met Leu Leu Ile Thr Glu Asp Ala Asn His Lys Phe Thr Gly Leu
 50 55 60
 Ile Gly Met Leu Tyr Ala Met Ser Arg Leu Gly Arg Glu Asp Thr Ile

65	Lys	Ile	Leu	Lys	Asp	Ala	Gly	Tyr	His	Val	Lys	Ala	Asn	Gly	Val	Asp
					85					90					95	
	Ile	Thr	Thr	Tyr	Arg	Gln	Asp	Ile	Asn	Gly	Lys	Glu	Met	Lys	Phe	Glu
				100					105					110		
	Val	Leu	Thr	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Ile	Gln	Val	Asn	Ile	Glu
			115					120					125			
	Ile	Glu	Ser	Arg	Lys	Ser	Tyr	Lys	Lys	Leu	Leu	Lys	Glu	Met	Gly	Glu
		130					135					140				
	Val	Ala	Pro	Glu	Tyr	Arg	His	Asp	Ser	Pro	Asp	Cys	Gly	Met	Ile	Ile
						150					155				160	
	Leu	Cys	Ile	Ala	Ala	Leu	Val	Ile	Thr	Lys	Leu	Ala	Ala	Gly	Asp	Arg
				165						170					175	
	Ser	Gly	Leu	Thr	Ala	Val	Ile	Arg	Arg	Ala	Asn	Asn	Val	Leu	Lys	Asn
				180					185					190		
	Glu	Ile	Lys	Arg	Tyr	Lys	Gly	Leu	Ile	Pro	Lys	Asp	Ile	Ala	Asn	Ser
			195					200					205			
	Phe	Tyr	Glu	Val	Phe	Glu	Lys	His	Pro	His	Leu	Ile	Asp	Val	Phe	Val
		210					215					220				
	His	Phe	Gly	Ile	Ala	Gln	Ser	Ser	Thr	Arg	Gly	Gly	Ser	Arg	Val	Glu
						230					235				240	
	Gly	Ile	Phe	Ala	Gly	Leu	Phe	Met	Asn	Ala	Tyr	Gly	Ser	Gly	Gln	Val
				245						250					255	
	Met	Leu	Arg	Trp	Gly	Val	Leu	Ala	Lys	Ser	Val	Lys	Asn	Ile	Met	Leu
				260					265					270		
	Gly	His	Ala	Ser	Val	Gln	Ala	Glu	Met	Glu	Gln	Val	Val	Glu	Val	Tyr
			275					280					285			
	Glu	Tyr	Ala	Gln	Lys	Leu	Gly	Gly	Glu	Ala	Gly	Phe	Tyr	His	Ile	Leu
		290					295					300				
	Asn	Asn	Pro	Lys	Ala	Ser	Leu	Leu	Ser	Leu	Thr	Gln	Phe	Pro	Asn	Phe
						310					315				320	
	Ser	Ser	Val	Val	Leu	Gly	Asn	Ala	Ala	Gly	Leu	Gly	Ile	Met	Gly	Glu
					325					330					335	
	Tyr	Arg	Gly	Thr	Pro	Arg	Asn	Gln	Asp	Leu	Tyr	Asp	Ala	Ala	Lys	Ala
				340					345					350		
	Tyr	Ala	Glu	Gln	Leu	Lys	Glu	Asn	Gly	Val	Ile	Asn	Tyr	Ser	Val	Leu
			355					360					365			
	Asp	Leu	Thr	Ala	Glu	Glu	Leu	Glu	Ala	Ile	Lys	His	Gln	Leu	Asn	Pro
		370					375				380					
	Lys	Glu	Asp	Asp	Val	Glu	Leu									
						390										
	385															

<210> 278
 <211> 391
 <212> PRT
 <213> Human respiratory syncytial virus

<400>	278														
Met	Ala	Leu	Ser	Lys	Val	Lys	Leu	Asn	Asp	Thr	Leu	Asn	Lys	Asp	Gln
1				5				10						15	
Leu	Leu	Ser	Ser	Ser	Lys	Tyr	Thr	Ile	Gln	Arg	Ser	Thr	Gly	Asp	Ser
			20					25					30		
Ile	Asp	Thr	Pro	Asn	Tyr	Asp	Val	Gln	Lys	His	Ile	Asn	Lys	Leu	Cys
		35					40					45			
Gly	Met	Leu	Leu	Ile	Thr	Glu	Asp	Ala	Asn	His	Lys	Phe	Thr	Gly	Leu
	50					55					60				
Ile	Gly	Met	Leu	Tyr	Ala	Met	Ser	Arg	Leu	Gly	Arg	Glu	Asp	Thr	Ile
	65				70					75				80	
Lys	Ile	Leu	Arg	Asp	Ala	Gly	Tyr	His	Val	Lys	Ala	Asn	Gly	Val	Asp
				85					90					95	
Val	Thr	Thr	His	Arg	Gln	Asp	Ile	Asn	Gly	Lys	Glu	Met	Lys	Phe	Glu
			100					105					110		
Val	Leu	Thr	Leu	Ser	Ser	Leu	Thr	Thr	Glu	Ile	Gln	Ile	Asn	Ile	Glu
		115					120					125			
Ile	Glu	Ser	Arg	Lys	Ser	Tyr	Lys	Lys	Met	Leu	Lys	Glu	Met	Gly	Glu
	130					135					140				
Val	Ala	Pro	Glu	Tyr	Arg	His	Asp	Ser	Pro	Asp	Cys	Gly	Met	Ile	Ile

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

<210> 279

<211> 241

<212> PRT

<213> Human respiratory syncytial virus

<400> 279

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

225
Phe

230

235

240

<210> 280
<211> 256
<212> PRT
<213> Human respiratory syncytial virus

<400> 280
Met Glu Thr Tyr Val Asn Lys Leu His Glu Gly Ser Thr Tyr Thr Ala
1 5 10 15
Ala Val Gln Tyr Asn Val Leu Glu Lys Asp Asp Asp Pro Ala Ser Leu
20 25 30
Thr Ile Trp Val Pro Met Phe Gln Ser Ser Met Pro Ala Asp Leu Leu
35 40 45
Ile Lys Glu Leu Ala Asn Val Asn Ile Leu Val Lys Gln Ile Ser Thr
50 55 60
Pro Lys Gly Pro Ser Leu Arg Val Met Ile Asn Ser Arg Ser Ala Val
65 70 75 80
Leu Ala Gln Met Pro Ser Lys Phe Thr Ile Cys Ala Asn Val Ser Leu
85 90 95
Asp Glu Arg Ser Lys Leu Ala Tyr Asp Val Thr Thr Pro Cys Glu Ile
100 105 110
Lys Ala Cys Ser Leu Thr Cys Leu Lys Ser Lys Asn Met Leu Thr Thr
115 120 125
Val Lys Asp Leu Thr Met Lys Thr Leu Asn Pro Thr His Asp Ile Ile
130 135 140
Ala Leu Cys Glu Phe Glu Asn Ile Val Thr Ser Lys Lys Val Ile Ile
145 150 155 160
Pro Thr Tyr Leu Arg Ser Ile Ser Val Arg Asn Lys Asp Leu Asn Thr
165 170 175
Leu Glu Asn Ile Thr Thr Thr Glu Phe Lys Asn Ala Ile Thr Asn Ala
180 185 190
Lys Ile Ile Pro Tyr Ser Gly Leu Leu Val Ile Thr Val Thr Asp
195 200 205
Asn Lys Gly Ala Phe Lys Tyr Ile Lys Pro Gln Ser Gln Phe Ile Val
210 215 220
Asp Leu Gly Ala Tyr Leu Glu Lys Glu Ser Ile Tyr Tyr Val Thr Thr
225 230 235 240
Asn Trp Lys His Thr Ala Thr Arg Phe Ala Ile Lys Pro Met Glu Asp
245 250 255

<210> 281
<211> 64
<212> PRT
<213> Human respiratory syncytial virus

<400> 281
Met Glu Asn Thr Ser Ile Thr Ile Glu Phe Ser Ser Lys Phe Trp Pro
1 5 10 15
Tyr Phe Thr Leu Ile His Met Ile Thr Thr Ile Ile Ser Leu Ile
20 25 30
Ile Ile Ser Ile Met Ile Ala Ile Leu Asn Lys Leu Cys Glu Tyr Asn
35 40 45
Ala Phe His Asn Lys Thr Phe Glu Leu Pro Arg Ala Arg Ile Asn Thr
50 55 60

<210> 282
<211> 574
<212> PRT
<213> Human respiratory syncytial virus

<220>

<400> 282

Met	Glu	Leu	Pro	Ile	Leu	Lys	Ala	Asn	Ala	Ile	Thr	Thr	Ile	Leu	Ala
1				5				10					15		
Ala	Val	Thr	Leu	Cys	Phe	Val	Ser	Ser	Gln	Asn	Ile	Thr	Glu	Phe	
			20					25					30		
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu
		35					40					45			
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile
	50					55					60				
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85				90						95	
Met	Gln	Ser	Thr	Pro	Ala	Ala	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100					105					110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Thr	Lys	Asn	Thr	Asn	Val	Thr
		115					120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Phe	Leu	Gly	Phe	Leu	Leu	Gly	Val
	130					135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Ile	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150				155						160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
		195					200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
	210					215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265					270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280						285		
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
	290					295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
		355					360					365			
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Asn	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	His	Asn	Val	Asn	Ala	Gly	Lys	Ser	Thr	Thr	Asn	Ile	Met	Ile	Thr
		515					520					525			
Thr	Ile	Ile	Ile	Val	Ile	Ile	Val	Ile	Leu	Leu	Ser	Leu	Ile	Ala	Val

