SEQUENCE LISTING

<110> Frazier, William
Manning, Pamela
Frey, Gerhard
Chang, Hwai Wen

<120> Therapeutic CD47 Antibodies

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<150> US 61/736301
<151> 2012-12-12

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<170> PatentIn version 3.5

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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
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1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
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Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

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

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65                  70                  75                  80

Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Ser Gln Asn
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Thr His Val Pro Arg Thr Phe Gly Gln Gly
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Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

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

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

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Asn
                85                  90                  95
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Thr His Val Pro Arg Thr Phe Gly Gln Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser

35 40 45

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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1               5                  10                  15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
            100                 105
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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 18

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

Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 19

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65 70 75 80

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 23

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 24

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 25

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

Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
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Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 27

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 28

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

<210> 29
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<212> PRT

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<400> 29

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

Glu Arg Ala Thr Leu Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 30

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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<400> 31

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

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
65 70 75 80

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

Thr His Val Pro Arg Thr Phe Gly Gln Gly
100 105

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tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

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tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

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gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

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tacctgcaga agccagggca gtctccacag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 40
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 40
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 41
<211> 318
<212> DNA
<213> Artificial Sequence

<220>

<223> light chain variable region

<400> 41
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atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 42
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 42
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atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 43
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 43
gaaattgtgt tgacacagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc cctcgaggtt cagtggcagt ggatctggga cagatttcac ctttaccatc 240

agtagcctgg aagctgaaga tgctgcaaca tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 44
<211> 318
<212> DNA

<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 44
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 45
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 45
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atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 46
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 46
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 47
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 47
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc catcaaggtt cagcggcagt ggatctggga cagaattcac tctcaccatc 240

agcagcctgc agcctgatga ttttgcaact tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 48
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 48
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 49
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 49
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

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

<220>
<223> light chain variable region

<400> 50
gaaattgtgt tgacacagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc cctcgaggtt cagtggcagt ggatctggga cagatttcac ctttaccatc 240

agtagcctgg aagctgaaga tgctgcaaca tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 51
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 51
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 52
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 52
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 53
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 53
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 54
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 54
gaaattgtgt tgacacagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60

ctctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc cctcgaggtt cagtggcagt ggatctggga cagatttcac ctttaccatc 240

agtagcctgg aagctgaaga tgctgcaaca tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 55
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 55
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60

atctcctgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

tatcagcaga aaccagggaa agctcctaag ctcctgatct ataaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt gggtcaggca ctgatttcac actgaaaatc 240

agcagggtgg aggctgagga tgttggagtt tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 56
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 56
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgca gatctagtca gagccttgta cacagtaatg gaaacaccta tttacattgg 120

taccagcaga aacctggcca ggctcccagg ctcctcatct ataaagtttc ctaccgattt 180

tctggggtcc catcaaggtt cagcggcagt ggatctggga cagaattcac tctcaccatc 240

agcagcctgc agcctgatga ttttgcaact tattactgtt ctcaaaatac acatgttcct 300

cggacgttcg gccaaggg 318

<210> 57
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 57

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

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

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

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

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

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

Thr Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 58
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 58

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 59
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 59

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

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

Tyr Val Phe Trp Val Arg Gln Ala Arg Gly Gln Arg Leu Glu Trp Ile

35 40 45

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 60
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 60

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 61
<211> 109
<212> PRT
<213> Artificial Sequence

<220>

<223> heavy chain variable region

<400> 61

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

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

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

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

Lys Asn Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 62
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 62

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

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

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

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

Lys Asn Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys

85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 63
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 63

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

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

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 64
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 64

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 65
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 65

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Val Phe Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 66
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 66

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

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

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65                  70                  75                  80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
            100                 105
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<210> 67
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 67

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

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

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65                  70                  75                  80
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Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 68
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 68

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 69
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 69

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 70
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 70

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

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

Tyr Val Phe Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 71
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 71

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 72
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 72

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

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

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 73
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 73

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 74
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 74

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 75
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 75

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

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

Tyr Val Phe Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 76
<211> 109
<212> PRT

<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 76

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

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

Tyr Val Phe Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu
35 40 45

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 77
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 77

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
            100                 105
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<210> 78
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 78

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

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

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65                  70                  75                  80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
            100                 105
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<210> 79
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 79

