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<120> Novel Modulators

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<170> PatentIn version 3.5

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

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

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

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

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Ala Pro Ala
    50                  55                  60

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

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

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

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

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

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

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
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85 90 95

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

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

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

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

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

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

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

Pro Val Glu Glu Glu Asp Val Ala Thr Tyr Tyr Cys Gln His Asn Arg
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Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
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Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
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Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn Lys Leu Leu Ile
        35                  40                  45
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Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
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Asp Thr Ile Thr Ile Thr Cys His Ala Ser Gln Asn Ile Asn Val Trp
20 25 30

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

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

Ser Gly Ser Gly Thr Gly Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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

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

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

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

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

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

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

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

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

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        35                  40                  45

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

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

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

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80
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Glu Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Tyr Pro Phe
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Thr Phe Gly Ser Gly Thr Lys Val Glu Ile Lys Arg
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Asp Ile Gln Met Thr Gln Ser Pro Ser Tyr Leu Ala Ala Ser Pro Gly
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Glu Thr Ile Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Ser Lys Tyr
20 25 30

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

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

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Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln His Ile Asn Lys Tyr
20 25 30

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

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

Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65 70 75 80

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

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

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20 25 30

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

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

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

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

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

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu Asn Ile His
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Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
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65 70 75 80

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Arg Val Thr Ile Ser Cys Ser Gly Ser Phe Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Val

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Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Gly Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
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Ser Pro His Val
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Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Ser Gly Trp

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Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Gly Pro Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp Ser Asn Thr
85 90 95

Gln

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<400> 26

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

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

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

Ile Tyr Asp Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Ser Gly Pro Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<400> 27

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

Arg Val Thr Ile Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ala Gly
20 25 30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65 70 75 80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
85 90 95

Leu Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

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

Ser Gly Trp Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Arg Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Gln Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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

Arg Val Thr Ile Ser Cys Ser Gly Asn Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly His Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<400> 31

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Asn Ser Asn Ile Gly Ser Arg
20 25 30

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

```
Ile Tyr Glu Asn Asn Lys Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Ala Gly Ser Asn
                85                  90                  95

Asn Leu Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 32

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Phe Ser Asn Ile Gly Gly Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Val Ser Leu
                85                  90                  95
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Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<400> 33

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<400> 34

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Pro Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 35

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Phe Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 36

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30
```

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 37
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<212> PRT
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<400> 37

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

Ile Tyr Arg Asn Tyr Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu

85 90 95

Thr Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 38
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<223> L-CDR3

<400> 38

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asn Ile Gly Ala Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 39
<211> 111
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<223> L-CDR3

<400> 39

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Trp Asp Asp Ser Leu
                85                  90                  95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<400> 40

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asp Thr Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<223> L-CDR3

<400> 41

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn

20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 42
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<220>
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<220>
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<400> 42

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

Arg Val Thr Ile Ser Cys Ser Gly Gly Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  43
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<212>  PRT
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<220>
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<223>  L-CDR2

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<223>  L-CDR3

<400>  43

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Pro His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  44
<211>  111
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<213> Homo sapiens

<220>
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<220>
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<223> L-CDR3

<400> 44

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65 70 75 80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
85 90 95

Leu Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<223> L-CDR3

<400> 46

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

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Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp His Ser
                85                  90                  95

Leu Ser Ala His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110

Gly
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<223> L-CDR3

<400> 47

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

Arg Val Thr Ile Ser Cys Ser Gly Thr Ser Ser Asn Phe Gly Arg Arg
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

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<212>  PRT
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<223>  L-CDR3

<400>  48

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

Arg Val Thr Ile Ser Cys Ser Gly Arg Ser Ser Asn Ile Gly Tyr Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95
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Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 49
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<223> L-CDR3

<400> 49

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

Arg Val Thr Ile Ser Cys Ser Gly Arg Ser Ser Asn Ile Glu Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<223> L-CDR3

<400> 50

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Asp Ser
                85                  90                  95

His Leu His Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 51
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<223> L-CDR2

