

SEQUENCE LISTING

<110> National Research Council Canada
 <120> AXL-SPECIFIC ANTIBODIES AND USES THEREOF
 <130> PAT 86600W-90
 <150> US 62/557,870
 <151> 2017-09-13
 <160> 188
 <170> PatentIn version 3.5
 <210> 1
 <211> 17
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> CDR L1-B consensus
 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> Xaa = S or T
 <220>
 <221> misc_feature
 <222> (14)..(14)
 <223> Xaa = I or N
 <400> 1
 Lys Ser Ser Gln Ser Leu Leu Asn Xaa Arg Thr Arg Lys Xaa Tyr Leu
 1 5 10 15
 Ala
 <210> 2
 <211> 7
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> CDR L2-B consensus
 <220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> Xaa is E, H or Q
 <220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> Xaa is S or T
 <400> 2

Trp Ala Ser Thr Arg Xaa Xaa
1 5

<210> 3
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR H1-B consensus

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is F or Y

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is I, S, or T

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is S, N, or K

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is F or Y

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> Xaa is G or W

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is i or M

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is N, S, or H

<400> 3

Gly Xaa Thr Phe Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 4
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR H2-B consensus

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is F, N, or Y

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is G, N, or D

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is S or T

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is A or T

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is N or D

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Xaa is S or R

<400> 4

Asn	Ile	Xaa	Pro	Xaa	Ser	Xaa	Ser	Xaa	Xaa	Tyr	Asn	Glu	Lys	Phe	Lys
1				5					10					15	

Xaa

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR H3-B consensus

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa is T or Y

<400> 5

Asp	Xaa	Tyr	Gly	Gly	Ser	Pro	Asp	Tyr
1				5				

<210> 6
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR L2-B consensus (2)

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is E or Q

<400> 6

Trp Ala Ser Thr Arg Xaa Ser
1 5

<210> 7
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR H1-B consensus (2)

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is F or Y

<400> 7

Gly Tyr Thr Phe Thr Ser Xaa Trp Ile Asn
1 5 10

<210> 8
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR H2-B consensus (2)

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is F or Y

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is G or D

<400> 8

Asn Ile Xaa Pro Xaa Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5 CDR L1-B

<400> 9

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

Ala

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5 CDR L2-B

<400> 10

Trp Ala Ser Thr Arg Gln Ser
1 5

<210> 11
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5/F107 & 8D12 CDR L3-B

<400> 11

Lys Gln Ser Tyr Asn Leu Trp Thr
1 5

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5 CDR H1-B

<400> 12

Gly Tyr Thr Phe Thr Ser Tyr Trp Ile Asn
1 5 10

<210> 13
<211> 17
<212> PRT

<213> Artificial Sequence

<220>

<223> F107-7H5 CDR H2-B

<400> 13

Asn	Ile	Tyr	Pro	Asp	Ser	Ser	Ser	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys
1				5					10					15	

Ser

<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-7H5 CDR H3-B

<400> 14

Asp	Thr	Tyr	Gly	Gly	Ser	Pro	Asp	Tyr
1				5				

<210> 15

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-8D12 CDR L1-B

<400> 15

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

Ala

<210> 16

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-8D12 CDR L2-B

<400> 16

Trp	Ala	Ser	Thr	Arg	Glu	Ser
1				5		

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-8D12 CDR H1-B

<400> 17

Gly Tyr Thr Phe Ile Ser Phe Trp Ile Asn
1 5 10

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-8D12 CDR H2-B

<400> 18

Asn Ile Phe Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ser

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-8D12 CDR H3-B

<400> 19

Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr
1 5

<210> 20

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR L1-B

<400> 20

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

<210> 21

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR L2-B

<400> 21

Tyr Ile Ser Arg Leu His Ser
1 5

<210> 22

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR L3-B

<400> 22

Gln Gln Gly Asn Thr Leu Pro Phe Thr
1 5

<210> 23

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR H1-B

<400> 23

Lys Tyr Gly Met Asn
1 5

<210> 24

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR H2-B

<400> 24

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 25

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR H3-B

<400> 25

Gly Gly Tyr Tyr Ser Asn Pro Ile Tyr Pro Met Asp Tyr

1 5 10

<210> 26
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-3C8 CDR L1-B

<400> 26

Ser Ala Ser Ser Ser Val Ser Tyr Met Tyr
1 5 10

<210> 27
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-3C8 CDR L2-B

<400> 27

Arg Thr Ser Asn Leu Ala Ser
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-3C8 CDR L3-B

<400> 28

Gln Gln Tyr His Asn Tyr Pro Pro Thr
1 5

<210> 29
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-3C8 CDR H1-B

<400> 29

Gly Tyr Thr Phe Thr Ser Tyr Trp Met His
1 5 10

<210> 30
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> F111-3C8 CDR H2-B