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Asn Tyr
```

20 25 30

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 80
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 80

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

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

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

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

Lys Asn Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val Val
65 70 75 80

Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 81
<211> 109

<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 81

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

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

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

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

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

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

Ala Arg Gly Gly Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105

<210> 82
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 82
gaggtccagc tgcagcagtt tggggctgaa ctggtgaagc ctggggcttc aatgaagttg 60

tcctgcaagg cttctggcta caccttcacc aactactatg tattctgggt gaaacagagg 120

cctggacaag gccttgagtg gattggagac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacaa ggccacactg actgtagaca agtcctccac cacaacatac 240

ttgcaactca gcagcctgac atctgaggac tctgcggtct attactgtac aagaggggtt 300

tatactatgg actactgggg tcaagga 327

<210> 83
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 83
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 84
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 84
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 85
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 85
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 86
<211> 327

<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 86
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcagtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcaccata tcagtagaca cgtccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgcggac acggctgtgt attactgtgc gagagggggt 300

tatactatgg actactgggg ccaggga 327

<210> 87
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 87
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtcagtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcaccata tcagtagaca cgtccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgcggac acggctgtgt attactgtgc gagagggggt 300

tatactatgg actactgggg ccaggga 327

<210> 88
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 88
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagagggggt 300

tatactatgg actactgggg ccaggga 327

<210> 89
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 89
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc ctggggctac agtgaaaatc 60

tcctgcaagg tttctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagggggt 300

tatactatgg actactgggg ccaggga 327

<210> 90
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 90
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg 60

acctgcacct tctctggcta caccttcacc aactactatg tattctggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag attcaccatc tccagagaca acgccaagaa ctcactgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagggggt 300

tatactatgg actactgggg ccaggga 327

<210> 91
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 91
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagagggggt 300

tatactatgg actactgggg ccaggga 327

<210> 92
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 92
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 93
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 93
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc ctggggctac agtgaaaatc 60

tcctgcaagg tttctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 94
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 94
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc ctggggctac agtgaaaatc 60

tcctgcaagg tttctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 95
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 95
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta caccttcacc aactactatg tattctggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 96
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 96
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 97
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 97
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 98
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 98
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcaccatc tcagccgaca agtccatcag caccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 99
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 99
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60

tcctgcaagg tttctggcta caccttcacc aactactatg tattctggat ccgccagccc 120

ccagggaagg ggctggagtg gattggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 100
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 100

gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta caccttcacc aactactatg tattctggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 101
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 101
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60

tcctgtaagg gttctggcta caccttcacc aactactatg tattctggat caggcagtcc 120

ccatcgagag gccttgagtg gctgggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 102
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 102
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg 60

acctgcacct tctctggcta caccttcacc aactactatg tattctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 103
<211> 327
<212> DNA
<213> Artificial Sequence

<220>

<223> heavy chain variable region

<400> 103
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 104
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 104
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 105
<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 105
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60

acctgcactg tctctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag actcaccatc tccaaggaca cctccaaaaa ccaggtggtc 240

cttacaatga ccaacatgga ccctgtggac acagccacgt attactgtgc aagaggggt 300

tatactatgg actactgggg ccaggga 327

<210> 106
<211> 327
<212> DNA

<213> Artificial Sequence

<220>
<223> heavy chain variable region

<400> 106
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc ctggggctac agtgaaaatc 60

tcctgcaagg tttctggcta caccttcacc aactactatg tattctgggt gcgacaggct 120

cgtggacaac gccttgagtg gataggtgac attaatcctg tcaatggtga tactaacttc 180

aatgagaaat tcaagaacag agtcacgatt accgcggaca aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggggtt 300

tatactatgg actactgggg ccaggga 327

<210> 107
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<223> complete light chain

<400> 107

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

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

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

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

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

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

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

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

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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<210> 108
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
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<400> 108
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tacctgcaga agccaggcca gtctccaaag ctcctgatct acaaagtttc ctaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaaatac acatgttcct 300

cggacgttcg gccaagggac caaggtggaa atcaaacgta cggtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

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<210> 109
<211> 446
<212> PRT
<213> Artificial Sequence

<220>
<223> complete heavy chain

<400> 109

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255
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Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

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

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

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

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

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

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

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

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

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
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Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

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

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<212> DNA
<213> Artificial Sequence

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tcctgcaagg cttctggcta caccttcacc aactactatg tattctgggt gaaacagagg 120

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cctggacaag gccttgagtg gattggagac attaatcctg tcaatggtga tactaacttc      180

aatgagaaat tcaagaacaa ggccacactg actgtagaca agtcctccac cacaacatac      240

ttgcaactca gcagcctgac atctgaggac tctgcggtct attactgtac aagagggggt      300

tatactatgg actactgggg ccagggaacg ctggtcaccg tcagctcagc ctccaccaag      360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc      420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc      480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc      540

ctcagcagcg tggtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac      600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac      660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc      720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc      780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc      840

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agtacaacag cacgtaccgt      900

gtggtcagcg tcctcaccgt cctgcaccag gactggctga atggcaagga gtacaagtgc      960

aaggtcagca acaaagccct cccagccccc atcgagaaaa ccatctccaa agccaaaggg     1020

cagccccgag aaccacaggt gtacaccctg cccccatccc gggatgagct gaccaagaac     1080

caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg     1140

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ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac     1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc     1320

tccctgtctc cgggtaaatg a                                               1341
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