530 535 540
 Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
 545 550 555 560
 Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Ser
 565 570

<210> 283
 <211> 83
 <212> PRT
 <213> Human respiratory syncytial virus

<400> 283
 Lys Arg Asp Pro Lys Thr Pro Ala Lys Met Leu Asn Lys Glu Thr Thr
 1 5 10 15
 Thr Asn Pro Thr Lys Asn Leu Thr Leu Lys Thr Thr Glu Arg Asp Thr
 20 25 30
 Ser Thr Ser Gln Ser Thr Val Leu Asp Thr Ser Thr Ser Lys His Ile
 35 40 45
 Ile Leu Gln Gln Ser Leu His Ser Thr Thr Pro Glu Asn Thr Pro Asn
 50 55 60
 Phe Thr Gln Thr Pro Thr Ala Ser Glu Pro Ser Thr Ser Asn Ser Thr
 65 70 75 80
 Gln Lys Thr

<210> 284
 <211> 21
 <212> PRT
 <213> Bufo gargarizans

<220>
 <223> Asian toad Buforin II

<400> 284
 Thr Arg Ser Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His
 1 5 10 15
 Arg Leu Leu Arg Lys
 20

<210> 285
 <211> 16
 <212> PRT
 <213> Homo sapiens

<220>
 <223> DPV3

<400> 285
 Arg Lys Lys Arg Arg Arg Glu Ser Arg Lys Lys Arg Arg Arg Glu Ser
 1 5 10 15

<210> 286
 <211> 17
 <212> PRT
 <213> Homo sapiens

<220>
 <223> DPV6

<400> 286
 Gly Arg Pro Arg Glu Ser Gly Lys Lys Arg Lys Arg Lys Arg Leu Lys
 1 5 10 15
 Pro

<210> 287
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<223> DPV7

<400> 287
Gly Lys Arg Lys Lys Lys Gly Lys Leu Gly Lys Lys Arg Asp Pro
1 5 10 15

<210> 288
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<223> DPV7b

<400> 288
Gly Lys Arg Lys Lys Lys Gly Lys Leu Gly Lys Lys Arg Pro Arg Ser
1 5 10 15
Arg

<210> 289
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> DPV3/10

<400> 289
Arg Lys Lys Arg Arg Arg Glu Ser Arg Arg Ala Arg Arg Ser Pro Arg
1 5 10 15
His Leu

<210> 290
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> DPV10/6

<400> 290
Ser Arg Arg Ala Arg Arg Ser Pro Arg Glu Ser Gly Lys Lys Arg Lys
1 5 10 15
Arg Lys Arg

<210> 291
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<223> DPV1047

<400> 291
Val Lys Arg Gly Leu Lys Leu Arg His Val Arg Pro Arg Val Thr Arg
1 5 10 15
Met Asp Val

<210> 292
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> DPV1048

<400> 292
Val Lys Arg Gly Leu Lys Leu Arg His Val Arg Pro Arg Val Thr Arg
1 5 10 15
Asp Val

<210> 293
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<223> DPV10

<400> 293
Ser Arg Arg Ala Arg Arg Ser Pro Arg His Leu Gly Ser Gly
1 5 10

<210> 294
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> DPV15

<400> 294
Leu Arg Arg Glu Arg Gln Ser Arg Leu Arg Arg Glu Arg Gln Ser Arg
1 5 10 15

<210> 295
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<223> DPV15b

<400> 295
Gly Ala Tyr Asp Leu Arg Arg Arg Glu Arg Gln Ser Arg Leu Arg Arg
1 5 10 15
Arg Glu Arg Gln Ser Arg
20

<210> 296
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> GALA

<400> 296
Trp Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala Glu His
1 5 10 15
Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
20 25 30

<210> 297
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<223> Human fibrinogen beta chain

<400> 297
Lys Gly Ser Trp Tyr Ser Met Arg Lys Met Ser Met Lys Ile Arg Pro
1 5 10 15
Phe Phe Pro Gln Gln
20

<210> 298
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<223> Human fibrinogen gamma chain precursor

<400> 298
Lys Thr Arg Tyr Tyr Ser Met Lys Lys Thr Thr Met Lys Ile Ile Pro
1 5 10 15
Phe Asn Arg Leu
20

<210> 299
<211> 20
<212> PRT
<213> Artificial sequence

<220>
<223> Human fibrinogen alpha chain

<400> 299
Arg Gly Ala Asp Tyr Ser Leu Arg Ala Val Arg Met Lys Ile Arg Pro
1 5 10 15
Leu Val Thr Gln
20

<210> 300
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<223> Human hCT (9-32)

<400> 300
Leu Gly Thr Tyr Thr Gln Asp Phe Asn Lys Phe His Thr Phe Pro Gln
1 5 10 15
Thr Ala Ile Gly Val Gly Ala Pro
20

<210> 301
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HN-1

<400> 301
Thr Ser Pro Leu Asn Ile His Asn Gly Gln Lys Leu
1 5 10

<210> 302
<211> 12
<212> PRT
<213> Influenza virus

<220>
<223> Influenza virus nucleoprotein (NLS)

<400> 302
Asn Ser Ala Ala Phe Glu Asp Leu Arg Val Leu Ser
1 5 10

<210> 303
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> KALA

<400> 303
Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala Leu Ala Lys His
1 5 10 15
Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Ala Cys Glu Ala
20 25 30

<210> 304
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Ku70

<400> 304
Val Pro Met Leu Lys Pro Met Leu Lys Glu
1 5 10

<210> 305
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> MAP

<400> 305
Lys Leu Ala Leu Lys Leu Ala Leu Lys Ala Leu Lys Ala Ala Leu Lys
1 5 10 15
Leu Ala

<210> 306
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> MPG

<400> 306
Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly
1 5 10 15
Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
20 25

<210> 307
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<223> Human Fibroblast growth factor 4

<400> 307
Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

<210> 308
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> Human N50 (NLS of NF-kB P50)

<400> 308
Val Gln Arg Lys Arg Gln Lys Leu Met
1 5

<210> 309
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Pep-1

<400> 309
Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
1 5 10 15
Lys Lys Arg Lys Val
20

<210> 310
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Pep-7

<400> 310

Ser Asp Leu Trp Glu Met Met Met Val Ser Leu Ala Cys Gln Tyr
 1 5 10 15

<210> 311
 <211> 16
 <212> PRT
 <213> Drosophila antennapedia

<220>
 <223> Fruit Fly Penetratin

<400> 311
 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
 1 5 10 15

<210> 312
 <211> 17
 <212> PRT
 <213> Drosophila antennapedia

<220>
 <223> Fruit Fly Penetratin variant

<400> 312
 Gly Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys
 1 5 10 15
 Lys

<210> 313
 <211> 7
 <212> PRT
 <213> Drosophila antennapedia

<220>
 <223> Fruit Fly Short Penetratin

<400> 313
 Arg Arg Met Lys Trp Lys Lys
 1 5

<210> 314
 <211> 17
 <212> PRT
 <213> Drosophila antennapedia

<220>
 <223> Fruit Fly Penetratin 42-58

<400> 314
 Glu Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys
 1 5 10 15
 Lys

<210> 315
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Poly Arginine R7

<400> 315
Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 316
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Poly Arginine R9

<400> 316
Arg Arg Arg Arg Arg Arg Arg Arg
1 5

<210> 317
<211> 16
<212> PRT
<213> Rattus norvegicus

<220>
<223> Rat pISL

<400> 317
Arg Val Ile Arg Val Trp Phe Gln Asn Lys Arg Cys Lys Asp Lys Lys
1 5 10 15

<210> 318
<211> 28
<212> PRT
<213> Mus musculus

<220>
<223> Prion mouse PrPc1-28

<400> 318
Met Ala Asn Leu Gly Tyr Trp Leu Leu Ala Leu Phe Val Thr Met Trp
1 5 10 15
Thr Asp Val Gly Leu Cys Lys Lys Arg Pro Lys Pro
20 25

<210> 319
<211> 18
<212> PRT
<213> Mus musculus

<220>
<223> Mouse pVEC

<400> 319
Leu Leu Ile Ile Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala His
1 5 10 15
Ser Lys

<210> 320
<211> 16
<212> PRT
<213> Mus musculus

<220>
<223> Mouse pVEC variant

<400> 320
 Leu Leu Ile Ile Leu Arg Arg Arg Ile Arg Lys Gln Ala His Ala His
 1 5 10 15

<210> 321
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> SAP

<400> 321
 Val Arg Leu Pro Pro Pro Val Arg Leu Pro Pro Pro Val Arg Leu Pro
 1 5 10 15
 Pro Pro

<210> 322
 <211> 7
 <212> PRT
 <213> Simian virus

<220>
 <223> SV-40 (NLS)

<400> 322
 Pro Lys Lys Lys Arg Lys Val
 1 5

<210> 323
 <211> 18
 <212> PRT
 <213> Sus scrofa

<220>
 <223> Porcine SynB1

<400> 323
 Arg Gly Gly Arg Leu Ser Tyr Ser Arg Arg Arg Phe Ser Thr Ser Thr
 1 5 10 15
 Gly Arg