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<222> (90)..(100)
<223> L-CDR3

<400> 51

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Gly Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Pro His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 52
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<220>
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<223> L-CDR3

<400> 52

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

Arg Val Thr Ile Ser Cys Ser Gly Asn Ser Ser Asn Ile Gly Asn Ser
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<400> 53

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
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85 90 95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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<223> L-CDR3

<400> 54

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Pro His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 55
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<223> L-CDR3

<400> 55

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Pro His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<400> 56

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 57
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<212> PRT
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<223> L-CDR2

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<222> (90)..(99)
<223> L-CDR3

<400> 57

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

Arg Val Thr Ile Ser Cys Ser Gly Gly Asn Ser Asn Ile Gly Ser Asn

20 25 30

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

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Gly Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 58
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<212> PRT
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<223> L-CDR3

<400> 58

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65 70 75 80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Ser
85 90 95

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 59
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<212> PRT
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<223> L-CDR2

<220>
<221> MISC_FEATURE
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<223> L-CDR3

<400> 59

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Pro His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 60
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<223> L-CDR3

<400> 60

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asp Thr Leu
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> Xaa can be any naturally occurring amino acid

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<223> L-CDR2

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<400> 61

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ile Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Pro His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 62

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 63
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<212> PRT
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<220>
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<223> L-CDR3

<400> 63

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

Arg Val Thr Ile Ser Cys Ser Gly Arg Asn Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Arg Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Asn Phe Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 64
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<212> PRT
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<223> Clone XPA.15.146 light chain

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<222> (26)..(33)
<223> L-CDR1

<220>
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<222> (51)..(53)
<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> L-CDR3

<400> 64

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

Arg Val Thr Ile Ser Cys Ser Gly Thr Asp Ser Asn Phe Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 65
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<223> L-CDR2

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<223> L-CDR3

<400> 65

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
20 25 30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65 70 75 80

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

Asn Gln Phe Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 66
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<212> PRT
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<223> L-CDR3

<400> 66

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

Arg Val Thr Ile Ser Cys Ser Gly Ile Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Pro
                85                  90                  95

Arg Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 67
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<223> L-CDR3

<400> 67

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

Arg Val Thr Ile Ser Cys Ser Gly Cys Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Ile Gly His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 68
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<223> L-CDR3

<400> 68

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

Arg Val Thr Ile Ser Cys Ser Gly Ile Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Pro
85 90 95

Arg Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 69
<211> 111
<212> PRT
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<223> L-CDR3

