

29272.sequence.listing.txt
SEQUENCE LISTING

<110> ADIENNE Srl
<120> Anti-CD 26 antibodies and uses thereof
<130> 6459-X-2972 EP
<150> EP13425029
<151> 2013-02-19
<160> 159
<170> PatentIn version 3.5
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Gln Gln Arg Ser Ser Tyr Pro Asn Thr
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Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr
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Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

Ser 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 Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
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Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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Glu Arg Val Thr Leu Thr Cys Lys Ala Ser Glu Asn Val Val Thr Tyr
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Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile
35 40 45

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

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

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

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

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

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

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

Ser 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 Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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

Ser 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 Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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

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Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
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1 5 10 15

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

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

Ser 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 Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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

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

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

Ser 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 Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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

Ser 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 Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
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Asp Ile Gln Met Ile Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
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Asn Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
 35 40 45

Ser 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 Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

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

Ser 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 Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
 85 90 95

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

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Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

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

Ser 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 Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
 85 90 95

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

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29272.sequence.listing.txt

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

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

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

Ser 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 Arg Met Glu Ala Glu
65     70     75     80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85     90     95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
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Asp Ile Leu Xaa Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20     25     30

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

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

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

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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Asp Val Leu Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

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

Ser 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 Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
85 90 95

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

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Asp Ile Val Met Thr Gln Thr Pro Ala Ile Met Ser Ala Ser Pro Gly
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Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Asn Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
Seite 10

35

40

45

Ser 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 Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
 85 90 95

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

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<212> PRT

<213> Artificial Sequence

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<400> 21

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

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

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

Ser 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 Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Asn Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Leu Lys Arg
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<223> VH group 1

<400> 22

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

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

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
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Glu Val Lys Leu Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser

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Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

Ala Arg Trp Thr Val Val Gly Pro Gly Tyr Phe Asp Val Trp Gly Ala
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Gly Thr Thr Val Thr Val Ser Ser
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Glu Val Gln Gly Val Glu Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Arg Ser Tyr
20 25 30

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

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

29272.sequence.listing.txt

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

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Gln Val Gln Leu Gln Gln Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

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29272.sequence.listing.txt

Glu Val Gln Leu Gln Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

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Gln Val Gln Leu Gln Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

29272.sequence.listing.txt

Gly Thr Thr Val Thr Val Ser Ser
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Glu Val Gln Leu Gln Gln Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 30
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Gln Val Lys Leu Gln Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

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Glu Val Lys Leu Gln Gln Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
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<210> 32
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Glu Val Lys Val Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

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Asp Val Gln Leu Gln Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

29272.sequence.listing.txt

Ala Arg Trp Thr Val Val Gly Pro Gly Tyr Phe Asp Val Trp Gly Ala
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Gly Thr Thr Val Thr Val Ser Ser
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Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Pro Val Thr Val Ser Ser
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Gln Val Gln Leu Lys Glu Ser 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 Arg Ser Tyr
20 25 30

29272.sequence.listing.txt

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

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<400> 36

Glu Val Met Leu Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT

<213> Artificial Sequence

<220>

<223> VH group 1

<220>

<221> misc_feature

<222> (3)..(3)

<223> Leu or Glu

<400> 37

Glu Val Xaa Leu Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 38

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> VH group 1

<400> 38

Asp Val Lys Leu Gln Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

29272.sequence.listing.txt

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 39
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 39

Glu Val Gln Leu Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 40
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 40

29272.sequence.listing.txt

Glu Val Gln Leu Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 41
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 41

Glu Val Gln Leu His Gln Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

29272.sequence.listing.txt

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 42
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1
<400> 42

Glu Val Lys Leu Met Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 43
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1

<220>
<221> misc_feature
<222> (1)..(1)
<223> Glu, Gln or Lys

<220>
<221> misc_feature
<222> (6)..(6)
<223> Glu, Gln or Lys

<400> 43

29272.sequence.listing.txt

Xaa Val Gln Leu Gln Xaa Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 44
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1
<400> 44

Glu Val Lys Val Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

29272.sequence.listing.txt

Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 45
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 45

Glu Val Gln Leu Lys Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 46
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> VH group 1

<220>
<221> misc_feature
<222> (113)..(113)
<223> Arg or Trp

<400> 46

Glu Val Gln Leu Gln Gln Ser 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 Arg Ser Tyr
20 25 30

29272.sequence.listing.txt

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Xaa Thr Thr Val Thr Val Ser Ser
115 120