<400> 30

Asn Ile Asn Pro Asn Ser Thr Ser Ala Asp Tyr Asn Glu Lys Phe Lys
1 5 10 15

Arg

<210> 31

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 CDR H3-B

<400> 31

Pro Leu Met Gly Pro Tyr Trp Tyr Phe Asp Val
1 5 10

<210> 32

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-10G1 CDR L1-B

<400> 32

Lys Ala Ser Gln Asp Val Thr Thr Ala Val Ala
1 5 10

<210> 33

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-10G1 CDR L2-B

<400> 33

Trp Ala Ser Thr Arg His Thr
1 5

<210> 34

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-10G1 CDR L3-B

<400> 34

Gln Gln His Phe Thr Thr Pro Leu Thr
1 5

<210> 35
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 CDR H1-B

<400> 35

Asn Tyr Gly Met Ser
1 5

<210> 36
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 CDR H2-B

<400> 36

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

Gly

<210> 37
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 CDR H3-B

<400> 37

Gly Ala Arg Ala Ser Tyr Phe Ala Met Asp Tyr
1 5 10

<210> 38
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5 VL

<400> 38

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

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

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 39
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5 VH

<400> 39

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

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

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

Gly Asn Ile Tyr Pro Asp Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

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

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

Thr Arg Asp Thr Tyr Gly Gly Ser Pro Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser

<210> 40
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F107-8D12 VL

<400> 40

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

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

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
 85 90 95

Ser Tyr Asn Leu Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 41
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> F107-8D12 VH

<400> 41

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

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

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

Gly Asn Ile Phe Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe

50

55

60

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

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

Ala Arg Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 42

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 VL

<400> 42

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

Glu Lys Val Thr Ile Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asn Tyr Pro Pro Thr
85 90 95

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

<210> 43

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 VH

<400> 43

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

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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 44

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 VL

<400> 44

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Ile Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Leu
65 70 75 80

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

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 45
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-5E9 VH

<400> 45

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

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

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

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Thr Thr Glu Asp Met Val Thr Tyr Phe Cys
85 90 95

Ala Lys Gly Gly Tyr Tyr Ser Asn Pro Ile Tyr Pro Met Asp Tyr Trp
100 105 110

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

<210> 46
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 VL

<400> 46

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

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 47
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 VH

<400> 47

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

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

Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu Glu Trp Val
35 40 45

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

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

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

Ala Arg Gly Ala Arg Ala Ser Tyr Phe Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Ser Ser Val Thr Val Ser Ser

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

<220>
 <223> Chimeric F107-7H5 light chain

<400> 48

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

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

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Gln Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
 85 90 95

Ser Tyr Asn Leu Trp 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> 49
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric F107-7H5 heavy chain

<400> 49

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

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

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

Gly Asn Ile Tyr Pro Asp Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

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

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

Thr Arg Asp Thr Tyr Gly Gly Ser Pro Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

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

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

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

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser

195

200

205

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

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

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

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

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

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

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

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

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

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

<210> 50

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

<220>
<223> Chimeric F107-8D12 light chain

<400> 50

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

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

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
85 90 95

Ser Tyr Asn Leu Trp 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> 51
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric F107-8D12 heavy chain

<400> 51

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

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

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

Gly Asn Ile Phe Pro Gly Ser Ser Ser Thr Asn Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

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

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

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

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

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr

210

215

220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 225 230 235 240

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

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

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

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

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

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

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

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
 355 360 365

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

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
 385 390 395 400

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

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
 420 425 430

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

<210> 52

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric F111-3C8 light chain

<400> 52

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

Glu Lys Val Thr Ile Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr His Asn Tyr Pro Pro Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu 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> 53

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric F111-3C8 heavy chain

<400> 53

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

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

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

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

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

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

Thr Arg Pro Leu Met Gly Pro Tyr Trp Tyr Phe Asp Val Trp Gly Thr
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 Lys 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	Asp	Glu	Leu	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

<210> 54
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Chimeric F111-5E9 light chain

<400> 54

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Ile Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Leu
65 70 75 80

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 55

<211> 451

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric F111-5E9 heavy chain

<400> 55

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

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

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

Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

Leu Gln Ile Asn Asn Leu Thr Thr Glu Asp Met Val Thr Tyr Phe Cys
85 90 95

Ala Lys Gly Gly Tyr Tyr Ser Asn Pro Ile Tyr Pro Met Asp Tyr Trp
100 105 110

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

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

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

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

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu

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

<210> 56
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Chimeric F107-10G1 light chain