<400> 69

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

Arg Val Thr Ile Ser Cys Ser Gly Arg Ser Ser Asn Ile Gly Tyr Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

```
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 70

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asp Thr Leu
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 71
<211> 111
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<213> Homo sapiens

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<223> L-CDR3

<400> 71

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

Arg Val Thr Ile Ser Cys Ser Gly Thr Ser Ser Asn Leu Gly Ser His
            20                  25                  30

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

Ile Tyr Asp Asn Asn Glu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 72
<211> 111
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<223> L-CDR3

<400> 72

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Asp Ser Leu
                85                  90                  95

Ser Val Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 73
<211> 111
<212> PRT
<213> Homo sapiens

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<223> L-CDR3

<400> 73

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Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15
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Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Asp Ser Leu
                85                  90                  95

Ser Val Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 74

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

Arg Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

Phe Asp Val His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
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65 70 75 80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
85 90 95

Leu Asn Gly Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 75
<211> 111
<212> PRT
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<223> L-CDR2

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<223> L-CDR3

<400> 75

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 76
<211> 111

<212> PRT
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<223> L-CDR2

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<223> L-CDR3

<400> 76

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu
65                  70                  75                  80

Arg Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser
                85                  90                  95

Leu Gly Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<223> L-CDR3

<400> 77

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Ser
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

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

<210> 78
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<212> PRT
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<222> (90)..(99)
<223> L-CDR3

<400> 78

Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln

1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 79
<211> 111
<212> PRT
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<223> L-CDR2

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<223> L-CDR3

<400> 79

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 80
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<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.064 light chain

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<223> L-CDR2

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<223> L-CDR3

<400> 80

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Arg Arg
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 81
<211> 111
<212> PRT
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<223> Clone XPA.15.068 light chain

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<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> L-CDR3

<400> 81

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asp Thr Leu
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 82
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<212> PRT
<213> Homo sapiens

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<223> Clona XPA.15.081 light chain

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<222> (26)..(33)
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<222> (51)..(53)
<223> L-CDR2

<220>
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<223> L-CDR3

<400> 82

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Thr Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Asp Thr Leu
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 83
<211> 111
<212> PRT
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<223> L-CDR2

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<222> (90)..(99)
<223> L-CDR3

<400> 83

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
85 90 95

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 84
<211> 111
<212> PRT
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<220>
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<223> Clone XPA.15.077 light chain

<220>
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<222> (26)..(33)
<223> L-CDR1

<220>
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<222> (51)..(53)
<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> L-CDR3

<400> 84

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Ser Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 85
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.086 light chain

<220>
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<222> (26)..(33)
<223> L-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> L-CDR3

<400> 85

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Ser Leu
                85                  90                  95
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Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 86
<211> 112
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.088 light chain

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<222> (26)..(33)
<223> L-CDR1

<220>
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<222> (51)..(53)
<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (90)..(100)
<223> L-CDR3

<400> 86

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

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

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

Ile Tyr Asp Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

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

Ser Gly Pro Val Leu Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 87
<211> 110
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.193 light chain

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<220>
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<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (92)..(99)
<223> LCDR3

<400> 87

Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Ser Ile Ser Cys Thr Gly Ser Ser Gly Ser Ile Gly Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

Ile Tyr Glu Asp Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

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

Ser Asn Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 88
<211> 108
<212> PRT
<213> Homo sapiens

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<222> (88)..(97)
<223> LCDR3

<400> 88

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

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

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

Gly Lys Asn Ile Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

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

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Asn Arg Asn His
85 90 95

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

<210> 89
<211> 115
<212> PRT
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<220>
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<220>
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<220>
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<222> (52)..(58)
<223> LCDR2

<220>
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<223> LCDR3

<400> 89

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

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

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

Val Leu Arg Tyr Lys Ser Asp Ser Asp Ser Glu Arg Asp Ser Gly Val
50 55 60

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

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

Leu Ile Trp His Asn Ser Ala Trp Val Phe Gly Gly Gly Thr Gln Leu
100 105 110

Thr Val Leu
115

<210> 90
<211> 110
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<223> Clone XPA.15.196 light chain

<220>
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<222> (26)..(33)
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<223> LCDR2

<220>
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<223> LCDR3

<400> 90

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

Thr Val Thr Ile Ser Cys Thr Gly Ser Gly Gly Ser Ile Gly Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

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

Gly Ser Ile His Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly

65 70 75 80

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

Thr Ile Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 91
<211> 110
<212> PRT
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<220>
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<220>
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<223> LCDR1

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<223> LCDR2

<220>
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<223> LCDR3

<400> 91

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

Thr Val Thr Ile Ser Cys Thr Gly Ser Gly Gly Ser Ile Gly Ser Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala Pro Thr Thr Val
35 40 45

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

Gly Ser Ile His Ser Ser Ser Asn Ser Ala Ser Leu Thr Ile Ser Gly
65 70 75 80

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

Thr Ile Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 92
<211> 108

<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (26)..(31)
<223> LCDR1

<220>
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<223> LCDR2

<220>
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<223> LCDR2

<400> 92

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

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Asn Lys Tyr Ala
            20                  25                  30

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

Glu Asp Thr Arg Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Ala Ser
    50                  55                  60

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

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

Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
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<210> 93
<211> 111
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.199 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
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<223> LCDR2

<220>
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<222> (91)..(100)
<223> LCDR3

<400> 93

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Gly Ser Asp Ile Gly Thr Tyr
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

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

Ser Thr Leu Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
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<210> 94
<211> 110
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.200 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
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<223> LCDR2

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<222> (9199)..(98)
<223> LCDR3

<400> 94