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

<220>
<223> VH group 1

<400> 47

Glu Val Gln Arg Val Glu Ser 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 Arg Ser Tyr
20 25 30

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

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

Lys Gly Lys Ala Thr Leu Thr Thr 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

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

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 48

29272.sequence.listing.txt

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

<220>
<223> CL

<400> 48

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

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

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
          35          40          45

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

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

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
          85          90          95

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
          100          105

```

<210> 49
<211> 336
<212> PRT
<213> Artificial Sequence

<220>
<223> CH1-CH2-CH3

<400> 49

```

Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Cys Gly
1          5          10          15

Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
          20          25          30

Phe Pro Glu Ser Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser
          35          40          45

Ser Val His Thr Phe Pro Ala Leu Leu Gln Ser Gly Leu Tyr Thr Met
          50          55          60

Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val
65          70          75          80

Thr Cys Ser Val Ala His Pro Ala Ser Ser Thr Thr Val Asp Lys Lys
          85          90          95

```

29272.sequence.listing.txt

Leu Glu Pro Ser Gly Pro Ile Ser Thr Ile Asn Pro Cys Pro Pro Cys
 100 105 110
 Lys Glu Cys His Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly Pro Ser
 115 120 125
 Val Phe Ile Phe Pro Pro Asn Ile Lys Asp Val Leu Met Ile Ser Leu
 130 135 140
 Thr Pro Lys Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro
 145 150 155 160
 Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala
 165 170 175
 Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Ile Arg Val Val
 180 185 190
 Ser Thr Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe
 195 200 205
 Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ser Pro Ile Glu Arg Thr
 210 215 220
 Ile Ser Lys Ile Lys Gly Leu Val Arg Ala Pro Gln Val Tyr Ile Leu
 225 230 235 240
 Pro Pro Pro Ala Glu Gln Leu Ser Arg Lys Asp Val Ser Leu Thr Cys
 245 250 255
 Leu Val Val Gly Phe Asn Pro Gly Asp Ile Ser Val Glu Trp Thr Ser
 260 265 270
 Asn Gly His Thr Glu Glu Asn Tyr Lys Asp Thr Ala Pro Val Leu Asp
 275 280 285
 Ser Asp Gly Ser Tyr Phe Ile Tyr Ser Lys Leu Asn Met Lys Thr Ser
 290 295 300
 Lys Trp Glu Lys Thr Asp Ser Phe Ser Cys Asn Val Arg His Glu Gly
 305 310 315 320
 Leu Lys Asn Tyr Tyr Leu Lys Lys Thr Ile Ser Arg Ser Pro Gly Lys
 325 330 335

<210> 50
 <211> 318
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL prevalent group 1

29272.sequence.listing.txt

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<400> 50
caaatgttc tcaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc      60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctgg aaataaaa                                     318
```

```
<210> 51
<211> 324
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> VL group 3
```

```
<400> 51
gacattgtaa tgaccaatc tcccaaattc atgtccatgt cagtaggaga gagggtcacc      60
ttgacctgca aggccagtga gaatgtgggt acttatgttt cctgggtatca acagaaacca      120
gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat      180
cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct      240
gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg      300
gggaccaagc tggaaataaa acgt                                     324
```

```
<210> 52
<211> 321
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> VL group 1
```

```
<400> 52
gatattgtgc tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc      60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctgg agctgaaacg t                                     321
```

```
<210> 53
<211> 320
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> VL group 1
```

```
<400> 53
gacattgagc tcaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc      60
```

29272.sequence.listing.txt

ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc	120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc	180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa	240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cgaggggggg	300
accaagctgg aaataaacgt	320

<210> 54
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 54 gatattgtgt tgacacagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc	60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc	120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc	180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa	240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cgaggggggg	300
accaagctgg aaataaaaacg t	321

<210> 55
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 55 gacattgtgc tgacacagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc	60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc	120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc	180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa	240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cgaggggggg	300
accaagctgg aaatcaaacg t	321

<210> 56
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 56 gacattgtga tgacgcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc	60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc	120

29272.sequence.listing.txt

acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctcg agatcaaacg t 321

<210> 57
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 57
 gacattgtga tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgtagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctgg aaataaaacg t 321

<210> 58
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 58
 gatattgtga tgactcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgtagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctgg aaataaaacg t 321