<210> 324
 <211> 10
 <212> PRT
 <213> Sus scrofa

<220>
 <223> Porcine SynB3

<400> 324
 Arg Arg Leu Ser Tyr Ser Arg Arg Arg Phe
 1 5 10

<210> 325
 <211> 17
 <212> PRT
 <213> Sus scrofa

<220>

<223> Porcine SynB4

<400> 325

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

<210> 326

<211> 14

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> HIV type I Tat 47-60

<400> 326

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
1 5 10

<210> 327

<211> 11

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> HIV type I Tat 47-57

<400> 327

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 328

<211> 10

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> HIV type I Tat 47-56

<400> 328

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg
1 5 10

<210> 329

<211> 9

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> HIV type I Tat 48-56

<400> 329

Gly Arg Lys Lys Arg Arg Gln Arg Arg
1 5

<210> 330

<211> 10

<212> PRT

<213> Human immunodeficiency virus

<220>

<223> HIV type I Tat 48-57

<400> 330
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 331
<211> 9
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 49-57

<400> 331
Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5

<210> 332
<211> 8
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 49-56

<400> 332
Arg Lys Lys Arg Arg Gln Arg Arg
1 5

<210> 333
<211> 13
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 48-60

<400> 333
Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln
1 5 10

<210> 334
<211> 5
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 48-52

<400> 334
Gly Arg Lys Lys Arg
1 5

<210> 335
<211> 36
<212> PRT
<213> Human immunodeficiency virus

<220>
<223> HIV type I Tat 37-72

<400> 335
Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
Page 125

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

<220>
<223> Transportan derivative

<400> 340
Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly
1 5 10

<210> 341
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Transportan derivative

<400> 341
Ile Asn Leu Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
1 5 10

<210> 342
<211> 34
<212> PRT
<213> Herpes simplex virus

<220>
<223> Herpes simplex virus 1 VP22

<400> 342
Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr
1 5 10 15
Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro
20 25 30
Val Asp

<210> 343
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> VT5

<400> 343
Asp Pro Lys Gly Asp Pro Lys Gly Val Thr Val Thr Val Thr Val Thr
1 5 10 15
Val Thr Gly Lys Gly Asp Pro Lys Pro Asp
20 25

<210> 344
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Signal sequence-based peptide

<400> 344
Gly Ala Leu Phe Leu Gly Trp Leu Gly Ala Ala Gly Ser Thr Met Gly
1 5 10 15

Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
20 25

<210> 345
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Amphiphilic model peptide

<400> 345
Lys Leu Ala Leu Lys Leu Ala Leu Lys Ala Leu Lys Ala Ala Leu Lys
1 5 10 15
Leu Ala

<210> 346
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Bacterial cell wall permeating

<400> 346
Lys Phe Phe Lys Phe Phe Lys Phe Phe Lys
1 5 10

<210> 347
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<223> Human LL-37

<400> 347
Leu Leu Gly Asp Phe Phe Arg Lys Ser Lys Glu Lys Ile Gly Lys Glu
1 5 10 15
Phe Lys Arg Ile Val Gln Arg Ile Lys Asp Phe Leu Arg Asn Leu Val
20 25 30
Pro Arg Thr Glu Ser
35

<210> 348
<211> 31
<212> PRT
<213> Sus scrofa

<220>
<223> Porcine cecropin P1

<400> 348
Ser Trp Leu Ser Lys Thr Ala Lys Lys Leu Glu Asn Ser Ala Lys Lys
1 5 10 15
Arg Ile Ser Glu Gly Ile Ala Ile Ala Ile Gln Gly Gly Pro Arg
20 25 30

<210> 349
<211> 30
<212> PRT
<213> Homo sapiens

<220>

<223> Human alpha defensin

<400> 349

Ala Cys Tyr Cys Arg Ile Pro Ala Cys Ile Ala Gly Glu Arg Arg Tyr
1 5 10 15
Gly Thr Cys Ile Tyr Gln Gly Arg Leu Trp Ala Phe Cys Cys
20 25 30

<210> 350

<211> 36

<212> PRT

<213> Homo sapiens

<220>

<223> Human beta defensin

<400> 350

Asp His Tyr Asn Cys Val Ser Ser Gly Gly Gln Cys Leu Tyr Ser Ala
1 5 10 15
Cys Pro Ile Phe Thr Lys Ile Gln Gly Thr Cys Tyr Arg Gly Lys Ala
20 25 30
Lys Cys Cys Lys
35

<210> 351

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Bactenecin

<400> 351

Arg Lys Cys Arg Ile Trp Ile Arg Val Cys Arg
1 5 10

<210> 352

<211> 42

<212> PRT

<213> Sus scrofa

<220>

<223> Porcine PR-39

<400> 352

Arg Arg Arg Pro Arg Pro Pro Tyr Leu Pro Arg Pro Arg Pro Pro Pro
1 5 10 15
Phe Phe Pro Pro Arg Leu Pro Pro Arg Ile Pro Pro Gly Phe Pro Pro
20 25 30
Arg Phe Pro Pro Arg Phe Pro Gly Lys Arg
35 40

<210> 353

<211> 13

<212> PRT

<213> Bos taurus

<220>

<223> Bovine Indolicidin

<400> 353

Ile Leu Pro Trp Lys Trp Pro Trp Trp Pro Trp Arg Arg

1 5 10

<210> 354
 <211> 27
 <212> PRT
 <213> Simian immunodeficiency virus

<220>
 <223> SIV MPS

<400> 354
 Gly Ala Leu Phe Leu Gly Trp Leu Gly Ala Ala Gly Ser Thr Met Gly
 1 5 10 15
 Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
 20 25

<210> 355
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pIs1

<400> 355
 Pro Val Ile Arg Arg Val Trp Phe Gln Asn Lys Arg Cys Lys Asp Lys
 1 5 10 15
 Lys

<210> 356
 <211> 330
 <212> PRT
 <213> Homo sapiens

<220>
 <223> hIgG1 heavy chain constant

<400> 356
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 1 5 10 15
 Ser Thr Ser 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 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> 357
 <211> 326
 <212> PRT
 <213> Homo sapiens

<220>
 <223> hIgG2 heavy chain constant

<400> 357

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
1				5				10						15	
Ser	Thr	Ser	Glu	Ser	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	Asn	Phe	Gly	Thr	Gln	Thr
65					70					75					80
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85					90						95	
Thr	Val	Glu	Arg	Lys	Cys	Cys	Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro
			100					105					110		
Pro	Val	Ala	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
		115					120					125			
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
	130					135					140				
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly
145					150					155					160
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn
				165					170					175	
Ser	Thr	Phe	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Val	His	Gln	Asp	Trp
			180					185					190		
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro
		195					200					205			
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Gln	Pro	Arg	Glu
	210					215					220				
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn
225					230					235					240
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
				245					250					255	
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr
			260				265						270		
Thr	Pro	Pro	Met	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys
		275					280					285			
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys
	290					295					300				
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
305					310					315					320
Ser	Leu	Ser	Pro	Gly	Lys										

<210> 358
 <211> 377
 <212> PRT
 <213> Homo sapiens

<220>
 <223> hIgG3 heavy chain constant

<400> 358
 Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 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
 Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
 100 105 110
 Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
 115 120 125
 Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
 130 135 140
 Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
 145 150 155
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 165 170 175
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 180 185 190
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
 195 200 205
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 210 215 220
 Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
 225 230 235
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 245 250 255
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
 260 265 270
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
 275 280 285
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 290 295 300
 Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
 305 310 315
 Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
 325 330 335
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
 340 345 350
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
 355 360 365
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 370 375

<210> 359
 <211> 327
 <212> PRT
 <213> Artificial Sequence

<220>

<223> hIgG4 heavy chain constant

<400> 359

Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
1				5				10					15		
Ser	Thr	Ser	Glu	Ser	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	Lys	Thr
65					70				75					80	
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85					90						95	
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro
			100					105					110		
Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys
		115					120					125			
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val
	130					135					140				
Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp
145					150				155					160	
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe
				165					170					175	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp
			180					185					190		
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu
		195					200					205			
Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
	210					215					220				
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys
225					230					235				240	
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
				245					250					255	
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
			260					265					270		
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
		275					280					285			
Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser
	290					295					300				
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
305					310					315					320
Leu	Ser	Leu	Ser	Leu	Gly	Lys									
				325											

<210> 360

<211> 231

<212> PRT

<213> Artificial sequence

<220>

<223> hIgG1 Fc

<400> 360

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

Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu
			100					105					110		
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg
		115					120					125			
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys
	130					135					140				
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp
145					150					155					160
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys
				165					170					175	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser
			180					185					190		
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser
		195					200					205			
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
	210					215					220				
Leu	Ser	Leu	Ser	Pro	Gly	Lys									
225					230										

<210> 361
 <211> 232
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> hIgG1 Fc

<400>	361														
Glu	Pro	Arg	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala
1				5					10					15	
Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
			20					25					30		
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
	50					55					60				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
65					70					75					80
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
				85					90					95	
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
			100					105					110		
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120					125			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
	130					135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg
145					150					155					160
His	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
				165					170					175	
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
			180					185					190		
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195					200					205			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
	210					215					220				
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
225					230										

<210> 362
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv6/11/21/22/23 Heavy chain

<400> 362
 Gln Val Lys Leu Leu Glu Gln Ser Gly Gly Gly Leu Val Gln Pro Gly
 1 5 10 15
 Gly Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Val Thr Phe Ser Ala
 20 25 30
 Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 Val Ser Gly Ile Ser Gly Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser
 50 55 60
 Val Lys Gly Arg Leu Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 65 70 75 80
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr
 85 90 95
 Cys Ala Ser His Leu Pro Asp Tyr Trp Asn Leu Asp Tyr Thr Arg Phe
 100 105 110
 Phe Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
 115 120 125
 Ser

<210> 363
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv6/11/21/22/23 Heavy CDR1