```
Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
```

1 5 10 15

Thr Val Thr Leu Thr Cys Gly Leu Thr Ser Gly Ser Val Ser Thr Ser
20 25 30

Tyr Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Met
35 40 45

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

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Gly Ile Tyr Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 95
<211> 116
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.201 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(58)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(105)
<223> LCDR2

<400> 95

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

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

His Asn Ile Tyr Trp Tyr Gln Glu Lys Pro Gly Ser Pro Pro Arg Tyr
35 40 45

Leu Leu Tyr Tyr Tyr Ser Asp Ser Ser Lys Gly Gln Gly Ser Gly Val
50 55 60

```
Pro Ser Arg Phe Ser Gly Ser Lys Asp Val Ser Thr Asn Thr Gly Ile
65                  70                  75                  80

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

Met Thr Trp Ser Ser Asn Gly Ser Gly Val Phe Gly Gly Gly Thr Gln
            100                 105                 110

Leu Thr Val Leu
        115
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<210> 96
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.202 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(100)
<223> LCDR3

<400> 96

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

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

His Asp Val His Trp Tyr Gln Gln Ile Pro Gly Arg Ala Pro Lys Leu
        35                  40                  45

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

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asn Ser
                85                  90                  95
```

Leu Ser Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 97
<211> 110
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.203 light chain

<220>
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<223> LCDR1

<220>
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<223> LCDR2

<220>
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<222> (91)..(99)
<223> LCDR3

<400> 97

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

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

Ser Tyr Pro Ser Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Met
35 40 45

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

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Gly Ile Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 98
<211> 115
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.204 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(58)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(104)
<223> LCDR3

<400> 98

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

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

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

Leu Leu Ser Tyr Asn Ser Asp Ser Asn Asn His Gln Gly Ser Gly Val
    50                  55                  60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65                  70                  75                  80

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

Met Ile Trp His Ile Asn Ala Trp Val Phe Gly Gly Gly Thr Lys Val
            100                 105                 110

Thr Val Leu
        115
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<210> 99
<211> 110
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.205 light chain

<220>
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<223> LCDR1

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<222> (51)..(53)
<223> LCDR2

<220>
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<222> (90)..(99)
<223> LCDR3

<400> 99

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

Arg Val Thr Ile Ser Cys Ile Gly Ser Arg Ser Asp Ile Gly Tyr Tyr
20 25 30

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

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

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

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

Gly Lys Gly Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 100
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.206 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(102)
<223> LCDR3

<400> 100

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

```
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95

Leu Ser Gly Pro Asn Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val
            100                 105                 110

Leu
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<210> 101
<211> 116
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.207 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(58)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(105)
<223> LCDR3

<400> 101

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

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

Tyr Asn Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Arg Tyr
        35                  40                  45
```

```
Leu Leu Tyr Tyr Tyr Ser Asp Ser Asn Lys Asp Gln Gly Ser Gly Val
    50                  55                  60

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

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

Met Thr Trp Ser Ser Asn Gly Ser Gly Val Phe Gly Gly Gly Thr Gln
            100                 105                 110

Leu Thr Val Leu
        115
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<210> 102
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.208 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (26)..(58)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(105)
<223> LCDR3

<400> 102

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

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

His Asn Ile Tyr Trp Tyr Gln Glu Lys Pro Gly Ser Pro Pro Arg Tyr
        35                  40                  45

Leu Leu Tyr Tyr Tyr Ser Asp Ser Ser Lys Gly Gln Gly Ser Gly Val
    50                  55                  60