<400> 56

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

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

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

Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

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

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

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

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

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

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

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

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

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

Phe Asn Arg Gly Glu Cys
210

<210> 57

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Chimeric F107-10G1 heavy chain

<400> 57

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

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

Gly Met Ser Trp Val Arg Gln Thr Ser Asp Lys Arg Leu Glu Trp Val
35 40 45

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

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

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

Ala Arg Gly Ala Arg Ala Ser Tyr Phe Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Ser Ser 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 Lys 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	Asp	Glu	Leu	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

<210> 58
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>

<223> rhAXL-ECD

<400> 58

Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp Cys
1 5 10 15

Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr Gln Ala
20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
85 90 95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr
100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser
115 120 125

Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
130 135 140

Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys
145 150 155 160

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
180 185 190

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

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
210 215 220

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

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

<210> 59

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain signal sequence

<400> 59

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

Gly Ala Tyr Gly
20

<210> 60

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain signal sequence

<400> 60

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Thr His Ala

<210> 61

<211> 339

<212> DNA

<213> Artificial Sequence

<220>

<223> F107-7H5 VL sequence

<400> 61

gacattgtga tgtcacagtc tccatcctcc ctggctgtgt cagcaggaga gaaggctact 60

atgagctgca aatccagtc gagtctgctc aacagtagaa cccgaaagat ctacttggct 120

tggtaccagc agaaaccagg tcagtctcct aaactgctga tctattgggc atccactagg 180

caatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc 240

atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctg 300

tggaacgttc gtggaggcac caagctggaa atcaaacgg 339

<210> 62

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> F107-7H5 VH sequence

<400> 62

cagggtccaac tgcagcagcc tggggctgag cttgtgaagc ctggggcttc agtgaaactg 60

tcctgcaagg cttctggcta cactttcacc agctactgga taaactgggt gaagcagagg 120

cctggacaag gccttgagtg gattggaaat atttatcctg atagtagtag tactaactac	180
aatgagaagt tcaagagcaa ggccacactg actgtagaca agtcctccac cacagcctac	240
atacagttca gcagcctgac atctgaggac tctgcggtct attattgtac aagagatacc	300
tatggtggta gccctgacta ctggggccaa ggcaccactc tcacagtctc ctca	354

<210> 63
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F107-8D12 VL sequence

<400> 63	
gacattgtga tgtcacagtc tccatcctcc ctggctgtgt cagcaggaga gagggtcact	60
atgagctgca aatccagtca gagtctgctc aacactagaa cccgaaagaa ctacttggct	120
tggtaccagc agaaaccagg gcagtctcct aaactgctga tctactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc	240
atcagcagtg tgcaggctga agacctggca gtttattact gcaagcaatc ttataatctg	300
tggacgttcg gtggaggcac caagctggaa atcaaa	336

<210> 64
 <211> 354
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F107-8D12 VH sequence

<400> 64	
caggtccaac tgcagcagcc tggggctgag cttgtgaagc ctggggcttc agtgcagctg	60
tcttgcaagg cttctggcta cactttcatc agcttctgga taaactgggt gaagcagagg	120
cctggacaag gccttgagtg gatgggaaat atttttcctg gtagtagtag tacgaactac	180
aatgagaagt tcaagagcaa ggccacactg actgtagaca aatcctccag cacagcctac	240
atgcagctca gcagcctgac atctgaggac tctgcggtct atttttgtgc aagagattac	300
tatggtggta gccctgacta ctggggccaa ggcaccactc tcacagtytc ctca	354

<210> 65
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F111-5E9 VL sequence

<400> 65	
gatatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc	60

atcagttgca gggcaagtca ggacattaac aattatttaa actggtatca gcagaaacca	120
gatggaactg ttaaactcct gatctactac atatcaagat tacactcagg agtcccatca	180
aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggagcta	240
gaagatgttg ccacttactt ttgccaacag ggtaatacgc ttccattcac gttcggctcg	300
gggacaaaagt tggaataaaa a	321

<210> 66
 <211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F111-5E9 VH sequence

<400> 66	
cagatccagt tgggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc	60
tcctgcaagg cttctgggta taccttcaca aaatatggaa tgaactgggt aaagcaggct	120
ccaggaaaagg gtttaaagtg gatgggctgg ataaacacct aactggaga gccaacatat	180
gctgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccag cactgcctat	240
ttgcagatca acaacctcac aactgaggac atggtcacat atttctgtgc aaaagggggg	300
tattatagta accctatcta tcctatggac tactggggtc aaggaacctc agtcaccgtc	360
tcctca	366

<210> 67
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F111-3C8 VL sequence

