SEQUENCE LISTING

<110> Medical Research Council
Matthews, David
Barlow, Jillian
McKenzie, Andrew

<120> Antibodies Against IL-25

<130> 4433.1001002

<150> US 61/101,293
<151> 2008-09-30

<150> GB 0817891.5
<151> 2008-09-30

<160> 41

<170> PatentIn version 3.3

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<223> Xaa is Ser or Thr

<220>
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<223> Xaa is Gly, Asp, Ala, Ser, Val, Asn, Lys, Tyr or Met

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<222> (48)..(48)
<223> Xaa is Met or Ile

<220>
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<223> Xaa is Asp, Asn or Gly

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Xaa Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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<400> 2

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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1 5 10 15

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

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

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

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

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

Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Val Ser Ser
115 120

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1 5 10 15

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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<400> 5

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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1 5 10 15

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

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<400> 7

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1 5 10 15

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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<400> 8

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 9
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<220>
<223> Synthetic sequence: Humanised VH domain

<400> 9

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
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85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

<210> 10
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<212> PRT
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<220>
<223> Synthetic sequence: Humanised VH domain

<400> 10

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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<223> Synthetic sequence: Humanised VH domain

<400> 11

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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<211> 122
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<220>
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<400> 12

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

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

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

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Ser Tyr Asn Gln Asn Phe

50 55 60

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

<210> 13
<211> 122
<212> PRT
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<400> 13

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

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

<220>
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<400> 14

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr Trp
100 105 110

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

<210> 15
<211> 107
<212> PRT
<213> Mus musculus

<400> 15

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 Ser Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

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

Tyr Tyr Thr Ser Ser 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 Pro
65 70 75 80

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

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

<210> 16
<211> 321
<212> DNA
<213> Mus musculus

<400> 16
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atcagctgca gcgcctccca gggcatcagc aactacctga actggtatca gcagaaggcc 120

gacggcaccg tcgagctgct gatctactac accagcagcc tgcacagcgg cgtgcccagc 180

cggtttagcg gcagcggctc cggcaccgac tacagcctga ccatctccaa cctggaaccc 240

gaggatatcg ccacctacta ctgccagcag tacagcaagc tgccctacac ctttggcggc 300

ggaacaaagc tggaaatcaa g 321

<210> 17
<211> 139
<212> PRT
<213> Mus musculus

<400> 17

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

Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
20 25 30

Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp
35 40 45

Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp

50 55 60

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

Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
85 90 95

Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
100 105 110

Cys Ala Arg Glu Gly Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr
115 120 125

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

<210> 18
<211> 417
<212> DNA
<213> Mus musculus

<400> 18
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ctgcagcaga gcggccctga gctggtgaag cctggcgcca gcatgaagat cagctgcaag 120

gccagcggct acagcttcac cgactacacc atgaactggg tgaagcagag ccacggcaag 180

aacctggaat ggatcggcct gatcaacccc tacaacggcg gcaccagcta caaccagaac 240

ttcaagggca aggccaccct gaccgtggac aagagcagca gcaccgccta catggaactg 300

ctgtctctga ccagcgagga cagcgccgtg tactactgcg ccagagaggg ctacgacggc 360

tacctgtact tcgccatgga ctactggggc cagggcacca gcgtgaccgt gagcagc 417

<210> 19
<211> 137
<212> PRT
<213> Homo sapiens

<400> 19

Leu Leu Leu Ala Val Leu Gln Gly Val Cys Ala Glu Val Arg Leu Val
1 5 10 15

Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser
20 25 30

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

Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Ile Gly Ile Ile Phe Pro
50 55 60

Gly Asp Ser Asp Thr Ile Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr
65 70 75 80

Ile Ser Val Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Ser Ser
85 90 95

Leu Lys Ala Thr Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gln Asn Pro
100 105 110

Pro Glu Tyr Ser Gly Ala Tyr His Asp Gly Trp Phe Asp Pro Trp Gly
115 120 125

Gln Gly Thr Leu Val Ile Val Ser Ser
130 135

<210> 20
<211> 411
<212> DNA
<213> Homo sapiens

<400> 20
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gaggtgaaaa agccggggga gtctctgaag atctcctgta aggcttctgg atacagtttt 120

accagtaact ggatcggctg ggtgcgccag atgcccggga aaggcctgga gtggattggg 180

atcatctttc ctggtgactc tgataccata tacagcccgt ccttccaagg ccaggtcacc 240

atttcagtcg acaagtccat caataccgcc tacctgcagt ggagcagcct gaaggccacg 300

gacaccgcca tgtattactg tgcgagacag aaccccccccg agtatagtgg cgcatatcat 360

gatgggtggt tcgacccctg gggccaggga accctggtca tcgtctcctc a 411

<210> 21
<211> 141
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: RHA VH domain

<400> 21

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

Val Cys Ala Glu Val Arg Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45

Thr Asp Tyr Thr Met Asn Trp Val Arg Gln Met Pro Gly Lys Gly Leu
50 55 60

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

Gln Asn Phe Lys Gly Gln Val Thr Ile Ser Val Asp Lys Ser Ile Asn
85 90 95

Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Thr Asp Thr Ala Met
100 105 110

Tyr Tyr Cys Ala Arg Glu Gly Tyr Asp Gly Tyr Leu Tyr Phe Ala Met
115 120 125

Asp Tyr Trp Gly Gln Gly Thr Leu Val Ile Val Ser Ser
130 135 140

<210> 22
<211> 424
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Nucleic acid encoding RHA VH domain