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

Leu Val Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Glu Tyr Tyr Cys
```

85 90 95

Met Thr Trp Ser Ser Asn Gly Ser Gly Val Phe Gly Gly Gly Thr Lys
100 105 110

Leu Thr Val Leu
115

<210> 103
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.209 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(99)
<223> LCDR3

<400> 103

Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Gly Leu Ser Ser Gly Ser Val Ser Thr Gly
20 25 30

Tyr Ser Pro Gly Trp Tyr Gln Gln Thr Pro Gly Gln Ala Pro Arg Thr
35 40 45

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

Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65 70 75 80

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

Gly Thr Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 104
<211> 112

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.211 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
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<222> (52)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(101)
<223> LCDR3

<400> 104

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

Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
                85                  90                  95

Leu Ser Gly Ser Gly Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105                 110
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<210> 105
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.212 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 105

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

Thr Ala Thr Ile Thr Cys Gly Gly Asp Asn Ile Ala Ser Lys Ser Val
20 25 30

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

Asp Asp Ser Val Arg Pro Ser Asp Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Ala Asn Thr Ala Thr Leu Thr Leu Thr Arg Val Glu Ala Gly
65 70 75 80

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

Pro Phe Phe Gly Pro Gly Thr Lys Val Thr Val Leu
100 105

<210> 106
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.213 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
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<222> (52)..(54)
<223> LCDR2

<220>
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<223> LCDR3

<400> 106

Gln Ala Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly

1 5 10 15

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

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

Leu Ile Tyr Ser Thr Ser Asn Lys His Ser Trp Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

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

Ala Gln Pro Trp Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 107
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.214 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> LCDR3

<400> 107

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

Thr Ala Thr Leu Thr Cys Thr Gly Asp Asn Asn Ile Val Gly Asp Gln
20 25 30

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

Ser Phe Arg Asn Asn Ser Arg Pro Ser Gly Ile Ser Glu Arg Phe Ser
50 55 60

```
Ala Ser Arg Ser Arg Asn Thr Ala Ser Leu Thr Ile Thr Arg Leu Gln
65                  70                  75                  80

Pro Glu Asp Ala Ala Asp Tyr Tyr Cys Ser Ala Trp Asp Ser Phe Leu
                85                  90                  95

Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110

<210>  108
<211>  108
<212>  PRT
<213>  Homo sapiens

<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.215 light chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(31)
<223>  LCDR1

<220>
<221>  MISC_FEATURE
<222>  (49)..(51)
<223>  LCDR2

<220>
<221>  MISC_FEATURE
<222>  (88)..(97)
<223>  LCDR3

<400>  108

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

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

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Pro Asp Ser Ser Asn Lys Leu
                85                  90                  95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

<210> 109
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.216 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(97)
<223> LCDR3

<400> 109

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

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

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

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

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

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

Gly Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 110
<211> 112
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (27)..(37)
<223> LCDR1

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<223> LCDR2

<220>
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<222> (94)..(100)
<223> LCDR3

<400> 110

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

Gln Pro Ala Ser Ile Ser Cys Lys Ala Ser Gln Ser Leu Leu Tyr Thr
            20                  25                  30

Asn Gly Asp Thr Tyr Val Ser Trp Tyr Val Gln Lys Pro Gly Gln Ala
        35                  40                  45

Pro Gln Leu Leu Phe Ser Asp Val Ser Ser Arg Phe Phe Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Ala 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 Val Gln Ala
                85                  90                  95

Met Tyr Leu Pro Leu Val Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> 111
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.218 light chain

<220>
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<222> (26)..(31)
<223> LCDR1

<220>
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<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 111

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

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

Leu Met Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 112
<211> 111
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.219 light chain

<220>
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<222> (26)..(34)
<223> LCDR1

<220>
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<222> (52)..(54)
<223> LCDR2

<220>
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<222> (91)..(100)
<223> LCDR3