<400> 67	
caaattgttc tcaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc	60
atatcctgca gtgccagctc aagtgtagt tacatgtatt ggtaccagca gaagccagga	120
tcctcccca aaccctggat ttatcgaca tccaacctgg cttctggagt ccctgctcgc	180
ttcagtggca gtgggtctgg gacctcttac tctctcaca tcagcagcat ggaggctgaa	240
gatgctgcca cttattactg ccagcagtat cataattacc caccacggt cgaggggggg	300
accaagctgg aaataaaacg g	321

<210> 68
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> F111-3C8 VH sequence

<400> 68
caggtccaac tgcagcagcc tggggctgaa ctgggcaagc ctgggacatc agtgaagctg 60
tcctgcaagg cttctggcta caccttcacc agctattgga tgcactgggt gaagcgggtg 120
cctggacaag gccttgagtg gattggaaat attaatccta atagtactag tgctgactac 180
aatgagaagt tcaagaggaa ggccacattg actgtagaca aatcctccag cacagcctac 240
atgcagctca gcaccctgac atctgaggac tctgcggtct actactgtac aagacccta 300
atgggtcctt actggtactt cgatgtctgg ggcacaggga ccacggtcac cgtctcctca 360

<210> 69
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> F107-10G1 VL sequence

<400> 69
gtcattgtga tgaccagtc tcacaaattc atgtccacat cagtaggaga cagggtcagt 60
atcacctgca aggccagtc ggatgtgact actgctgtag cctggtatca acaaaaacca 120
gggcaatctc ctaaactact gatttactgg gcatccacc ggcacactgg agtccctgat 180
cgcttcacag gcagtggatc tgggacagat tattctctca ccatcagcaa tgtgcagact 240
gaagacctgg cattttatta ctgtcagcaa cattttacca ctctctcac gttcgggtgt 300
gggaccaagt tggagctgaa a 321

<210> 70
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> F107-10G1 VH sequence

<400> 70
gaagtgaacc tgggtggagtc tgggggaggc gtagtgaagc ctggagcgtc tctgaaactc 60
tcctgtgaag cctctggatt cactttcagt aactatggca tgtcttgggt tcgccagact 120
tcagacaaga ggctggagtg ggtcgcattc attagtgggt gtggtggtag aacctactat 180
ctagacaatg taaagggccg attcatcatc tccagagaga atgccaagaa caccctgtac 240
ctgcaaatga gtagtctgaa gtctgaggac acggccttgt tttactgtgc aagaggagct 300
cgggcctctt actttgctat ggactactgg ggtcaaggaa gttcagtcac cgtctcctca 360

<210> 71
<211> 469
<212> PRT
<213> Artificial Sequence

<220>

<223> (rh)AXL-ECD His8

<400> 71

Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp Cys
1 5 10 15

Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr Gln Ala
20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
85 90 95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr
100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser
115 120 125

Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
130 135 140

Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys
145 150 155 160

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
180 185 190

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

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
210 215 220

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

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

<210> 72
 <211> 909
 <212> PRT

<213> Artificial Sequence

<220>

<223> AXL - full length His6

<400> 72

Met Ala Trp Arg Cys Pro Arg Met Gly Arg Val Pro Leu Ala Trp Cys
1 5 10 15

Leu Ala Leu Cys Gly Trp Ala Cys Met Ala Pro Arg Gly Thr Gln Ala
20 25 30

Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn Ile Thr Gly Ala Arg
35 40 45

Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln Val Gln Gly Glu Pro
50 55 60

Pro Glu Val His Trp Leu Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp
65 70 75 80

Ser Thr Gln Thr Gln Val Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp
85 90 95

Ile Val Val Ser Gln Leu Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr
100 105 110

Gly Gln Tyr Gln Cys Leu Val Phe Leu Gly His Gln Thr Phe Val Ser
115 120 125

Gln Pro Gly Tyr Val Gly Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu
130 135 140

Pro Glu Asp Arg Thr Val Ala Ala Asn Thr Pro Phe Asn Leu Ser Cys
145 150 155 160

Gln Ala Gln Gly Pro Pro Glu Pro Val Asp Leu Leu Trp Leu Gln Asp
165 170 175

Ala Val Pro Leu Ala Thr Ala Pro Gly His Gly Pro Gln Arg Ser Leu
180 185 190

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

Asn Ala Lys Gly Val Thr Thr Ser Arg Thr Ala Thr Ile Thr Val Leu
210 215 220

Pro Gln Gln Pro Arg Asn Leu His Leu Val Ser Arg Gln Pro Thr Glu

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

485

490

495

Arg Tyr Arg Val Arg Lys Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr
500 505 510

Leu Asn Ser Leu Gly Ile Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp
515 520 525