<400> 363
 Ala Tyr Ala Met Ser
 1 5

<210> 364
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv6/11/21/22/23 Heavy CDR2

<400> 364
 Gly Ile Ser Gly Ser Gly Asp Ser Thr Asp Tyr Ala Asp Ser Val Lys
 1 5 10 15
 Gly

<210> 365
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv6/11/21/22/23 Heavy CDR3

<400> 365
 His Leu Pro Asp Tyr Trp Asn Leu Asp Tyr Thr Arg Phe Phe Tyr Tyr
 1 5 10 15
 Met Asp Val

<210> 366
 <211> 120
 <212> PRT

<213> Artificial Sequence

<220>

<223> Rsv13/19H Heavy chain

<400> 366

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

<210> 367

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv13/19H Heavy CDR1

<400> 367

Gly	Tyr	Thr	Met	His
1				5

<210> 368

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv13/19H Heavy CDR2

<400> 368

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

<210> 369

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv13/19H Heavy CDR3

<400> 369

Ala	Pro	Ile	Ala	Pro	Tyr	Phe	Asp	His
1				5				10

<210> 370

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv 6/11/21/22 Light chain

<400> 370

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

<210> 371

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv 6/11/21/22 Light CDR1

<400> 371

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

<210> 372

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv 6/11/21/22 Light CDR2

<400> 372

```
Gly Ala Ser Asn Arg Ala Thr
 1          5
```

<210> 373

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv 6/11/21/22 Light CDR3

<400> 373

```
Gln Gln Tyr Asp Ile Ser Pro Tyr Thr
 1          5
```

<210> 374

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> Rsv23 Light Chain

<400> 374
 Met Ala Glu Leu Thr Gln Ser Pro Val Thr Leu Ser Val Ser Pro Gly
 1 5 10 15
 Glu Arg Val Ala Leu Ser Cys Lys Ala Ser Gln Asn Ile Asn Asp Asn
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Arg Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Gly Ser Pro Tyr
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr
 100 105

<210> 375
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv23 Light CDR1

<400> 375
 Lys Ala Ser Gln Asn Ile Asn Asp Asn Leu Ala
 1 5 10

<210> 376
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv23 Light CDR2

<400> 376
 Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 377
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv23 Light CDR3

<400> 377
 Gln Gln Tyr Gly Gly Ser Pro Tyr Thr
 1 5

<210> 378
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv13/19 Light Chain

<400> 378
 Met Ala Glu 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 Thr Gln Ser Val Ser Asn Phe
 20 25 30
 Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Thr Leu Leu Ile
 35 40 45
 Tyr Asp Ala Ser Thr Ser Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Met Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Leu Ala Met Tyr Tyr Cys Gln Ala Ser Ile Asn Thr Pro Leu
 85 90 95
 Phe Gly Gly Gly Thr Arg Ile Asp Met Arg Arg Thr
 100 105

<210> 379
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv13/19 Light CDR1

<400> 379
 Arg Ala Thr Gln Ser Val Ser Asn Phe Leu Asn
 1 5 10

<210> 380
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv13/19 Light CDR2

<400> 380
 Asp Ala Ser Thr Ser Gln Ser
 1 5

<210> 381
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Rsv13/19 Light CDR3

<400> 381
 Gln Ala Ser Ile Asn Thr Pro Leu
 1 5

<210> 382
 <211> 574
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Respiratory Syncytial Virus Strain A2 F protein

<400> 382
 Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
 1 5 10 15
 Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
 20 25 30
 Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
 35 40 45

Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile
	50					55					60				
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85					90					95	
Met	Gln	Ser	Thr	Pro	Pro	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100					105					110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
		115					120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Phe	Leu	Gly	Phe	Leu	Leu	Gly	Val
	130					135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150					155					160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
		195					200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
	210					215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn	
225					230				235					240	
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265							
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280					285			
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
	290					295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
		355					360					365			
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Ile	Asn	Leu	Cys	Asn	Val
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Met	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	His	Asn	Val	Asn	Ala	Gly	Lys	Ser	Thr	Thr	Asn	Ile	Met	Ile	Thr
		515					520					525			
Thr	Ile	Ile	Ile	Val	Ile	Ile	Val	Ile	Leu	Leu	Ser	Leu	Ile	Ala	Val
	530					535					540				
Gly	Leu	Leu	Leu	Tyr	Cys	Lys	Ala	Arg	Ser	Thr	Pro	Val	Thr	Leu	Ser
545					550				555						560
Lys	Asp	Gln	Leu	Ser	Gly	Ile	Asn	Asn	Ile	Ala	Phe	Ser	Asn		
				565					570						

<210> 383
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> VH-g1(a/b)-REV primer

 <400> 383
 acaagatttg ggctcaacty tcttgtcc 28

 <210> 384
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5'L vLambda 1 primer

 <400> 384
 ggtcctgggc ccagtctgtg ctg 23

 <210> 385
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5'L vLambda 2 primer

 <400> 385
 ggtcctgggc ccagtctgcc ctg 23

 <210> 386
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5'L vLambda 3 primer

 <400> 386
 gctctgtgac ctcctatgag ctg 23

 <210> 387
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5'L vLambda 4/5 primer

 <400> 387
 ggtctctctc scagcytgtg ctg 23

 <210> 388
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 5'L vLambda 6 primer

 <400> 388
 gttcttgggc caattttatg ctg 23

 <210> 389
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> 5' L vLambda 7 primer

<400> 389
ggtccaattc ycaggctgtg gtg 23

<210> 390
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' L vLambda 8 primer

<400> 390
gagtggattc tcagactgtg gtg 23

<210> 391
<211> 6822
<212> DNA
<213> Artificial Sequence

<220>
<223> 28d11/pCAL vector

<400> 391
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gttccgcgtt acataactta cggtaaatgg cccgcctggc tgaccgcccacgaccccccg 120
cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga ctttccattg 180
acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc aagtgtatca 240
tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgctt ggcattatgc 300
ccagtacatg accttatggg actttcctac ttggcagtag atctacgtat tagtcatcgc 360
tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc ggtttgactc 420
acgggggattt ccaagtcttc accccattga cgtcaatggg agtttgtttt ggcacaaaaa 480
tcaacgggac tttccaaaat gtcgtaacaa ctccgccccca ttgacgcaaa tgggcggtag 540
gcgtgtacgg tgggagggtc atataagcag agctgggtta gtgaaccgtc agatccgcta 600
gcgattacgc caagctcgaa attaaccctc actaaaggga acaaaagctg gagctccacc 660
cgggtggcgg ccgcccacca tggactggac ctggcggatc ctgttcctgg tggccgcggc 720
cacgggggac cacagccagc tgcagctgca ggagtcgggc ccaggactgg tgaaggtttc 780
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caaggggccc agcgtgttcc ccctggcccc cagcagcaag agcaccagcg gcggcaccgc 1560
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cagcctgagc agcgtggtga ccgtgccag cagcagcctg ggcacccaga cctacatctg 1740
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cctctccctg	tctccgggta	aacgggccaa	gcgggcaccc	gtgaagcaga	ccctgaactt	2520
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cggagggacc	aagctgaccg	tcctaagtca	gccccaggct	gccccctcgg	tcactctgtt	3000
cccgcctcc	tctgaggagc	ttcaagccaa	caaggccaca	ctggtgtgtc	tcataagtga	3060
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<220>
 <223> 30D8 Light Chain

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His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35     40     45
Asp Asp Arg Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50     55     60
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65     70     75     80
Asp Glu Ala Asp Tyr Cys Gln Val Trp Asp Ser Ser Arg Asp Gln
85     90     95
Ala Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100    105    110
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115    120    125
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130    135    140
Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Pro Val Lys Ala
145    150    155    160
Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165    170    175
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180    185    190
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195    200    205
Ile Ala Pro Thr Glu Cys
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<210> 396
 <211> 224
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 30D8 Fab Heavy Chain

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

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

<210> 398
 <211> 228
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 104E5 Fab Heavy Chain

<400> 398
Gln Val Gln Leu Glu Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser	Val	Lys	Val	Ser	Cys	Lys	Pro	Ser	Gly	Gly	Thr	Phe	Asp	Thr	Tyr
Thr	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Leu
Gly	Arg	Ile	Ile	Pro	Ser	Leu	Gly	Glu	Thr	Asn	Tyr	Ala	His	Lys	Leu
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ala	Thr	Ser	Val	Val	Tyr
Met	Asp	Leu	Ser	Asp	Leu	Thr	Ser	Glu	Asp	Ala	Ala	Val	Tyr	Tyr	Cys
Ala	Phe	Arg	Ile	Thr	Gly	Pro	Val	Asp	Trp	Val	Trp	Asp	Tyr	Gly	Met
Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Ser	Val	Ser	Ser	Ala	Ser	Ser
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu
Pro	Lys	Ser	Cys												

<210> 399
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 38F10 Light Chain

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

<210> 400
 <211> 227
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 38F10 Fab Heavy Chain

<400> 400
 Glu Val Gln Leu Leu Glu Ser Gly Gly Asp Val Val Gln Pro Gly Lys
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Ile Thr Asp Phe
 20 25 30
 Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Leu Ile Ser Tyr Asn Glu Val Asn Ile His Tyr Gly Glu Ser Val
 50 55 60
 Arg Gly Arg Phe Thr Ile Ser Arg Asp Ile Ala Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Asn Gly Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys
 85 90 95
 Ala Arg Asp Val Trp Glu Asp Ser Trp Leu Ser Leu Ala Cys Phe Gln
 100 105 110
 Glu Trp Gly Gln Gly Ser Leu Val Val Val Ser Ser Ala Ser Thr Lys
 115 120 125
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 165 170 175
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 180 185 190
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 195 200 205
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 210 215 220
 Lys Ser Cys
 225