<210> 59
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 59
 gacattgtga tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgtagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240

29272.sequence.listing.txt

gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctcg agatcaaacg t 321

<210> 60
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 60
 gatattgtga tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgttaagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctgg aaataaaacg t 321

<210> 61
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 61
 gatattgtga tgacgcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgttaagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctcg agatcaaacg t 321

<210> 62
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 62
 gatattgtga tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgttaagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300

accaagctgg agatcaaacg t 321

<210> 63
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 63
 gacattgtga tgacgcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgttaagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacgtt cggagggggg 300
 accaagctgg agctgaaacg t 321

<210> 64
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 64
 gacattgtga tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgttaagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacgtt cggagggggg 300
 accaagctgg agctgaaacg t 321

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

<220>
 <223> VL group 1

<400> 65
 gatattgtga tgacgcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
 ataacctgca gtgccagctc aagtgttaagt tacatgaact ggttccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacgtt cggagggggg 300
 accaagctgg agctgaaacg t 321

29272.sequence.listing.txt

<210> 66
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> VL group 1

<400> 66
gatattgtga tgacacagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc 120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
ttcagtgga gtggatctgg gacctcttac tctctcaca tcagccgaat ggaggctgaa 240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacgtt cggagggggg 300
accaagctgg agctgaaacg t 321

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

<220>
<223> VL group 1

<400> 67
gacattcaga tgactcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc 120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgcttgc 180
ttcagtgga gtggatctgg gacctcttac tctctcaca tcagccgaat ggaggctgaa 240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacgtt cggagggggg 300
accaagctcg agatcaaacg t 321

<210> 68
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> VL group 1

<400> 68
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ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc 120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
ttcagtgga gtggatctgg gacctcttac tctctcaca tcagccgaat ggaggctgaa 240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacgtt cggagggggg 300
accaagctcg agatcaaacg t 321

<210> 69
<211> 321
<212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 69

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gatattcaga tgaccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc      60
ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctcg agatcaaacg t                                     321

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<210> 70

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 70

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ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctcg agatcaaacg t                                     321

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<210> 71

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 71

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ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctgg aaataaaacg t                                     321

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<210> 72

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 72
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 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctgg aaatcaaacg t 321

<210> 73
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<400> 73
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 ataacctgca gtgccagctc aagtgttaagt tacatgaact gggtccagca gaagccaggc 120
 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctcg agatcaaacg t 321

<210> 74
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VL group 1

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> a, t, g or c

<400> 74
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 acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc 180
 ttcagtggca gtggatctgg gacctcttac tctctcacia tcagccgaat ggaggctgaa 240
 gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg 300
 accaagctgg agctgaaacg t 321

<210> 75
 <211> 321
 <212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 75

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ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctcg agatcaaacg t                                     321

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<210> 76

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 76

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ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctcg agatcaaacg t                                     321

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<210> 77

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> VL group 1

<400> 77

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ataacctgca gtgccagctc aagtgtaagt tacatgaact ggttccagca gaagccaggc      120
acttctccca aactctggat ttatagcacc tccaacctgg cttctggagt ccctgctcgc      180
ttcagtggca gtggatctgg gacctttac tctctcaca tcagccgaat ggaggctgaa      240
gatgctgcca cttattactg ccagcaaagg agtagttacc cgaacacggt cggagggggg      300
accaagctgg agctgaaacg t                                     321

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<210> 78

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

<400> 78
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 79
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 79
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 80
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 80
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 81
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

29272.sequence.listing.txt

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> a, t, g or c

<400> 81
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 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca 360

<210> 82
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 82
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 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca 360

<210> 83
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 83
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 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca 360

<210> 84
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>

<223> VH group 1

<400> 84
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 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 85
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 85
 gaagtgaagt tggaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 86
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 86
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 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 87
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 87

29272.sequence.listing.txt

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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca	360

<210> 88
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 88	
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cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca	360

<210> 89
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 89	
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cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca	360

<210> 90
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 90	
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120

29272.sequence.listing.txt

cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc caggttactt cgatgtctgg ggcgcagga ccacggtcac cgtctcctca	360

<210> 91
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 91	
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cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
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<210> 92
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 92	
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cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc caggttactt cgatgtctgg ggcgcagga ccacggtcac cgtctcctca	360