Val Met Val Asp Arg His Lys Val Ala Leu Gly Lys Thr Leu Gly Glu
530 535 540

Gly Glu Phe Gly Ala Val Met Glu Gly Gln Leu Asn Gln Asp Asp Ser
545 550 555 560

Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg
565 570 575

Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe
580 585 590

Asp His Pro Asn Val Met Arg Leu Ile Gly Val Cys Phe Gln Gly Ser
595 600 605

Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys
610 615 620

His Gly Asp Leu His Ser Phe Leu Leu Tyr Ser Arg Leu Gly Asp Gln
625 630 635 640

Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile
645 650 655

Ala Ser Gly Met Glu Tyr Leu Ser Thr Lys Arg Phe Ile His Arg Asp
660 665 670

Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val
675 680 685

Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg
690 695 700

Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser
705 710 715 720

Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ser Phe Gly
725 730 735

Val Thr Met Trp Glu Ile Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly

740

745

750

Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Arg Gly Asn Arg Leu
 755 760 765

Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg
 770 775 780

Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg
 785 790 795 800

Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro
 805 810 815

Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu
 820 825 830

Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro
 835 840 845

Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly
 850 855 860

Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala
 865 870 875 880

Asp Arg Gly Ser Pro Ala Ala Pro Gly Gln Glu Asp Gly Ala Tyr Leu
 885 890 895

Glu Cys Gly Arg Tyr Ala Ser His His His His His
 900 905

<210> 73

<211> 118

<212> PRT

<213> Artificial Sequence

<220>

<223> F155-3C7 VH

<400> 73

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

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

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

Gly Asn Ile Phe Pro Gly Ser Asn Ser Ser Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

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

Val Arg Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser
115

<210> 74
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 VL

<400> 74

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

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

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Ala Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Ile Tyr Tyr Cys Lys His
85 90 95

Ser Tyr Asn Leu Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Arg
100 105 110

<210> 75
<211> 118
<212> PRT
<213> Artificial Sequence

<220>

<223> F149-4G4 VH

<400> 75

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

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

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

Gly Trp Ile Asn Thr Tyr Leu Gly Glu Pro Thr Tyr Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65 70 75 80

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

Thr Arg Gly Thr Met Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Ala Leu Thr Val Ser Ser
115

<210> 76

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> F149-4G4 VL

<400> 76

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

Glu Glu Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

Tyr Leu His Trp Tyr Gln Gln Lys Ser Gly Ala Ser Pro Lys Leu Trp
35 40 45

Ile Tyr Ser Thr Ser Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Val Glu

65

70

75

80

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

Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Val Lys
100 105

<210>	77
<211>	8
<212>	PRT
<213>	Artificial Sequence

<220>
<223> F107-10G1 CDR H1-A

<400> 77

Gly Phe Thr Phe Ser Asn Tyr Gly
1 5

<210>	78
<211>	8
<212>	PRT
<213>	Artificial Sequence

<220>
<223> F107-10G1 CDR H2-A

<400> 78

Ile Ser Gly Gly Gly Gly Arg Thr
1 5

<210>	79
<211>	13
<212>	PRT
<213>	Artificial Sequence

<220>
<223> F107-10G1 CDR H3-A

<400> 79

Ala Arg Gly Ala Arg Ala Ser Tyr Phe Ala Met Asp Tyr
1 5 10

<210>	80
<211>	6
<212>	PRT
<213>	Artificial Sequence

<220>
<223> F107-10G1 CDR L1-A

<400> 80

Gln Asp Val Thr Thr Ala

1

5

<210> 81
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 CDR L2-A

<400> 81

Trp Ala Ser Thr
1

<210> 82
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-10G1 CDR L3-A

<400> 82

Gln Gln His Phe Thr Thr Pro Leu Thr
1 5

<210> 83
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-5E9 CDR H1-A

<400> 83

Gly Tyr Thr Phe Thr Lys Tyr Gly
1 5

<210> 84
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-5E9 CDR H2-A

<400> 84

Ile Asn Thr Tyr Thr Gly Glu Pro
1 5

<210> 85
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> F111-5E9 CDR H3-A