<400> 22
atggggtcaa ccgccatcct tggcctcctc ctggctgttc tccaaggagt ctgtgccgaa 60

gtgcgccttg tgcagtctgg agcagaagtg aaaaagccgg gggagtctct gaagatctct 120

tgcaaggctt ctggatacag ttttaccgac tacaccatga actgggtgcg ccagatgccc 180

gggaaaggcc tggagtggat tgggcttatt aatccttaca atggtggtac tagctacaac 240

cagaatttca agggccaagt caccatttca gtcgacaagt ccatcaatac cgcctacctg 300

cagtggagca gcctgaaggc cacggacacc gccatgtatt actgtgcgag agagggctat 360

gatggttacc tttactttgc tatggactac tggggccagg gaaccctggt catcgtctcc 420

tcag 424

<210> 23
<211> 127
<212> PRT
<213> Homo sapiens

<400> 23

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

Asp Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
35 40 45

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn
100 105 110

Ser Ala Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 24
<211> 381
<212> DNA
<213> Homo sapiens

<400> 24
atgagggtcc ctgctcagct cctgggactc ctgctgctct ggctcccaga taccagatgt 60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 120

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 180

gggaaagttc ctaaactcct gatctatgct gcatccactt tgcaatcagg ggtcccatct 240

cggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 300

gaagatgttg caacttatta ctgtcaaaag tataacagtg ccccgtacac ttttggccag 360

gggaccaagc tggagatcaa a 381

<210> 25
<211> 127
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: Humanised 2c3 VK domain RKA

<400> 25

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

Asp Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
20 25 30

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Gln Gly
35 40 45

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro
50 55 60

Lys Leu Leu Ile Tyr Tyr Thr Ser Ser Leu His Ser Gly Val Pro Ser
65 70 75 80

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

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

Lys Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
115 120 125

<210> 26
<211> 381
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Nucleic acid encoding humanised 2c3 VK domain RKA

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atgagggtcc ctgctcagct cctgggactc ctgctgctct ggctcccaga taccagatgt 60

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 120

atcacttgca gtgcatccca gggcattagc aattatctga attggtatca gcagaaacca 180

gggaaagttc ctaaactcct gatctattac acatcaagtt tacactcagg ggtcccatct 240

cggttcagcg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 300

gaagatgttg caacttatta ctgtcagcag tatagcaagc tgccgtacac gtttggccag 360

gggaccaagc tggagatcaa a 381

<210> 27
<211> 121
<212> PRT
<213> Homo sapiens

<400> 27

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

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

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

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

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

Leu Glu Leu Asn Ser Leu Arg Ser Glu Asp Thr Gly Val Tyr Tyr Cys
85 90 95

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 28
<211> 363
<212> DNA
<213> Homo sapiens

<400> 28
gaggtgcagc tggtggagtc tggggctgag gtgaagaagc ctggggcctc agtgaaagtt 60

tcgtgcaagg cttctggata ctccttcagt agttatggta tacattgggt gcgccaggcc 120

cccggacaaa ggcttgagtg gatgggatgg atcaacggtg gcactggttt tacaaaatat 180

tcacagaatt ttcagggcag agtcacccta accagggaca cttccgcgag cacagcctac 240

ttggaactga acagcctgag atctgaagac acgggtgtat attactgtgc gagggatccc 300

tacaataact acgcggcgga acttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 29
<211> 11
<212> PRT
<213> Mus musculus

<400> 29

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

<210> 30
<211> 7
<212> PRT
<213> Mus musculus

<400> 30

Tyr Thr Ser Ser Leu His Ser
1 5

<210> 31
<211> 9
<212> PRT
<213> Mus musculus

<400> 31

Gln Gln Tyr Ser Lys Leu Pro Tyr Thr
1 5

<210> 32
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<212> PRT
<213> Mus musculus

<400> 32

Asp Tyr Thr Met Asn
1 5

<210> 33
<211> 13

<212> PRT
<213> Mus musculus

<400> 33

Glu Gly Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr
1 5 10

<210> 34
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: Heavy Chain CDR1

<400> 34

Gly Tyr Thr Met Asn
1 5

<210> 35
<211> 17
<212> PRT
<213> Mus musculus

<400> 35

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

Gly

<210> 36
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic sequence: Heavy Chain CDR3

<400> 36

Glu Asp Tyr Asp Gly Tyr Leu Tyr Phe Ala Met Asp Tyr
1 5 10

<210> 37
<211> 19
<212> PRT
<213> Homo sapiens

<400> 37

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

Val Cys Ala

<210> 38
<211> 20
<212> PRT
<213> Mus musculus

<400> 38

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

Asp Thr Arg Cys
20

<210> 39
<211> 22
<212> PRT
<213> Homo sapiens

<400> 39

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

Leu Pro Asp Thr Arg Cys
20

<210> 40
<211> 423
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Nucleic acid encoding RH2.5 R71V

<400> 40
atgggcagca cagccattct gggcctgctg ctggccgtgc tgcagggcgt gtgcgccgag 60

gtgcagctgg tcgagagcgg agccgaggtg aagaagccag gcgccagcgt caaggtgtcc 120

tgcaaggcca gcggctacag cttctccggc tacaccatga actgggtgcg gcaggcccca 180

ggccagaggc tggaatggat gggcctgatc aacccctaca acggcggcac cagctacaac 240

cagaacttca agggcagggt gacactgacc gtggatacca gcgccagcac cgcctacctg 300

gaactgaaca gcctgagaag cgaggacacc ggcgtgtact actgcgccag agaggactac 360

gacggctacc tgtacttcgc catggactac tggggccagg gcaccctggt gaccgtgagc 420

agc 423

<210> 41
<211> 15
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic sequence: Kozak consensus sequence

<400> 41
aagcttgccg ccacc 15