<210> 93
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 <212> DNA
 <213> Artificial Sequence

<220>
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac	180

29272.sequence.listing.txt

aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggtactt cgatgtctgg ggcgcagga ccacggtcac cgtctcctca 360

<210> 94
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 94
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggtactt cgatgtctgg ggcgcagga ccacggtcac cgtctcctca 360

<210> 95
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 95
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cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
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<210> 96
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 96
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cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300

29272.sequence.listing.txt

gtagtaggcc cagggctactt cgatgtctgg ggcgcagggga ccacgggtcac cgtctcctca 360

<210> 97
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<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 97
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggga ccacgggtcac cgtctcctca 360

<210> 98
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 98
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggga ccacgggtcac cgtctcctca 360

<210> 99
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 99
gaggtgcagc ttcaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggga ccacgggtcac cgtctcctca 360

29272.sequence.listing.txt

<210> 100
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 100
 gaggtacagc ttcaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggtactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 101
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 101
 gaggtgcagc tgcaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggtactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 102
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 102
 caggtgcagc tgcaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
 tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
 cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac 180
 aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
 atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
 gtagtaggcc cagggtactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 103
 <211> 360

29272.sequence.listing.txt

<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 103
caggttcaac tgcaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggactt cgatgtctgg ggcgcagga ccacggtcac cgtctcctca 360

<210> 104
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 104
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggactt cgatgtctgg ggcgcagga ccacggtcac cgtctcctca 360

<210> 105
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 105
gaggtccagc tgcaacagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggactt cgatgtctgg ggcgcagga ccactctcac agtctcctca 360

<210> 106
<211> 360
<212> DNA
<213> Artificial Sequence

29272.sequence.listing.txt

<220>

<223> VH group 1

<400> 106

cagggtcaagc tgcaggagtc aggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 107

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

<400> 107

cagggtgaagc tgcaggagtc tggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 108

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

<400> 108

gagggtgaagc tgcagcagtc tggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 109

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

29272.sequence.listing.txt

<400> 109
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 110
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 110
gaggtgaagg tgggtggagtc aggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 111
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 111
gaggtgaagg tgggtggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg 120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac 180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac 240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg 300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca 360

<210> 112
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> VH group 1

<400> 112
gatgtgcagc ttcaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg 60

29272.sequence.listing.txt

tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 113
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 113 gaggtgcagc tgcagcagtc tggagctgaa ctggtaaagc ctggggcctc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg cccaggtcac cgtctcctca	360

<210> 114
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 114 caggtgcagc tgaaggagtc aggagctgaa ctggtaaagc ctggggcctc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 115
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 115 gaggtgatgc tggtggagtc tggagctgaa ctggtaaagc ctggggcctc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180

29272.sequence.listing.txt

aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 116
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<220>
 <221> misc_feature
 <222> (7)..(7)
 <223> a, g or c

<400> 116	
gaagtgnagc tggtaggagtc tggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 117
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 117	
gatgtaaagc ttcaggagtc tggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 118
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 118	
gaggtgcaac tggtaggagtc aggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60

29272.sequence.listing.txt

tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 119
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<400> 119 gaggtgcagc tgggtggagtc tggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg cctcagtcac cgtctcctca	360

<210> 120
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> VH group 1

<220>
 <221> misc_feature
 <222> (6)..(6)
 <223> a, t, g or c

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> a, t, g or c

<400> 120 gaggtncagc tgcancagtc tggagctgaa ctggtaaagc ctggggccttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggctactt cgatgtctgg ggcgcagggg ccacgggtcac cgtctcctca	360

<210> 121
 <211> 360
 <212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

<400> 121

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gaggtgaagc tgatggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg      60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg      120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac      180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac      240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg      300
gtagtaggcc caggg tactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca      360
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<210> 122

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

<220>

<221> misc_feature

<222> (1)..(1)

<223> a, g or c

<220>

<221> misc_feature

<222> (6)..(6)

<223> a, t, g or c

<220>

<221> misc_feature

<222> (16)..(16)

<223> a, g or c

<400> 122

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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg      120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac      180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac      240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg      300
gtagtaggcc caggg tactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca      360
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<210> 123