<400> 85

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

<210> 86

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR L1-A

<400> 86

Gln Asp Ile Asn Asn Tyr
1 5

<210> 87

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR L2-A

<400> 87

Tyr Ile Ser Arg
1

<210> 88

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-5E9 CDR L3-A

<400> 88

Gln Gln Gly Asn Thr Leu Pro Phe Thr
1 5

<210> 89

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-8D12 CDR H1-A

<400> 89

Gly Tyr Thr Phe Ile Ser Phe Trp
1 5

<210> 90
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-8D12 CDR H2-A

<400> 90

Ile Phe Pro Gly Ser Ser Ser Thr
1 5

<210> 91
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-8D12 CDR H3-A

<400> 91

Ala Arg Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr
1 5 10

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-8D12 CDR L1-A

<400> 92

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

<210> 93
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-8D12 CDR L2-A

<400> 93

Trp Ala Ser Thr
1

<210> 94
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-8D12 CDR L3-A

<400> 94

Lys Gln Ser Tyr Asn Leu Trp Thr
1 5

<210> 95

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-7H5 CDR H1-A

<400> 95

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 96

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-7H5 CDR H2-A

<400> 96

Ile Tyr Pro Asp Ser Ser Ser Thr
1 5

<210> 97

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-7H5 CDR H3-A

<400> 97

Thr Arg Asp Thr Tyr Gly Gly Ser Pro Asp Tyr
1 5 10

<210> 98

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> F107-7H5 CDR L1-A

<400> 98

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

<210> 99

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

<220>
<223> F107-7H5 CDR L2-A

<400> 99

Trp Ala Ser Thr
1

<210> 100
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F107-7H5 CDR L3-A

<400> 100

Lys Gln Ser Tyr Asn Leu Trp Thr
1 5

<210> 101
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR H1-A

<400> 101

Gly Tyr Ile Phe Thr Asn Phe Trp
1 5

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR H2-A

<400> 102

Ile Phe Pro Gly Ser Asn Ser Ser
1 5

<210> 103
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR H3-A

<400> 103

Val Arg Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr
1 5 10

<210> 104
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR L1-A

<400> 104

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

<210> 105
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR L2-A

<400> 105

Trp Ala Ser Thr
1

<210> 106
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR L3-A

<400> 106

Lys His Ser Tyr Asn Leu Trp Thr
1 5

<210> 107
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F111-3C8 CDR H1-A

<400> 107

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 108
<211> 8
<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 CDR H2-A

<400> 108

Ile Asn Pro Asn Ser Thr Ser Ala
1 5

<210> 109

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 CDR H3-A

<400> 109

Thr Arg Pro Leu Met Gly Pro Tyr Trp Tyr Phe Asp Val
1 5 10

<210> 110

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 CDR L1-A

<400> 110

Ser Ser Val Ser Tyr
1 5

<210> 111

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 CDR L2-A

<400> 111

Arg Thr Ser Asn
1

<210> 112

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F111-3C8 CDR L3-A

<400> 112

Gln Gln Tyr His Asn Tyr Pro Pro Thr

1 5

<210> 113
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F149-4G4 CDR H1-A

<400> 113

Gly Tyr Thr Phe Thr Tyr Tyr Gly
1 5

<210> 114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F149-4G4 CDR H2-A

<400> 114

Ile Asn Thr Tyr Leu Gly Glu Pro
1 5

<210> 115
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> F149-4G4 CDR H3-A

<400> 115

Thr Arg Gly Thr Met Ser Tyr Ser Phe Asp Tyr
1 5 10

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

<220>
<223> F149-4G4 CDR L1-A

<400> 116

Ser Ser Ser Val Ser Ser Ser Tyr
1 5

<210> 117
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> F149-4G4 CDR L2-A

<400> 117

Ser Thr Ser Lys

1

<210> 118

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F149-4G4 CDR L3-A

<400> 118

His Gln Tyr Ser Gly Asp Pro Leu Thr

1

5

<210> 119

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb001

<400> 119

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

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

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

Ala Ala Ile Thr Thr Leu Asp Ile Ala Asn Tyr Arg Asp Ser Val Lys
50 55 60

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

Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Arg Tyr His Cys Ala
85 90 95

Ala Phe Gln Ser Asp Gln Asn Tyr Trp Gly Gln Gly Thr Gln Val Thr
100 105 110

Val Ser Ser
115

<210> 120
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002

<400> 120

Gln Val Gln Leu Val Asp Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Thr Ser Thr Arg Thr Val Ser Ser Ala
20 25 30

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

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

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

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

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

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

<210> 121
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb003

<400> 121

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

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

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

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

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

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

Ala Arg Arg Gly Gly Ala Arg Gly Glu Tyr Asp Tyr Trp Asp Gln Gly
100 105 110

Thr Gln Val Thr Val Ser Ser
115

<210> 122
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb004

<400> 122

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

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

Glu Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val
35 40 45

Ala Ala Val Thr Arg Asn Gly Asp Ser Val Val Tyr Ala Asp Ser Leu
50 55 60

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

Leu His Met Asn Ile Leu Gln Pro Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