<400> 112

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Ile Gly Leu Tyr
20 25 30

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

```
Met Ile Tyr Asp Val Ser Tyr Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

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

Ser Thr Leu Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 113
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.220 light chain

<220>
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<222> (26)..(31)
<223> LCDR1

<220>
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<222> (49)..(51)
<223> LCDR2

<220>
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<222> (88)..(97)
<223> LCDR3

<400> 113

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

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

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

Asp Arg Asn Ser Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

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

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
                85                  90                  95
```

Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 114
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.221 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 114

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

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

His Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 115
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.222 light chain

<220>
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<222> (26)..(31)
<223> LCDR1

<220>
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<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 115

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

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

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

Val Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105
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<210> 116
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.223 light chain

<220>
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<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE

<222> (88)..(97)
<223> LCDR3

<400> 116

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

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

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

Gly Asn Thr Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80

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

Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105
```

<210> 117
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.224 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 117

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80

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

Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
            100                 105

<210>  118
<211>  108
<212>  PRT
<213>  Homo sapiens

<220>
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<223>  Clone XPA.15.225 light chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(31)
<223>  LCDR1

<220>
<221>  MISC_FEATURE
<222>  (49)..(51)
<223>  LCDR2

<220>
<221>  MISC_FEATURE
<222>  (88)..(97)
<223>  LCDR3

<400>  118

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

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

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

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

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Glu His
```

85 90 95

His Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 119
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.226 light chain

<220>
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<222> (26)..(31)
<223> LCDR1

<220>
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<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 119

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

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

Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 120
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.227 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 120

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
    50                  55                  60

Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65                  70                  75                  80

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

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

<210> 121
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.228 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> LCDR3

<400> 121

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Asn Ser Asn Ile Gly Ser Asn
20 25 30

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

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

Gly Ser Arg Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Phe Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Pro Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105 110

<210> 122
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.229 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (90)..(98)
<223> LCDR3

<400> 122

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

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn

20 25 30

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

Ile Phe Asp Asn Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Asn Pro Leu Phe Gly Gly Ser Thr Gln Leu Thr Val Leu
100 105

<210> 123
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.230 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 123

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

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

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

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80

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

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

<210> 124
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.231 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(31)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (49)..(51)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(97)
<223> LCDR3

<400> 124

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

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

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

Asp Arg Asn Ser Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

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

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

Ala Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
            100                 105
```

<210> 125
<211> 109
<212> PRT

<213> Homo sapiens

<220>
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<223> Clone XPA.15.232 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(96)
<223> LCDR3

<400> 125

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

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

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

Ile Phe Asp Asn Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Asn Pro Leu Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
            100                 105
```

<210> 126
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.233 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>

<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (88)..(96)
<223> LCDR3

<400> 126

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

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

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

Ile Phe Asp Asn Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
50 55 60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95

Asn Pro Leu Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 127
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.234 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
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<222> (88)..(96)
<223> LCDR3

<400> 127

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

```
Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30

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

Ile Phe Asp Asn Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Asn Pro Leu Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
            100                 105


<210>  128
<211>  110
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.235 light chain

<220>
<221>  MISC_FEATURE
<222>  (27)..(37)
<223>  LCDR1

<220>
<221>  MISC_FEATURE
<222>  (55)..(57)
<223>  LCDR2

<220>
<221>  MISC_FEATURE
<222>  (94)..(98)
<223>  LCDR3

<400>  128

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 Tyr Ser
            20                  25                  30

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

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

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

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

Thr His Trp Ser Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110

<210>  129
<211>  107
<212>  PRT
<213>  Homo sapiens

<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.236 light chain

<220>
<221>  MISC_FEATURE
<222>  (27)..(32)
<223>  LCDR1

<220>
<221>  MISC_FEATURE
<222>  (50)..(52)
<223>  LCDR2

<220>
<221>  MISC_FEATURE
<222>  (99)..(105)
<223>  LCDR3

<400>  129

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

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

Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
        35                  40                  45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Thr Asn Ser Leu Glu Ala
65                  70                  75                  80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 130
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.237 light chain

<220>
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<222> (27)..(32)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 130

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

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

Tyr Ala Ala Ser Arg Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys
100 105

<210> 131
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.226 light chain

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.238 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(32)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 131

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

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

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 132
<211> 112
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.239 light chain

<220>
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<222> (27)..(37)
<223> LCDR1

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<222> (55)..(57)
<223> LCDR2

<220>
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<222> (94)..(100)
<223> LCDR3

<400> 132

Asp Ile Val Met Thr Gln Ser 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 Leu His Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala 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 Met Gln Ala
85 90 95

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

<210> 133
<211> 106
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.241 light chain

<220>
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<222> (27)..(32)
<223> LCDR1

<220>
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<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(104)
<223> LCDR3

<400> 133

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Thr Asn
20 25 30

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

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

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

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

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

<210> 134
<211> 106
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.242 light chain

<220>
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<222> (27)..(32)
<223> LCDR1

<220>
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<223> LCDR2

<220>
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<222> (99)..(104)
<223> LCDR3

<400> 134

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

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

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

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

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

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Phe Tyr Ser Asn Pro Ser
```