<210> 401
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G3 Light Chain

<400> 401
 Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Asp Gly Asn Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Gln Leu Leu Ile Tyr Thr Leu Ser Tyr Arg Ala Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 65 70 75 80
 Ile Ser Arg Val Glu Ala Asp Asp Val Gly Ile Tyr Tyr Cys Met Gln
 85 90 95
 Arg Met Glu Phe Pro Phe Thr Phe Gly Gln Gly Thr Arg Leu Asp Ile
 100 105 110
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

<400> 403
Ala Ile Arg Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Phe
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Arg Ala Pro Lys Leu Leu Ile
Page 150

<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR1

<400> 405
Gly Phe Thr Phe Ser Gly His Thr Ile Ala
1 5 10

<210> 406
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR2

<400> 406
Trp Val Ser Thr Asn Asn Gly Asn Thr Glu Tyr Ala Gln Lys Ile Gln
1 5 10 15
Gly

<210> 407
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VH CDR3

<400> 407
Glu Trp Leu Val Met Gly Gly Phe Ala Phe Asp His
1 5 10

<210> 408
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VL CDR1

<400> 408
Gly Ala Asn Asn Ile Gly Ser Gln Asn Val His
1 5 10

<210> 409
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 30D8 VL CDR2

<400> 409
Asp Asp Arg Asp Arg Pro Ser
1 5

<210> 410
<211> 12
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<213> Artificial Sequence

<220>

<223> 30D8 VL CDR3

<400> 410

Gln Val Trp Asp Ser Ser Arg Asp Gln Ala Val Ile
1 5 10

<210> 411

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 104E5 VH CDR1

<400> 411

Gly Gly Thr Phe Asp Thr Tyr Thr Ile Ser
1 5 10

<210> 412

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> 104E5 VH CDR2

<400> 412

Arg Ile Ile Pro Ser Leu Gly Glu Thr Asn Tyr Ala His Lys Leu Gln
1 5 10 15
Gly

<210> 413

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 104E5 VH CDR3

<400> 413

Arg Ile Thr Gly Pro Val Asp Trp Val Trp Asp Tyr Gly Met Asp Val
1 5 10 15

<210> 414

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 104E5 VL CDR1

<400> 414

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

<210> 415

<211> 7

<212> PRT

<213> Artificial Sequence

<220>
<223> 104E5 VL CDR2

<400> 415
Ala Val Ser Asn Leu Gln Ser
1 5

<210> 416
<211> 9
<212> PRT
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<220>
<223> 104E5 VL CDR3

<400> 416
Gln Gln Ser Phe Ser Ile Pro Leu Thr
1 5

<210> 417
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR1

<400> 417
Gly Phe Ser Ile Thr Asp Phe Gly Ile His
1 5 10

<210> 418
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR2

<400> 418
Leu Ile Ser Tyr Asn Glu Val Asn Ile His Tyr Gly Glu Ser Val Arg
1 5 10 15
Gly

<210> 419
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR3

<400> 419
Asp Val Trp Glu Asp Ser Trp Leu Ser Leu Ala Cys Phe Gln Glu
1 5 10 15

<210> 420
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
 <223> 38F10 VL CDR1
 <400> 420
 Arg Ala Ser Gln Ser Ile Ser Asn Trp Leu Ala
 1 5 10

<210> 421
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<220>
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 <400> 421
 Lys Ala Ser Asn Leu Glu Asp
 1 5

<210> 422
 <211> 10
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<220>
 <223> 38F10 VL CDR3
 <400> 422
 Gln Gln Tyr Asn Ser Tyr Ser Gly Leu Ser
 1 5 10

<210> 423
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<220>
 <223> 14G3 VH CDR1
 <400> 423
 Gly Ala Ser Ile Ser Ser Asp Asn His Tyr Trp Ser
 1 5 10

<210> 424
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G3 VH CDR2
 <400> 424
 Ser Ile Tyr Tyr Thr Gly Gly Thr Asn Tyr Asn Pro Ser Leu Lys Ser
 1 5 10 15

<210> 425
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 14G3 VH CDR3

<400> 425
Gly Leu Phe Phe Ile Thr Ala Arg Pro Tyr Trp Tyr Phe Asp Leu
1 5 10 15

<210> 426
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VL CDR1

<400> 426
Arg Ser Ser Gln Ser Leu Leu Asp Ser Asp Asp Gly Asn Thr Tyr Leu
1 5 10 15
Asp

<210> 427
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VL CDR2

<400> 427
Thr Leu Ser Tyr Arg Ala Ser
1 5

<210> 428
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VL CDR3

<400> 428
Met Gln Arg Met Glu Phe Pro Phe Thr
1 5

<210> 429
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 90D3 VH CDR1

<400> 429
Gly Phe Thr Leu Lys Asn Tyr Glu Met Asn
1 5 10

<210> 430
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 90D3 VH CDR2

<400> 430

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

<210> 431
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 90D3 VH CDR3

<400> 431
 Gly Phe Ser Ile Asp Lys Tyr Asp Ser Ser Val Asp Glu Tyr
 1 5 10

<210> 432
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 90D3 VL CDR1

<400> 432
 Arg Ala Ser Gln Ser Ile Ser Asn Phe Leu Asn
 1 5 10

<210> 433
 <211> 7
 <212> PRT
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<220>
 <223> 90D3 VL CDR2

<400> 433
 Ala Ala Ser Ser Leu Gln Gly
 1 5

<210> 434
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 90D3 VL CDR3

<400> 434
 Gln Gln Thr Tyr Ile Ser Leu Tyr Thr
 1 5

<210> 435
 <211> 7
 <212> PRT
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<220>
 <223> 58c5 VH CDR1

<400> 435
 Ser Asp Asn Tyr Tyr Trp Thr

1 5

<210> 436
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> sc5 VH CDR1

<400> 436
Gly Ser Asn Trp Trp Asn
1 5

<210> 437
<211> 5
<212> PRT
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<220>
<223> 30D8 VH CDR1

<400> 437
Gly His Thr Ile Ala
1 5

<210> 438
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 104E5 VH CDR1

<400> 438
Thr Tyr Thr Ile Ser
1 5

<210> 439
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 38F10 VH CDR1

<400> 439
Asp Phe Gly Ile His
1 5

<210> 440
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 14G3 VH CDR1

<400> 440
Ser Asp Asn His Tyr Trp Ser
1 5

<210> 441
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 90D3 VH CDR1

<400> 441
Asn Tyr Glu Met Asn
1 5

<210> 442
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 30D8 Light Chain

<400> 442
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caggccccctg ttttggtcgt ctatgatgat cgcgaccggc cctcagggat ccctgaccga 180
ttctctggct ccaactcttg gaatacggcc accctgacca tcagcagggt cgaggccggg 240
gatgaggccg actattactg tcagggtgtg gatagtagtc gtgatcaggc cgtaattttt 300
ggcggaggga ccaagctgac cgtcctaggc cagcccaagg ctgccccctc ggtcactctg 360
ttcccgccct cctctgagga gcttcaagcc aacaaggcca cactgggtgtg tctcataagt 420
gacttctacc cgggagccgt gacagtggcc tggaaggcag atagcagccc cgtcaaggcg 480
ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctac 540
ctgagcctga cgcctgagca gtggaagtcc cacagaagct acagctgcca ggtcacgcat 600
gaagggagca ccgtggagaa gacaattgcc cctacagaat gctca 645

<210> 443
<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> 30D8 Fab Heavy Chain

<400> 443
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tcctgcaaga cttctggttt caccttttagc ggtcatacta tcgcctgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggttgg gtcagcacta ataattgaaa cacagagtat 180
gcacagaaga tccagggcag agtcaccatg actatggaca catcaacgag cacagtctac 240
atggagttga ggagcctgac atctgacgac acggccgtgt atttctgtgc gagagagtgg 300
ctggctcatg ggggcttcgc ctttgaccac tggggccagg gaaccctgct caccgtctcc 360
tcagcctcca ccaagggccc atcggctctc cccctggcac cctcctccaa gagcacctct 420
ggggggcacag cggccctggg ctgcctgggt aaggactact tccccgaacc ggtgacgggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggctgt cctacagtcc 540
tcaggactct actccctcag cagcgtgggt accgtgccct ccagcagctt gggcaccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gagagttgag 660
cccaaattctt gt 672

<210> 444
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> 104E5 Light Chain

<400> 444
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atcacttgcc gggcaagtca gaacattaag acctatttaa attggtatca gcagaaacca 120
gggagagccc ctaaaactct gatctctgct gtgtccaatt taaaaagtgg ggtccccgtca 180

aggttcagtg	gcaccggatc	tgggacagat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagattttg	caacttacta	ctgtcagcag	agtttcagta	ttccgctcac	tttcggcgga	300
ggggccaagg	tggagatcaa	acgaactgtg	gctgcaccat	ctgtcttcat	cttcccgcga	360
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cccagagagg	ccaaagtaca	gtggaagggtg	gataacgccc	tccaatcggg	taactcccag	480
gagagtgtca	cagagcagga	cagcaaggac	agcacctaca	gcctcagcag	caccctgacg	540
ctgagcaaag	cagactacga	gaaacacaaa	ctctacgcct	gcgaagtcac	ccatcagggc	600
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<210> 445

