

SEQUENCE LISTING

<110> Opsidio, LLC

<120> ANTI-STEM CELL FACTOR ANTIBODIES AND METHODS OF USE THEREOF

<130> OPSL-001/01WO 336059-2005

<150> US 62/900,927

<151> 2019-09-16

<160> 50

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Mus musculus

<400> 1

Ser	Tyr	Trp	Met	Asn
1				5

<210> 2

<211> 17

<212> PRT

<213> Mus musculus

<400> 2

Gln	Ile	Tyr	Pro	Gly	Asp	Gly	Asp	Thr	His	Tyr	Asn	Gly	Lys	Phe	Lys
1				5				10						15	

Gly

<210> 3

<211> 7

<212> PRT

<213> Mus musculus

<400> 3

Ser	Asn	Trp	Val	Gly	Ser	Tyr
1				5		

<210> 4
 <211> 16
 <212> PRT
 <213> Mus musculus

<400> 4

Lys Ser Ser Gln Ser Leu Leu Glu Ser Asp Gly Lys Thr Tyr Leu Asn
 1 5 10 15

<210> 5
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 5

Leu Val Ser Arg Leu Asp Ser
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 6

Trp Gln Gly Thr His Leu Pro Gln Thr
 1 5

<210> 7
 <211> 116
 <212> PRT
 <213> Mus musculus

<400> 7

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ala
115

<210> 8
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5H10 Heavy chain variable region VH1

<400> 8

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 9
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5H10 Heavy chain variable region VH2

<400> 9

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

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

<220>
<223> Humanized 5H10 Heavy chain variable region VH3

<400> 10

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 11
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5H10 Heavy chain variable region VH4

<400> 11

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 12
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Humanized 5H10 Heavy chain variable region VH5

<400> 12

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 13

<211> 112

<212> PRT

<213> Mus musculus

<400> 13

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

Gln Thr Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

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

35

40

45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 14

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 5H10 Light chain variable region VK1

<400> 14

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly

85

90

95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 15

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 5H10 Light chain variable region VK2

<400> 15

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 16

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 5H10 Light chain variable region VK3

<400> 16

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 17

<211> 112

<212> PRT

<213> Artificial Sequence

<220>

<223> Humanized 5H10 Light chain variable region VK4

<400> 17

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

<210> 18
 <211> 348
 <212> DNA
 <213> Mus musculus

<400> 18
 caggttcagc tgcagcagtc tggggctgag ctcgtgaggc ctgggtcctc agtgaagatt 60
 tcctgcaagt cttctggcta tgcattcagt agctactgga tgaactgggt gaagcagagg 120
 cctggacagg gtcttgagt gattggacag atttatcctg gagatgggtga tactcactac 180
 aatggaaagt tcaagggcaa agccacactg actgcagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctaac atctgaggac tctgcggtct atttctgttc aagttcaaac 300
 tgggtcggga gttactgggg ccaagggact ctggtcaccg tctcctca 348

<210> 19
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized heavy chain variable region VH1

<400> 19
 cagggtccagc tggtgcaatc tggggctgag ctgaagaagc ctgggtcctc ggtgaagatt 60

tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gaagcagagg	120
cctggacaag ggcttgagt gattggacag atctatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacgctg accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgac atctgaggac tctgccgtgt atttctgttc aagttcaaac	300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca	348

<210> 20
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized heavy chain variable region VH2

<400> 20	
caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaagatt	60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gaagcagagg	120
cctggacaag ggcttgagt gattggacag atctatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacgctg accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtgt atttctgttc aagttcaaac	300
tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca	348

<210> 21
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized heavy chain variable region VH3

<400> 21	
caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaagggt	60
tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt ggcacagagg	120
cctggacaag ggcttgagt gattggacag atctatcctg gagatgggtga tactcactac	180
aatggaaagt tcaagggcaa agccacgctg accgcggaca aatccacgag cacagcctac	240

atggagctga gcagcctgag atctgaggac acggccgtgt atttctgttc aagttcaaac 300
 tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca 348

<210> 22
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized heavy chain variable region VH4

<400> 22
 caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaagggtt 60
 tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gcgacagagg 120
 cctggacaag ggcttgagt gattggacag atctatcctg gagatgggtga tactcactac 180
 aatggaaaagt tcaagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac acggccgtgt atttctgttc aagttcaaac 300
 tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca 348

<210> 23
 <211> 348
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized heavy chain variable region VH5

<400> 23
 caggtccagc tgggtgcaatc tggggctgag gtgaagaagc ctgggtcctc ggtgaagggtt 60
 tcctgcaagt cttctggata tgcattcagc agctattgga tgaactgggt gcgacagagg 120
 cctggacaag ggcttgagt gattggacag atctatcctg gagatgggtga tactcactac 180
 aatggaaaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac 240
 atggagctga gcagcctgag atctgaggac acggccgtgt attactgttc aagttcaaac 300
 tgggtcggga gttactgggg ccaaggaacc ctggtcaccg tctcctca 348