85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 135
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.243 light chain

<220>
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<222> (27)..(32)
<223> LCDR1

<220>
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<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 135

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

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

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

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

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

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

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

<210> 136
<211> 107
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.244 light chain

<220>
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<222> (27)..(32)
<223> LCDR1

<220>
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<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 136

```
Asp 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 Ala Ser Gln Gly Ile Ser Ser Ala
            20                  25                  30

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

Tyr Asp Ala Ser Ser Leu Glu Arg Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

Glu Asp Phe Ala Ser Tyr Tyr Cys His Gln Phe Asn Ser Tyr Pro Asp
                85                  90                  95

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

<210> 137
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.245 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(32)
<223> LCDR1

<220>
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<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 137

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

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

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

Tyr Thr Thr Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

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

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

<210> 138
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.246 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (100)..(106)
<223> LCDR3

<400> 138

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Leu Ser Ser Ser

20 25 30

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

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

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

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

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

<210> 139
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.247 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(37)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (55)..(57)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (94)..(1010)
<223> LCDR3

<400> 139

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

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

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

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

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

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

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


<210>  140
<211>  107
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.248 light chain

<220>
<221>  MISC_FEATURE
<222>  (27)..(32)
<223>  LCDR1

<220>
<221>  MISC_FEATURE
<222>  (50)..(52)
<223>  LCDR2

<220>
<221>  MISC_FEATURE
<222>  (99)..(105)
<223>  LCDR3

<400>  140

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

Glu Thr Val Thr Ile Ser Cys Arg Ala Ser Gln Asn Ile Gly Val Ser
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Val Leu Ile
        35                  40                  45

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


<210>  141
<211>  107
<212>  PRT
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<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.249 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(32)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 141

```
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 Ser Cys Arg Ala Ser Gln Ser Ile Thr Ser Tyr
            20                  25                  30

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

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

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

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

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

<210> 142
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.250 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(32)
<223> LCDR1

<220>

<221> MISC_FEATURE
<222> (50)..(52)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (99)..(105)
<223> LCDR3

<400> 142

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

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

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

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

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

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

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

<210> 143
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.272 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(100)
<223> LCDR3

<400> 143

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

```
Ser Ile Thr Ile Ser Cys Leu Gly Thr Ile Asn Asp Val Gly Leu Tyr
            20                  25                  30

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

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

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

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

Ser Asn Phe Trp Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
            100                 105                 110
```

<210> 144
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.275 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(34)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (52)..(54)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (91)..(99)
<223> LCDR3

<400> 144

```
Gln Thr Val Val Thr Gln Glu Pro Ser Phe Ser Val Ser Pro Gly Gly
1               5                   10                  15

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

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

Leu Ile Tyr Asn Thr Asn Thr Arg Ser Ser Gly Val Pro Asp Arg Phe
    50                  55                  60
```

```
Ser Gly Ser Ile Leu Gly Asn Lys Ala Ala Leu Thr Ile Thr Gly Ala
65                  70                  75                  80

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

Asp Ile Trp Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly
            100                 105                 110
```