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> 104E5 Fab Heavy Chain

<400> 445

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cctggacaac	gtcttgagtg	gctgggaagg	atcatccctt	cacttggtga	aacaaactat	180
gcacacaaac	tccagggcag	agtcacgatt	accgcggaca	aagccacgag	tgtcgtctat	240
atggacctga	gcgacctgac	atccgaggac	gcggccgtct	attactgtgc	atttcgtata	300
actggacctg	tcgactgggt	ctgggactat	gggatggacg	tctggggcca	agggaccacg	360
gtcagcgtct	cgtcagcctc	cagcaagggc	ccatcggtct	tccccctggc	accctcctcc	420
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ccggtgacgg	tgctcgtgaa	ctcaggcgcc	ctgaccagcg	gcgtgcacac	cttccccggt	540
gtcctacagt	cctcaggact	ctactccctc	agcagcgtgg	tgaccgtgcc	ctccagcagc	600
ttgggcaccc	agacctacat	ctgcaacgtg	aatcacaagc	ccagcaacac	caagggtggac	660
aagagagttg	agcccaaatc	ttgt				684

<210> 446

<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> 38F10 Light Chain

<400> 446

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tggtatcagc	aaaaaccagg	gaaagcccct	aaactcctca	tccagaaggc	gtccaattta	180
gaagatggcg	tcccctcacg	gttcaccgcc	agtggatttg	ggacagaatt	cactctcacc	240
atcagcagcc	tacagcctga	tgatttcgca	acttattact	gtcaacagta	taatagttac	300
tcaggccctca	gtttcggcgg	agggaccaag	gtggacatca	aacgaactgt	ggctgcacca	360
tctgtcttca	tcttcccggc	atctgatgag	cagttgaaat	ctggaactgc	ctctgtttgtg	420
tgcttctgta	ataacttcta	tcccagagag	gccaaagtac	agtgggaagg	ggataacgcc	480
ctccaatcgg	gtaactccca	ggagagtgtc	acagagcagg	acagcaagga	cagcacctac	540
agcctcagca	gcaccctgac	gctgagcaaa	gcagactacg	agaaacacaa	agtctacgcc	600
tgcgaagtca	cccatacagg	cctgagctcg	cccgtcacaa	agagcttcaa	caggggagag	660
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<210> 447

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> 38F10 Fab Heavy Chain

<400> 447

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cgccaggctc	caggcaaggg	gctggagtgg	gtggccctta	ttcatataaa	cgaagtaaat	180
atacactatg	gcgagtccgt	gaggggcccgc	ttcaccatct	ccagagacat	tgccaagaac	240
acagtatatc	tgagatgaa	tggcctgaga	cctgaagaca	cgggtgtgta	tttttgtgcg	300
agggatgtct	gggaggactc	gtggctgtca	cttgctgtct	tccaggaatg	gggccagggc	360

tccctggtcg	tcgtctcatc	agcctccacc	aagggcccat	cggtcttccc	cctggcaccc	420
tcctccaaga	gcacctctgg	gggcacagcg	gccctgggct	gcctgggtcaa	ggactacttc	480
cccgaaccgg	tgacgggtgtc	gtggaactca	ggcgccctga	ccagcggcgt	gcacaccttc	540
ccggctgtcc	tacagtcctc	aggactctac	tccctcagca	gcgtggtgac	cgtgccctcc	600
agcagcttgg	gcacccagac	ctacatctgc	aacgtgaatc	acaagcccag	caacaccaag	660
gtggacaaga	aagttgagcc	caaatcttgt	ggtcggccag	gccggccgca	ccatcaccat	720
cacat						726

<210> 448
 <211> 663
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 14G3 Light Chain

<400> 448						
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tggtacctgc	agaagccagg	gcagtctcca	cagctcctga	tctatacact	ttcctatcgg	180
gcctctggag	tcccagacag	gttcagtggc	agtgggtcag	gcactgattt	cacactgaaa	240
atcagcaggg	tggaggctga	cgatgttggg	atttattact	gcattgcaacg	tatggagttt	300
cccttcacct	tcgggcaagg	gacacgactg	gacattaaac	gaactgtggc	tgaccatct	360
gtcttcatct	tcccgccatc	tgatgagcag	ttgaaatctg	gaactgcctc	tgttgtgtgc	420
ctgctgaata	acttctatcc	cagagaggcc	aaagtacagt	ggaagggtgga	taacgccctc	480
caatcgggta	actcccagga	gagtgtcaca	gagcaggaca	gcaaggacag	cacctacagc	540
ctcagcagca	ccctgacgct	gagcaaagca	gactacgaga	aacacaaagt	ctacgcctgc	600
gaagtcaccc	atcagggcct	gagctcgccc	gtcacaaga	gcttcaacag	gggagagtgc	660
taa						663

<210> 449
 <211> 684
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 14G3 Fab Heavy Chain

<400> 449						
caggtgcagc	tgcaggagtc	gggcccagga	ctggtgaagc	cttcacagac	cctgtcccctc	60
acctgcactg	tctctggtgc	ctccatcagc	agtgataatc	actactggag	ttggattcga	120
cagccccccg	ggaagggcct	ggagtggatt	gcttccatct	attacactgg	tggcaccaac	180
tacaaccctg	ccctcaagag	tcgactcgcc	ttatcaatag	acacgtccgg	ggaccagttc	240
tccttgaagc	tgagctctgt	gactgccgca	gacacggccg	tctattactg	tgtcaggggc	300
ttgtttttca	taacagctcg	tccctactgg	tacttcgatc	tctggggccg	tggcaccctg	360
gtcgctgtct	ctcagcctc	caccaaggcg	ccatcggtct	tccccctggc	accctcctcc	420
aagagcacct	ctggggggcac	agcggccctg	ggctgcctgg	tcaaggacta	cttccccgaa	480
ccggtgacgg	tgtcgtggaa	ctcaggcgcc	ctgaccagcg	gcgtgcacac	cttcccggct	540
gtcctacagt	cctcaggact	ctactccctc	agcagcgtgg	tgaccgtgcc	ctccagcagc	600
ttgggcaccc	agacctacat	ctgcaacgtg	aatcacaagc	ccagcaacac	caaggtggac	660
aagagagtgtg	agcccaaatac	ttgt				684

<210> 450
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 90D3 Light Chain

<400> 450						
gccatccggg	tgacccagtc	tccatcctcc	ctgtctgcat	ctgtaggaga	cagagtcagc	60
atcacttgcc	gggcaagtca	gagtattagc	aactttttta	atgggtatca	gcagaaacca	120
gggagagccc	cgaaactcct	gatctctgct	gcatccagtt	tgcaagggtg	ggtcccatca	180
agattcagtg	gcagtggatc	tgggacagat	ttcactctca	ccatcagcag	tctgcaacct	240
gaagattttg	caacttacta	ctgtcaacag	acttacattt	ccctgtacac	ctttggccag	300
gggaccaaac	tggagatcaa	acgaactgtg	gctgcaccat	ctgtcttcat	cttcccgcga	360
tctgatgagc	agttgaaatc	tggaaactgcc	tctgtttgtg	gcctgctgaa	taacttctat	420

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cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

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<210> 451
<211> 723
<212> DNA
<213> Artificial Sequence

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<220>
<223> 90D3 Fab Light Chain

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<400> 451
gcgccgcac aggtgcagct ggtggagtcg gggggaggcc tggtaaagcc tggagggtcc 60
ctgagactct cgtgtgtagg ctctggattc accctcaaga attatgagat gaattgggtc 120
cgccaggctc cagggcaggg gctacaatat atttcataca tcagtagcag tggcaatgtc 180
gttaagtacg tagactctgt gcagggccga ttcaccatct ccagagacaa cgccgggaat 240
tcgctgtatc tccaaatgaa caacctgagg gccgaggaca cggccactta ttactgtgtg 300
agaggttttt cgatcgataa gtatgatagc agtgttgatg aatactgggg ccagggaatc 360
gcggtcacgc tctctcagc ctccaccaag ggcccatcgg tcttccccct ggcaccctcc 420
tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtaagga ctacttcccc 480
gaaccggtga cggtgtcgtg gaactcaggc gccctgacca gcggcgtgca caccttcccg 540
gctgtcctac agtcctcagg actctactcc ctcagcagcg tggtgaccgt gccctccagc 600
agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 660
gacaagaaag ttgagcccaa atcttgtggt cggccaggcc ggccgcacca tcaccatcac 720
cat 723

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<210> 452
<211> 227
<212> PRT
<213> Artificial Sequence

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<220>
<223> 56E11 Heavy Chain

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<400> 452
Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1      5      10      15
Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser Ile Asn Ser Asn
20      25      30
Asn Tyr Phe Trp Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35      40      45
Trp Ile Gly Asn Ile Tyr Tyr Gly Gly Ser Thr His Tyr Asn Ala Ser
50      55      60
Leu Gln Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Ser Gln Phe
65      70      75      80
Ser Leu Lys Leu Asn Ser Val Thr Ser Ala Asp Thr Ala Val Tyr Tyr
85      90      95
Cys Ala Ala Ser Glu Ser Ile Phe Trp Asp Tyr Tyr Tyr Gly Leu Asp
100     105     110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115     120     125
Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130     135     140
Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145     150     155     160
Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165     170     175
Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180     185     190
Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195     200     205
Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
210     215     220
Lys Ser Cys
225

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<210> 453
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 56E11 Light Chain

<400> 453
 Gln Ala Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Arg Leu
 35 40 45
 Ile Ile Ser Glu Val Thr Lys Arg Pro Ser Gly Val Pro Gly Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser
 85 90 95
 Arg His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Ile Ala Pro Ala Glu Cys Ser
 210 215