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

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

<210> 123

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

<220>
<223> NRC-sdAb005

<400> 123

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Ile Asn
20 25 30

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

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

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

Gln Met Asn Asn Leu Lys Pro Glu Asp Thr Ala Ile Tyr Tyr Cys Arg
85 90 95

Ala Trp Gly Thr Gly Thr Ile Ser Thr Met Tyr Trp Gly Gln Gly Thr
100 105 110

Gln Val Thr Val Ser Ser
115

<210> 124
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb006

<400> 124

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

Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ile Phe Gly Phe Asn
20 25 30

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

Ala Ser Ile Ser Asn Ser Lys Arg Thr Met Tyr Ala Asp Ser Val Lys

50

55

60

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

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

Ala Trp Gly Ile Ile Thr Ser Ala Thr Val Tyr Trp Gly Gln Gly Thr
 100 105 110

Gln Val Thr Val Ser Ser
 115

<210> 125

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb007

<400> 125

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

Ser Leu Arg Leu Ser Cys Ala Thr Ser Thr Arg Thr Val Ser Ser Ala
 20 25 30

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

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

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

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

Ile Ile Trp Arg Thr Ser Asp Leu Thr Gly Arg Phe Asn Thr Trp Gly
 100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120

<210> 126

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb008

<400> 126

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ser Gly Met Ile Asn
20 25 30

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

Ala Arg Arg Ser Thr Gly Gly Thr Thr Asn Tyr Ala Asp Ser Val Lys
50 55 60

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

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

Ile Ile Trp Arg Thr Ser Asp Leu Thr Gly Arg Phe Asn Thr Trp Gly
100 105 110

Gln Gly Thr Gln Val Thr Val Ser Ser
115 120

<210> 127

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb001 CDR1-A

<400> 127

Ala Ser Ile Ser Ser Phe Asp Ile
1 5

<210> 128

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb001 CDR2-A

<400> 128

Ile Thr Thr Leu Asp Ile Ala

1 5

<210> 129
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb001 CDR3-A

<400> 129

Ala Ala Phe Gln Ser Asp Gln Asn Tyr
1 5

<210> 130
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002 CDR1-A

<400> 130

Thr Arg Thr Val Ser Ser Ala Val
1 5

<210> 131
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002 CDR2-A

<400> 131

Ile Thr Asn Ser Gly Asn Ile
1 5

<210> 132
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002 CDR3-A

<400> 132

Ala Ala Lys Trp Ser Phe Ser Ser Gly Tyr Gly Asp Leu Arg Arg Ala
1 5 10 15

Ala Met Tyr Asp Tyr
20

<210> 133

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

<220>
<223> NRC-sdAb003 CDR1-A

<400> 133

Gly Val Thr Leu Asp Tyr Thr Ala
1 5

<210> 134
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb003 CDR2-A

<400> 134

Ile Thr Ser Gly Gly Asn Thr
1 5

<210> 135
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb003 CDR3-A

<400> 135

Ala Ala Arg Arg Gly Gly Ala Arg Gly Glu Tyr Asp Tyr
1 5 10

<210> 136
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb004 CDR1-A

<400> 136

Arg Gly Ala Phe Asp Thr Tyr Glu
1 5

<210> 137
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb004 CDR2-A

<400> 137

Val Thr Arg Asn Gly Asp Ser Val
1 5

<210> 138
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb004 CDR3-A

<400> 138

Ala Ala Asn Trp Arg Pro Leu Arg Thr Ser Ser Gly Ala Asp Asp Tyr
1 5 10 15

Ala Asp

<210> 139
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb005 CDR1-A

<400> 139

Gly Ser Ile Ser Ser Ile Asn Thr
1 5

<210> 140
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb005 CDR2-A

<400> 140

Ser Asp Ser Gly Ala Asn Arg
1 5

<210> 141
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb005 CDR3-A

<400> 141

Arg Ala Trp Gly Thr Gly Thr Ile Ser Thr Met Tyr
1 5 10

<210> 142
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb006 CDR1-A

<400> 142

Glu Ser Ile Phe Gly Phe Asn Thr
1 5

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

<220>
<223> NRC-sdAb006 CDR2-A

<400> 143

Ile Ser Asn Ser Lys Arg Thr
1 5

<210> 144
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb006 CDR3-A

<400> 144

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

<210> 145
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb007 CDR1-A

<400> 145

Thr Arg Thr Val Ser Ser Ala Val
1 5

<210> 146
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb007 CDR2-A

<400> 146

Ile Ser Asn Ser Gly Ser Val
1 5

<210> 147

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb007 CDR3-A

<400> 147

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

<210> 148

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb008 CDR1-A

<400> 148

Gly Ser Ser Gly Met Ile Asn Thr
1 5

<210> 149

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb008 CDR2-A

<400> 149

Arg Ser Thr Gly Gly Thr Thr
1 5

<210> 150

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb008 CDR3-A

<400> 150

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

<210> 151

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

<220>
<223> F155-3C7 CDR H1-B

<400> 151

Asn Phe Trp Ile Asn
1 5

<210> 152
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR H2-B

<400> 152

Asn Ile Phe Pro Gly Ser Asn Ser Ser Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Asn