<211> 360

<212> DNA

<213> Artificial Sequence

<220>

<223> VH group 1

<400> 123

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gaggtgaagg tggaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg      60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg      120
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29272.sequence.listing.txt

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cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac      180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac      240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg      300
gtagtaggcc cagggactt  cgatgtctgg ggcgcaggga cctcagtcac cgtctcctca      360
```

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<210> 124
<211> 360
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> VH group 1
```

```
<400> 124
gaggtgcagc tgaaggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg      60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg      120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac      180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac      240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg      300
gtagtaggcc cagggactt  cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca      360
```

```
<210> 125
<211> 360
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> VH group 1
```

```
<220>
<221> misc_feature
<222> (337)..(337)
<223> a, t or c
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<400> 125
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tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg      120
cctgaacagg gacttgagtg gattggatgg atttttcctg gagatggtag tactaagtac      180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac      240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg      300
gtagtaggcc cagggactt  cgatgtctgg ggcgcangga ccacggtcac cgtctcctca      360
```

```
<210> 126
<211> 360
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> VH group 1
```

```
<400> 126
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29272.sequence.listing.txt

gaggtgcagc ggggtggagtc tggagctgaa ctggtaaagc ctggggcttc agtgaagttg	60
tcctgcaagg cttctggcta caccttcaga agttatgata taaactgggt gagacagagg	120
cctgaacagg gacttgagt gattggatgg atttttcctg gagatggtag tactaagtac	180
aatgagaagt tcaagggcaa ggccacactg actacagaca aatcctccag cacagcctac	240
atgcagctca gcaggctgac atctgaggac tctgctgtct atttctgtgc aagatggacg	300
gtagtaggcc cagggtactt cgatgtctgg ggcgcaggga ccacggtcac cgtctcctca	360

<210> 127
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CL

<400> 127 cgggctgatg ctgcaccaac tgtatccatc ttcccacat ccagtgaagca gttaacatct	60
ggaggtgcct cagtcgtgtg cttcttgaac aacttctacc ccaaagacat caatgtcaag	120
tggaagattg atggcagtga acgacaaaat ggcgtcctga acagttggac tgatcaggac	180
agcaaagaca gcacctacag catgagcagc accctcacgt tgaccaagga cgagtatgaa	240
cgacataaca gttatacctg tgaggccact cacaagacat caacttcacc cattgtcaag	300
agcttcaaca ggaatgagtg t	321

<210> 128
 <211> 1008
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CH1-CH2-CH3

<400> 128 gccaaaacaa caccctcatc agtctatcca ctggcccctg ggtgtggaga tacaactggt	60
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tggaactctg gatccctgtc cagcagtgtg cacaccttcc cagctctcct gcagtctgga	180
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gggcccattt caacaatcaa cccctgtcct ccatgcaagg agtgtcaca atgcccagct	360
cctaacctcg aggggtggacc atccgtcttc atcttccctc caaatatcaa ggatgtactc	420
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gacgtccaga tcagctggtt tgtgaacaac gtggaagtac acacagctca gacacaaacc	540
catagagagg attacaacag tactatccgg gtggtcagca ccctcccat ccagcaccag	600
gactggatga gtggcaagga gttcaaatgc aaggtcaaca acaaagacct cccatcacc	660
atcgagagaa ccatctcaa aattaaagg ctagtcagag ctccacaagt atacatcttg	720
ccgccaccag cagagcagtt gtccaggaaa gatgtcagtc tacttgcct ggtcgtgggc	780

29272.sequence.listing.txt

ttcaaccctg gagacatcag tgtggagtgg accagcaatg ggcatacaga ggagaactac	840
aaggacaccg caccagtcct ggactctgac ggttcttact tcatatatag caagctcaat	900
atgaaaacaa gcaagtggga gaaaacagat tccttctcat gcaacgtgag acacgagggt	960
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Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	Asn
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<220>
 <223> CDR-L2 Light Group1

<400> 130

Ser	Thr	Ser	Asn	Leu	Ala	Ser
1				5		

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 <223> CDR-L1 Light Group3

<400> 131

Lys	Ala	Ser	Glu	Asn	Val	Val	Thr	Tyr	Val	Ser
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 <223> CDR-L2 Light Group3

<400> 132

Gly	Ala	Ser	Asn	Arg	Tyr	Thr
1				5		

<210> 133
 <211> 10
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<213> Artificial Sequence

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<223> CDR-H1 Heavy

<400> 133

Gly Tyr Thr Phe Arg Ser Tyr Asp Ile Asn
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<210> 134

<211> 17

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<223> CDR-H2 Heavy

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

<210> 135

<211> 7

<212> PRT

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<223> ABR1 Light group 1

<400> 135

Ser Ser Val Ser Tyr Met Asn
1 5

<210> 136