<210> 454
 <211> 236
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 17C9 Heavy Chain

<400> 454
 Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Val Arg Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Asp Ser Phe Asn Asp Tyr
 20 25 30
 Phe Trp Thr Trp Ile Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Ser His Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ala Val Thr Ala Ala Asp Thr Thr Val Tyr Phe Cys Ala
 85 90 95
 Arg Gly Val Arg Ser Arg Pro Pro Pro Ser Tyr Arg Gly Ser Gly Ser
 100 105 110
 Pro Pro Tyr Tyr His Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
 115 120 125
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 130 135 140
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys

145	Leu	Val	Lys	Asp	Tyr	150	Phe	Pro	Glu	Pro	Val	155	Thr	Val	Ser	Trp	Asn	160	Ser
	Gly	Ala	Leu	165	Thr	Ser	Gly	Val	His	Thr	170	Phe	Pro	Ala	Val	Leu	175	Gln	Ser
	Ser	Gly	Leu	180	Tyr	Ser	Leu	Ser	Ser	Val	185	Val	Thr	Val	Pro	Ser	Ser	Ser	
	Leu	Gly	195	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn		
	Thr	Lys	210	Val	Asp	Lys	Arg	215	Val	Glu	Pro	Lys	Ser	Cys					
225							230						235						

<210> 455
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 17C9 Light Chain

<400>	455																		
Glu	Ile	Val	Leu	5	Thr	Gln	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Ser	Val	Gly			
1	Asp	Arg	Val	20	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Asn	Ile	Asn	Thr	Trp		
	Leu	Ala	Trp	35	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile		
	Tyr	Ala	Ala	50	Ser	Phe	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly		
	Ser	Gly	Ser	65	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Leu	Gln	Pro		
	Glu	Asp	Phe	80	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Ala	Asn	Ser	Phe	Pro	Arg		
	Thr	Phe	Gly	95	Gln	Gly	Thr	Lys	Val	Glu	Val	Lys	Arg	Thr	Val	Ala	Ala		
	Pro	Ser	Val	110	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly		
	Thr	Ala	Ser	125	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala		
	Lys	Val	Gln	140	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln		
	Glu	Ser	Val	155	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser		
	Ser	Thr	Leu	170	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr		
	Ala	Cys	Glu	185	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser		
	Phe	Asn	Arg	200	Gly	Glu	Cys												
				210															

<210> 456
 <211> 221
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 69F6 Heavy Chain

<400>	456																		
Gln	Met	Gln	Leu	5	Val	Gln	Ser	Gly	Ala	Glu	Val	Arg	Lys	Pro	Gly	Glu			
1	Ser	Leu	Lys	20	Ile	Ala	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr		
	Trp	Ile	Ala	35	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Leu		
	Gly	Ile	Ile	40	Phe	Pro	Asn	Asp	Ser	Asp	Ala	Thr	Tyr	Ser	Pro	Ser	Phe		

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

<210> 457
 <211> 216
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 69F6 Light Chain

<400> 457	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1	Asp	Arg	Val	Thr	Ile	Ser	Cys	Gln	Ala	Ser	Gln	Asp	Ile	Ser	Asn	Tyr
	Leu	Asn	Trp	20	Gln	Gln	Lys	Pro	25	Gly	Lys	Ala	Pro	Arg	Leu	Ile
	Tyr	Asp	Ala	35	Ser	Tyr	Leu	Asp	40	Thr	Gly	Val	Pro	Ser	Arg	Phe
	50	Ser	Gly	Ser	Gly	Thr	Asp	Phe	55	Thr	Phe	Thr	Ile	60	Ser	Leu
	65	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	70	Cys	Gln	Gln	Tyr	75	Asp	Asp
	Gly	Phe	Thr	Phe	85	Gly	Pro	Gly	Thr	Lys	Val	Asp	Val	Lys	Arg	Thr
	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	100	Pro	Pro	Ser	Asp	Glu	Gln	Leu
	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	115	Leu	Leu	Asn	Asn	Phe	Tyr	Pro
	130	Glu	Ala	Lys	Val	Gln	Trp	Lys	120	Val	Asp	Asn	Ala	Gln	Ser	Gly
	145	Ser	Gln	Glu	Ser	Val	Thr	Glu	135	Gln	Asp	Ser	Lys	Asp	Ser	Thr
	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	150	Lys	Ala	Asp	Tyr	Glu	Lys	His
	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	165	Gln	Gly	Leu	Ser	Ser	Pro	Val
	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	180					205		
	210						215									

<210> 458
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 56E11 VH CDR1

<400> 458

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

<210> 459

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 56E11 VH CDR2

<400> 459

Asn Ile Tyr Tyr Gly Gly Ser Thr His Tyr Asn Ala Ser Leu Gln Ser
1 5 10 15

<210> 460

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 56E11 VH CDR3

<400> 460

Ser Glu Ser Ile Phe Trp Asp Tyr Tyr Tyr Gly Leu Asp Val
1 5 10

<210> 461

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> 56E11 VL CDR1

<400> 461

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 462

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> 56E11 VL CDR2

<400> 462

Glu Val Thr Lys Arg Pro Ser
1 5

<210> 463

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> 56E11 VL CDR3

<400> 463

Ser Ser Tyr Ala Gly Ser Arg His Val Val
1 5 10

<210> 464
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR1

<400> 464
Gly Asp Ser Phe Asn Asp Tyr Phe Trp Thr
1 5 10

<210> 465
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR2

<400> 465
Glu Ile Ser His Ser Gly Ser Thr Asn Tyr Ser Pro Ser Leu Lys Ser
1 5 10 15

<210> 466
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR3

<400> 466
Gly Val Arg Ser Arg Pro Pro Pro Ser Tyr Arg Gly Ser Gly Ser Pro
1 5 10 15
Pro Tyr Tyr His Tyr Gly Met Asp Val
20 25

<210> 467
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VL CDR1

<400> 467
Arg Ala Ser Gln Asn Ile Asn Thr Trp Leu Ala
1 5 10

<210> 468
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VL CDR2

<400> 468
Ala Ala Ser Phe Leu Gln Ser

1 5

<210> 469
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VL CDR3

<400> 469
Gln Gln Ala Asn Ser Phe Pro Arg Thr
1 5

<210> 470
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR1

<400> 470
Gly Tyr Ser Phe Thr Ser Tyr Trp Ile Ala
1 5 10

<210> 471
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR2

<400> 471
Ile Ile Phe Pro Asn Asp Ser Asp Ala Thr Tyr Ser Pro Ser Phe Gln
1 5 10 15
Gly

<210> 472
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR3

<400> 472
Gln Tyr Tyr Leu Gly Ser Phe Glu Ser
1 5

<210> 473
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VL CDR1

<400> 473
Gln Ala Ser Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 474
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 69F6 VL CDR2

<400> 474
 Asp Ala Ser Tyr Leu Asp Thr
 1 5

<210> 475
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 69F6 VL CDR3

<400> 475
 Gln Gln Tyr Asp Asp Leu Arg Gly Gly Phe Thr
 1 5 10

<210> 476
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 56E11 Light Chain

<400> 476
 caggctgtgc tgactcagcc tccctccgcg tccgggtctc ctggacagtc agtcaccatc 60
 tcctgcactg gaaccagcag tgacgttggg ggttataatt atgtctcctg gtaccaacaa 120
 caccgccgga aagccccag actcataatt tctgaagtca ctaagcggcc ctcaggggtc 180
 cctggtcgct tctccggctc caagtctggc aacacggcct ccctgaccgt ctctgggctc 240
 caggctgagg atgaggctga ttattactgc agctcatatg caggcagcag gcatgtggtt 300
 ttcggcgagg ggaccaagtt gaccgtcctc ggtcagccca aggctgcccc ctcggtcact 360
 ctgttcccgc cctcctctga ggagcttcaa gccaacaagg ccacactggg gtgtctcata 420
 agtgacttct acccgggagc cgtgacagtg gcctggaagg cagatagcag ccccgtaag 480
 tcgggagtg agaccaccac accctccaaa caaagcaaca acaagtacgc ggccagcagc 540
 tacctgagcc tgacgcctga gcagtggaa tccccagaa gctacagctg ccaggtcacg 600
 catgaaggga gcaccgtgga gaagacaatt gcccctgcag aatgctca 648

<210> 477
 <211> 681
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 56E11 Heavy Chain

<400> 477
 gaggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
 acctgcagtg tctctggtgt ctccatcaac agcaacaatt atttctgggc ctggatccgc 120
 cagccccag gcaaggggct ggagtggatt ggggaatatct attatgggtg gagcaccac 180
 tacaatgcgt ccctgcagag tcgagtcacc atatccgtag acacgtcaa gagccagttc 240
 tccctgaagc tgaactctgt gacctccgcc gacacggctg tgtattactg tgcggcttcc 300
 gagtctatct tttgggacta ctactacggc ctggacgtct ggggccaagg gaccacggtc 360
 accgtctcct ctgcctccac caagggccca tcggtcttcc ccctggcacc ctcctccaag 420
 agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaaccg 480
 gtgacgggtg cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540
 ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg 600

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ggcaccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660
aaagttgagc ccaaattcttg t 681