<210> 24
<211> 336
<212> DNA
<213> Mus musculus

<400> 24
gatgttgatga tgaccagac tccactcact ttgtcggta ccattggaca aacagcctcc 60
atctcttgca agtcaagtca gaggctctta gaaagtgatg gaaagacata tttgaattgg 120
ttgtcacaga ggccaggcca gtctccaaag cgcctaattct atctgggtgtc tagactggac 180
tctggagtcc ctgacagggt cactggcagt ggatcaggga cagatttcac actgaaaatc 240
agcagagtgg aggctgagga tttgggagtt tattattgtt ggcaaggcac acatcttcct 300
cagacgttcg gtggaggcac caagctggag atcaaa 336

<210> 25
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain variable region VK1

<400> 25
gatgttgatga tgactcagtc tccactcact ctgtcggta cccttggaca gccggcctcc 60
atctcctgca agtctagtca aagcctctta gaaagtgatg gaaagaccta cttgaattgg 120
ttgcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac 180
tctgggggtcc cagacagatt cactggcagt gggtcaggca ctgatttcac actgaaaatc 240
agcagggtgg aggctgagga tgttgggggt tattactgct ggcaaggcac acatcttcct 300
cagactttcg gcggaggggac caaggtggag atcaaa 336

<210> 26
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized light chain variable region VK2

<400> 26

gatgttgatga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc	60
atctcctgca agtctagtca aagcctctta gaaagtgatg gaaagaccta cttgaattgg	120
ttgcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180
tctgggggtcc cagacagatt cactggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgggggtt tattactgct ggcaaggcac acatcttcct	300
cagactttcg gcggagggac caaggtggag atcaaa	336

<210> 27
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized light chain variable region VK3

<400> 27	
gatgttgatga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc	60
atctcctgca agtctagtca aagcctctta gaaagtgatg gaaagaccta cttgaattgg	120
ttgcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180
tctgggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc	240
agcaggggtgg aggctgagga tgttgggggtt tattactgct ggcaaggcac acatcttcct	300
cagactttcg gcggagggac caaggtggag atcaaa	336

<210> 28
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Humanized light chain variable region VK4

<400> 28	
gatgttgatga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc	60
atctcctgca agtctagtca aagcctctta gaaagtgatg gaaagaccta cttgaattgg	120
tttcagcaga ggccaggcca atctccaagg cgcctaattt atctggtttc tagactggac	180

tctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgaaaatc 240
 agcaggggtgg aggctgagga tggtgggggtt tattactgct ggcaaggcac acatcttcct 300
 cagactttcg gcggagggac caaggtggag atcaaa 336

<210> 29
 <211> 40
 <212> PRT
 <213> Homo sapiens

<400> 29

Pro Glu Lys Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro
 1 5 10 15

Pro Val Ala Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg
 20 25 30

Lys Ala Lys Asn Pro Pro Gly Asp
 35 40

<210> 30
 <211> 21
 <212> PRT
 <213> Homo sapiens

<400> 30

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

Asn Pro Pro Gly Asp
 20

<210> 31
 <211> 8
 <212> PRT
 <213> Homo sapiens

<400> 31

Ser Ser Asn Arg Lys Ala Lys Asn
 1 5

<210> 32
<211> 14
<212> PRT
<213> Homo sapiens

<400> 32

Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
1 5 10

<210> 33
<211> 14
<212> PRT
<213> Homo sapiens

<400> 33

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg Lys
1 5 10

<210> 34
<211> 29
<212> PRT
<213> Homo sapiens

<400> 34

Asp Ser Arg Val Ser Val Thr Lys Pro Phe Met Leu Pro Pro Val Ala
1 5 10 15

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg
20 25

<210> 35
<211> 7
<212> PRT
<213> Homo sapiens

<400> 35

Ser Asn Arg Lys Ala Lys Asn
1 5

<210> 36
<211> 13
<212> PRT
<213> Homo sapiens

<400> 36

Ala Ser Ser Leu Arg Asn Asp Ser Ser Ser Ser Asn Arg
1 5 10

<210> 37
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> VH5 CDR2

<400> 37

Gln Ile Tyr Pro Gly Asp Gly Asp Thr His Tyr Asn Gly Lys Phe Gln
1 5 10 15

Gly

<210> 38
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> VH0 IgG4 heavy chain

<400> 38

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr

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

<210> 39
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VK0 Kappa light chain

<400> 39

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

Gln Thr Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Ser Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Lys Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 40

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> heavy chain constant region

<400> 40

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 Pro Cys Pro Ala Pro
100 105 110

Glu Phe Glu 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> 41
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 41

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

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

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

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

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

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

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

<210> 42
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 5H10 VH1 Heavy Chain

<400> 42

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 43
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5H10 VH2 Heavy Chain

<400> 43

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440

<210> 44
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5H10 VH3 Heavy Chain

<400> 44

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 245 250 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 45
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H10 VH4 Heavy Chain

<400> 45

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 46
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H10 VH5 Heavy Chain

<400> 46

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

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

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

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

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

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

Ser Ser Ser Asn Trp Val Gly Ser Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

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

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

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

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

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

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

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
210 215 220

Cys Pro Ala Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu Phe Pro
 225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 245 250 255

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 305 310 315 320

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
 405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 47
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> 5H10 VK1 Light Chain

<400> 47

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 48
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5H10 VK2 Light Chain

<400> 48

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 49

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> 5H10 VK3 Light Chain

<400> 49

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 50
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 5H10 VK4 Light Chain

<400> 50

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Glu Ser
 20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45

Pro Arg Arg Leu Ile Tyr Leu Val Ser Arg Leu Asp Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95

Thr His Leu Pro Gln Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140

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

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215