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> ABR2 Light group 1

<400> 136

Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser
1 5 10

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<211> 8

<212> PRT

<213> Artificial Sequence

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<223> ABR3 Light group 1

<400> 137

Gln Gln Arg Ser Ser Tyr Pro Asn
1 5

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 <212> PRT
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 <223> ABR1* Light group 3

<400> 138

Glu Asn Val Val Thr Tyr Val Ser
 1 5

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 <223> ABR3* Light group 3

<400> 140

Gly Gln Gly Tyr Ser Tyr Pro Tyr
 1 5

<210> 141
 <211> 9
 <212> PRT
 <213> Artificial Sequence

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 <223> ABR1h Heavy group 1

<400> 141

Tyr Thr Phe Arg Ser Tyr Asp Ile Asn
 1 5

<210> 142
 <211> 14
 <212> PRT
 <213> Artificial Sequence

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<400> 142

Trp Ile Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Lys Tyr
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5

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

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 <223> ABR3h Heavy group 3

<400> 143

Arg Trp Thr Val Val Gly Pro Gly Tyr Phe Asp Val
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<210> 144
 <211> 766
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<220>
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Met Lys Thr Pro Trp Lys Val Leu Leu Gly Leu Leu Gly Ala Ala Ala
 1 5 10 15

Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
 20 25 30

Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr
 35 40 45

Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser
 50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn
 65 70 75 80

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

Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln
 100 105 110

Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
 115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
 130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val
 145 150 155 160

29272.sequence.listing.txt

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile
165 170 175

Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp
180 185 190

Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
225 230 235 240

Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr
245 250 255

Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn
260 265 270

Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr
275 280 285

Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr
290 295 300

Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln
305 310 315 320

Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg
325 330 335

Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly
340 345 350

Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly
355 360 365

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile
370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly
385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
420 425 430

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu

435

440

445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu
 450 455 460
 Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr
 465 470 475 480
 Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp
 485 490 495
 Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys
 500 505 510
 Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met
 515 520 525
 Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu
 530 535 540
 Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg
 545 550 555 560
 Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
 565 570 575
 Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
 580 585 590
 Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
 595 600 605
 Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile
 610 615 620
 Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
 625 630 635 640
 Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
 645 650 655
 Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
 660 665 670
 Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val
 675 680 685
 Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
 690 695 700
 Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser
 705 710 715 720

29272.sequence.listing.txt

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro
755 760 765

<210> 145
<211> 766
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<220>
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Leu Val Thr Val Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr
20 25 30

Asp Asp Ala Ala Ala Asp Ser Arg Arg Thr Tyr Thr Leu Thr Asp Tyr
35 40 45

Leu Lys Ser Thr Phe Arg Val Lys Phe Tyr Thr Leu Gln Trp Ile Ser
50 55 60

Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Leu Phe Asn
65 70 75 80

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

Glu Leu Gly Tyr Ser Thr Asn Asp Tyr Ser Val Ser Pro Asp Arg Gln
100 105 110

Phe Ile Leu Phe Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr
115 120 125

Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr
130 135 140

Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Ile Thr Trp Ser Pro Val
145 150 155 160

Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Asn
165 170 175

29272.sequence.listing.txt

Glu Pro Asn Leu Ser Ser Gln Arg Ile Thr Trp Thr Gly Lys Glu Asn
180 185 190

Val Ile Tyr Asn Gly Val Thr Asp Trp Val Tyr Glu Glu Glu Val Phe
195 200 205

Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala
210 215 220

Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe
225 230 235 240

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

Pro Lys Ala Gly Ala Glu Asn Pro Thr Val Lys Phe Phe Val Val Asp
260 265 270

Thr Arg Thr Leu Ser Pro Asn Ala Ser Val Thr Ser Tyr Gln Ile Val
275 280 285

Pro Pro Ala Ser Val Leu Ile Gly Asp His Tyr Leu Cys Gly Val Thr
290 295 300

Trp Val Thr Glu Glu Arg Ile Ser Leu Gln Trp Ile Arg Arg Ala Gln
305 310 315 320

Asn Tyr Ser Ile Ile Asp Ile Cys Asp Tyr Asp Glu Ser Thr Gly Arg
325 330 335

Trp Ile Ser Ser Val Ala Arg Gln His Ile Glu Ile Ser Thr Thr Gly
340 345 350

Trp Val Gly Arg Phe Arg Pro Ala Glu Pro His Phe Thr Ser Asp Gly
355 360 365

Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Lys His Ile
370 375 380

Cys His Phe Gln Thr Asp Lys Ser Asn Cys Thr Phe Ile Thr Lys Gly
385 390 395 400

Ala Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr
405 410 415

Tyr Ile Ser Asn Glu His Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr
420 425 430

Arg Ile Gln Leu Asn Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu
435 440 445

29272.sequence.listing.txt

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Ala Ser Phe Ser Asn Lys
450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Phe Gly Pro Gly Leu Pro Leu Tyr
465 470 475 480

Thr Leu His Ser Ser Ser Ser Asp Lys Glu Leu Arg Val Leu Glu Asp
485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asp Val Gln Met Pro Ser Lys
500 505 510

Lys Leu Asp Val Ile Asn Leu His Gly Thr Lys Phe Trp Tyr Gln Met
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Ile
530 535 540

Glu Val Tyr Ala Gly Pro Cys Ser Gln Lys Val Asp Thr Val Phe Arg
545 550 555 560

Leu Ser Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu
595 600 605

Ala Thr Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asp Lys Arg Ile
610 615 620

Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu
625 630 635 640

Gly Ala Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val
645 650 655

Ser Lys Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp Tyr Tyr Arg Asn Ser Thr Val
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Leu Ser
705 710 715 720

Lys Ala Leu Val Asp Ala Gly Val Asp Phe Gln Thr Met Trp Tyr Thr

725

730

735

Asp Glu Asp His Gly Ile Ala Ser Asn Met Ala His Gln His Ile Tyr
 740 745 750

Thr His Met Ser His Phe Leu Lys Gln Cys Phe Ser Leu Pro
 755 760 765

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<220>
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<400> 146

Asp Tyr Asp Glu Ser Ser Gly Arg Trp Asn Cys Leu Val Ala Arg
 1 5 10 15

<210> 147
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> >CD26 EPITOPE 2

<400> 147

Asp Val Thr Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu
 1 5 10 15

<210> 148
 <211> 13
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> >CD26 EPITOPE 3

<400> 148

Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala Tyr Ala Gln
 1 5 10

<210> 149
 <211> 15
 <212> PRT
 <213> Homo sapiens

<220>
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29272.sequence.listing.txt

<400> 149

Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr Thr Leu His
1 5 10 15

<210> 150

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> >CD26 EPITOPE 5

<400> 150

Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met Ile Leu Pro
1 5 10

<210> 151

<211> 16

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> >CD26 EPITOPE 6

<400> 151

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

<210> 152

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> >CD26 EPITOPE 7

<400> 152

Pro Asn Gly Thr Phe
1 5

<210> 153

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<223> > CD26 EPITOPE 8

<400> 153

Thr Thr Gly Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe
1 5 10 15

29272.sequence.listing.txt

<210> 154
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 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> >CD26 EPITOPE 9

<400> 154

Arg Phe Arg Pro Ser Glu Pro His Phe
 1 5

<210> 155
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> >CD26 EPITOPE 10

<400> 155

Thr Phe Ile Thr Lys Gly Thr Trp Glu Val Ile Gly
 1 5 10

<210> 156
 <211> 9
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> >CD26 EPITOPE 11

<400> 156

Asp Tyr Leu Tyr Tyr Ile Ser Asn Glu
 1 5

<210> 157
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE
 <223> >CD26 EPITOPE 12

<400> 157

Ser Cys Glu Leu Asn Pro Glu Arg Cys Gln Tyr Tyr
 1 5 10

<210> 158
 <211> 6
 <212> PRT
 <213> Homo sapiens

29272.sequence.listing.txt

<220>
<221> MISC_FEATURE
<223> >CD26 EPITOPE 13

<400> 158

Ser Gly Pro Gly Leu Pro
1 5

<210> 159
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> >CD26 EPITOPE 14

<400> 159

Ala Thr Gln Glu Arg
1 5