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<210> 478
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 17C9 Light Chain

```

<400> 478
gaaattgtgt tgaccagtc tccttcacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc ggccagtcga gaattattaat acctggttgg cctgggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatcctttt tgcaaagtgg ggtcccatca 180
aggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcaa cttgcagcct 240
gaagattttg caacttactt ttgtcaacag gctaacagtt tccttcggac cttcggccag 300
gggaccaagg tggaagtcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
cccagagagg ccaaagtaca gtggaagggt gataacgccc tccaatcggg taactcccag 480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

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<210> 479
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 17C9 Heavy Chain

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<400> 479
caggtacagc tgcagcagtg gggcgagga ctggtgaggc cttcggagac cctgtccctc 60
acctgcgctg tctatggtga ctccittcaat gattacttct ggacgtggat ccgccagacc 120
ccaggaaagg ggctggagtg gattggggaa atcagtcata gtggaagcac caactacagc 180
cagtcctcca agagtcgagt caccatatca gttgacacgt ccaagaacca gttctccctg 240
aaactcagcg ctgtgaccgc cgcggacacg actgtgtatt tctgtgcgag aggtgtccgc 300
tcccagaccc ctccgagtta ccgtggctcg ggctccccc cttactacca ttacggtatg 360
gacgtctggg gccaaaggac cacggtcacc gtctcctcag cctccaccaa gggcccctcg 420
gtcttccccc tggcaccctc ctccaagagc acctctgggg gcacagcggc cctgggctgc 480
ctggtcaagg actacttccc cgaaccggtg acggtgtcgt ggaactcagg cgccctgacc 540
agcggcgctg acaccttccc ggctgtccta cagtcctcag gactctactc cctcagcagc 600
gtggtgaccg tgccctccag cagcttgggc acccagacct acatctgcaa cgtgaatcac 660
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<210> 480
 <211> 648
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 69F6 Light Chain

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<400> 480
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gggaaagccc ctaggctcct gatctacgat gcatcctatt tgacacagag ggtcccatca 180
aggttcagtg gaagtggatc tgggacagat tttactttca ccatcagcag cctacagcct 240
gaagattttg caacatatta ctgtcaacaa tatgatgatc tccggggggg gttcactttc 300
ggccctggga ccaaagtggg cgtcaaacga actgtggctg caccatctgt cttcatcttc 360
ccgccatctg atgagcagtt gaaatctgga actgcctctg ttgtgtgcct gctgaataac 420
ttctatccca gagaggccaa agtacagtgg aagggtggata acgccctcca atcgggtaac 480
tcccagaga gtgtcacaga gcaggacagc aaggacagca cctacagcct cagcagacc 540
ctgacgctga gcaaagcaga ctacgagaaa cacaagctct acgcctgcga agtcacccat 600
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<210> 481

<211> 663
<212> DNA
<213> Artificial Sequence

<220>
<223> 69F6 Heavy Chain

<400> 481
cagatgcagc tgggtgcagtc tggagcagag gtgagaaagc cgggggagtc tctgaagatc 60
gcctgtaagg gttccggata cagttttacc agctactgga tcgcctgggt gcgccagatg 120
cccgggaaag gcctggaatg gctggggatc atctttccta atgactctga tgccacatac 180
agcccgtcct tccaaggcca ggtcaccatg tcagtcgaca agtccatcag caccgcctac 240
ctgcagtgga acagcctgaa ggcctcggac accgccgtgt atttttgtgc gagacagtat 300
tatcttggct cgtttgaatc ctggggccaa ggaaccacgg tcaccgtctc ctcagcctcc 360
accaagggcc catcggtctt ccccctggca ccctcctcca agagcacctc tgggggcaca 420
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480
tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tcctacagtc ctcaggactc 540
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagtga gcccaaattc 660
tgt 663

<210> 482
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> 56E11 VH CDR1

<400> 482
Ser Asn Asn Tyr Phe Trp Ala
1 5

<210> 483
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 17C9 VH CDR1

<400> 483
Asp Tyr Phe Trp Thr
1 5

<210> 484
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> 69F6 VH CDR1

<400> 484
Ser Tyr Trp Ile Ala
1 5

<210> 485
<211> 574
<212> PRT
<213> Respiratory syncytial virus

<220>
<223> F Protein

<400> 485

Met	Glu	Leu	Leu	Ile	Leu	Lys	Ala	Asn	Ala	Ile	Thr	Thr	Ile	Leu	Thr
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			20					25					30		
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu
		35					40					45			
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile
	50					55					60				
Lys	Lys	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Ala	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85					90					95	
Met	Gln	Ser	Thr	Gln	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100					105					110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
		115					120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Phe	Leu	Gly	Phe	Leu	Leu	Gly	Val
		130				135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150					155					160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
		195					200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
		210				215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265					270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280						285		
Met	Ser	Ile	Ile	Lys	Glu	Glu	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro
		290				295					300				
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
		355					360					365			
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	His	Asn	Val	Ile	Ala	Gly	Lys	Ser	Thr	Thr	Asn	Ile	Met	Ile	Thr
		515					520					525			
Thr	Ile	Ile	Ile	Val	Ile	Ile	Val	Ile	Leu	Leu	Ser	Leu	Ile	Ala	Val

Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485				490						495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	His	Asn	Val	Ile	Ala	Gly	Lys	Ser	Thr	Thr	Asn	Ile	Met	Ile	Thr
		515					520					525			
Thr	Ile	Ile	Ile	Val	Ile	Ile	Val	Ile	Leu	Leu	Ser	Leu	Ile	Ala	Val
	530					535					540				
Gly	Leu	Leu	Leu	Tyr	Cys	Lys	Ala	Arg	Ser	Thr	Pro	Val	Thr	Leu	Ser
545					550					555					560
Lys	Asp	Gln	Leu	Ser	Gly	Ile	Asn	Asn	Ile	Ala	Phe	Ser	Asn		
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<210> 487
 <211> 574
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 58C5 MARM F protein

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Ala	Val	Thr	Phe	Cys	Phe	Ala	Ser	Gly	Gln	Asn	Ile	Thr	Glu	Glu	Phe
			20					25					30		
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu
		35					40					45			
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Lys	Ile
	50					55					60				
Lys	Lys	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Ala	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85				90						95	
Met	Gln	Ser	Thr	Gln	Ala	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100				105						110		
Arg	Phe	Lys	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
		115					120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Phe	Leu	Gly	Phe	Leu	Leu	Gly	Val
	130					135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150					155					160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
		195					200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
	210					215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Leu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu
				245					250					255	
Leu	Leu	Ser	Leu	Ile	Asn	Asp	Met	Pro	Ile	Thr	Asn	Asp	Gln	Lys	Lys
			260					265					270		
Leu	Met	Ser	Asn	Asn	Val	Gln	Ile	Val	Arg	Gln	Gln	Ser	Tyr	Ser	Ile
		275					280					285			
Met	Ser	Ile	Ile	Lys	Glu	Gly	Val	Leu	Ala	Tyr	Val	Val	Gln	Leu	Pro

	290					295				300					
Leu	Tyr	Gly	Val	Ile	Asp	Thr	Pro	Cys	Trp	Lys	Leu	His	Thr	Ser	Pro
305					310					315					320
Leu	Cys	Thr	Thr	Asn	Thr	Lys	Glu	Gly	Ser	Asn	Ile	Cys	Leu	Thr	Arg
				325					330					335	
Thr	Asp	Arg	Gly	Trp	Tyr	Cys	Asp	Asn	Ala	Gly	Ser	Val	Ser	Phe	Phe
			340					345					350		
Pro	Gln	Ala	Glu	Thr	Cys	Lys	Val	Gln	Ser	Asn	Arg	Val	Phe	Cys	Asp
		355					360					365			
Thr	Met	Asn	Ser	Leu	Thr	Leu	Pro	Ser	Glu	Val	Asn	Leu	Cys	Asn	Val
	370					375					380				
Asp	Ile	Phe	Asn	Pro	Lys	Tyr	Asp	Cys	Lys	Ile	Met	Thr	Ser	Lys	Thr
385					390					395					400
Asp	Val	Ser	Ser	Ser	Val	Ile	Thr	Ser	Leu	Gly	Ala	Ile	Val	Ser	Cys
				405					410					415	
Tyr	Gly	Lys	Thr	Lys	Cys	Thr	Ala	Ser	Asn	Lys	Asn	Arg	Gly	Ile	Ile
			420					425					430		
Lys	Thr	Phe	Ser	Asn	Gly	Cys	Asp	Tyr	Val	Ser	Asn	Lys	Gly	Val	Asp
		435					440					445			
Thr	Val	Ser	Val	Gly	Asn	Thr	Leu	Tyr	Tyr	Val	Asn	Lys	Gln	Glu	Gly
	450					455					460				
Lys	Ser	Leu	Tyr	Val	Lys	Gly	Glu	Pro	Ile	Ile	Asn	Phe	Tyr	Asp	Pro
465					470					475					480
Leu	Val	Phe	Pro	Ser	Asp	Glu	Phe	Asp	Ala	Ser	Ile	Ser	Gln	Val	Asn
				485					490					495	
Glu	Lys	Ile	Asn	Gln	Ser	Leu	Ala	Phe	Ile	Arg	Lys	Ser	Asp	Glu	Leu
			500					505					510		
Leu	His	Asn	Val	Ile	Ala	Gly	Lys	Ser	Thr	Thr	Asn	Ile	Met	Ile	Thr
		515					520					525			
Thr	Ile	Ile	Ile	Val	Ile	Ile	Val	Ile	Leu	Leu	Ser	Leu	Ile	Ala	Val
	530					535					540				
Gly	Leu	Leu	Leu	Tyr	Cys	Lys	Ala	Arg	Ser	Thr	Pro	Val	Thr	Leu	Ser
545					550					555					560
Lys	Asp	Gln	Leu	Ser	Gly	Ile	Asn	Asn	Ile	Ala	Phe	Ser	Asn		
				565					570						