<210> 153
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR H3-B

<400> 153

Asp Tyr Tyr Gly Gly Ser Pro Asp Tyr
1 5

<210> 154
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR L1-B

<400> 154

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

Ala

<210> 155

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

<220>
<223> F155-3C7 CDR L2-B

<400> 155

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 156
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> F155-3C7 CDR L3-B

<400> 156

Lys His Ser Tyr Asn Leu Trp Thr
1 5

<210> 157
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> F149-4G4 CDR H1-B

<400> 157

Tyr Tyr Gly Ile Asn
1 5

<210> 158
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> F149-4G4 CDR H2-B

<400> 158

Trp Ile Asn Thr Tyr Leu Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 159
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> F149-4G4 CDR H3-B

<400> 159

Gly Thr Met Ser Tyr Ser Phe Asp Tyr
1 5

<210> 160

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> F149-4G4 CDR L1-B

<400> 160

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

<210> 161

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> F149-4G4 CDR L2-B

<400> 161

Ser Thr Ser Lys Leu Ala Ser
1 5

<210> 162

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> F149-4G4 CDR L3-B

<400> 162

His Gln Tyr Ser Gly Asp Pro Leu Thr
1 5

<210> 163

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb001 CDR1-B

<400> 163

Phe Asp Ile Met Gly
1 5

<210> 164
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb001 CDR2-B

<400> 164

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

<210> 165
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb001 CDR3-B

<400> 165

Phe	Gln	Ser	Asp	Gln	Asn	Tyr
1				5		

<210> 166
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002 CDR1-B

<400> 166

Ser	Ala	Val	Met	Ala
1				5

<210> 167
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002 CDR2-B

<400> 167

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

<210> 168
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb002 CDR3-B

<400> 168

Lys Trp Ser Phe Ser Ser Gly Tyr Gly Asp Leu Arg Arg Ala Ala Met
1 5 10 15

Tyr Asp Tyr

<210> 169

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb003 CDR1-B

<400> 169

Tyr Thr Ala Ile Gly
1 5

<210> 170

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb003 CDR2-B

<400> 170

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

<210> 171

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb003 CDR3-B

<400> 171

Arg Arg Gly Gly Ala Arg Gly Glu Tyr Asp Tyr
1 5 10

<210> 172

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb004 CDR1-B

<400> 172

Thr Tyr Glu Ile Gly

1 5

<210> 173
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb004 CDR2-B

<400> 173

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

Ala

<210> 174
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb004 CDR3-B

<400> 174

Asn Trp Arg Pro Leu Arg Thr Ser Ser Gly Ala Asp Asp Tyr Ala Asp
1 5 10 15

<210> 175
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb005 CDR1-B

<400> 175

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

<210> 176
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb005 CDR2-B

<400> 176

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

<210> 177

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

<220>
<223> NRC-sdAb005 CDR3-B

<400> 177

Trp Gly Thr Gly Thr Ile Ser Thr Met Tyr
1 5 10

<210> 178
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb006 CDR1-B

<400> 178

Phe Asn Thr Met Gly
1 5

<210> 179
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb006 CDR2-B

<400> 179

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

<210> 180
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb006 CDR3-B

<400> 180

Trp Gly Ile Ile Thr Ser Ala Thr Val Tyr
1 5 10

<210> 181
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb007 CDR1-B

<400> 181

Ser Ala Val Met Ala
1 5

<210> 182
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb007 CDR2-B

<400> 182

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

<210> 183
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb007 CDR3-B

<400> 183

Ile Trp Arg Thr Ser Asp Leu Thr Gly Arg Phe Asn Thr
1 5 10

<210> 184
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb008 CDR1-B

<400> 184

Ile Asn Thr Met Gly
1 5

<210> 185
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NRC-sdAb008 CDR2-B

<400> 185

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

<210> 186
<211> 13
<212> PRT

<213> Artificial Sequence

<220>

<223> NRC-sdAb008 CDR3-B

<400> 186

Ile Trp Arg Thr Ser Asp Leu Thr Gly Arg Phe Asn Thr
1 5 10

<210> 187

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Fc peptide

<400> 187

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
1 5 10 15

Lys

<210> 188

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> A20.1 peptide

<400> 188

Glu Phe Val Ala Ala Gly Ser Ser Thr Gly Arg
1 5 10