<210> 145
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.282 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (90)..(98)
<223> LCDR3

<400> 145

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

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

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

Ile Phe Asp Asn Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Asn Pro Leu Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
            100                 105                 110
```

<210> 146
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.284 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (90)..(98)
<223> LCDR3

<400> 146

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

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

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

Ile Phe Asp Asn Asp Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
                85                  90                  95

Asn Pro Leu Phe Gly Gly Gly Thr Gln Leu Thr Val Leu Gly
            100                 105                 110
```

<210> 147
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.293 light chain

<220>
<221> MISC_FEATURE
<222> (27)..(38)

<223> LCDR1

<220>
<221> MISC_FEATURE
<222> (56)..(58)
<223> LCDR2

<220>
<221> MISC_FEATURE
<222> (95)..(101)
<223> LCDR3

<400> 147

```
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 Leu Asp Ser
            20                  25                  30

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

Ser Pro Gln Leu Leu Met Tyr Ser Leu Ser Tyr Arg Ala Ser Gly Val
    50                  55                  60

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

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

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

Lys Arg
```

<210> 148
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.110 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> L-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> L-CDR2

<220>
<221> MISC_FEATURE

<222> (97)..(101)
<223> L-CDR3

<400> 148

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Arg Asn
            20                  25                  30

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

Ile Tyr Asn Asn Asp Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Pro Val Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110

Gly
```

<210> 149
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.120 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> L-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(53)
<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (90)..(99)
<223> L-CDR3

<400> 149

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Ser Ala Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 150
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.163 light chain

<220>
<221> MISC_FEATURE
<222> (26)..(34)
<223> L-CDR1

<220>
<221> MISC_FEATURE
<222> (52)..(54)
<223> L-CDR2

<220>
<221> MISC_FEATURE
<222> (91)..(100)
<223> L-CDR3

<400> 150

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

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

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

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

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu

65 70 75 80

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

Asn Gln Phe Val Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 151
<211> 119
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Clone XPA.015.172 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(108)
<223> H-CDR3

<400> 151

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
115

<210> 152
<211> 119
<212> PRT
<213> Mus musculus

<220>
<221> MISC_FEATURE
<223> Clone XPA.015.189 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(108)
<223> H-CDR3

<400> 152

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
        115
```

<210> 153
<211> 119
<212> PRT
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<400> 153

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
        115
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<400> 154

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
115

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<223> H-CDR3

<400> 155

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
115

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<400> 156

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

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

```
Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
        35                  40                  45

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

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

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

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

Thr Val Ser Ser
        115


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<400>  157

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

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

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Lys Trp Ile
        35                  40                  45

Gly Asp Ile Asn Pro Asn Asn Gly Gly Ser Asn Tyr Asn Gln Lys Phe
    50                  55                  60
```

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

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

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

Thr Val Ser Ser
115

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<223> H-CDR3

<400> 158

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

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

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

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

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

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

Ala Arg Arg Arg Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val

100 105 110

Thr Val Ser Ser
115

<210> 159
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<212> PRT
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<223> H-CDR3

<400> 159

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
115

<210> 160
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<212> PRT
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<223> H-CDR3

<400> 160

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
115

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<400> 161

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
        115
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<400> 162

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

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

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

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

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

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

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

Thr Ser Val Thr Val Ser Ser
        115
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<400> 163

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

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

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

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

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

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

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

Thr Val Ser Ser
115

<210> 164
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<212> PRT
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<223> H-CDR3

<400> 164

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

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

Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

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

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

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

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

Thr Val Ser Ser
115

<210> 165
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<212> PRT
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<400> 165

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

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

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

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

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

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

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

Gly Thr Thr Leu Ile Val Ser Ser
        115                 120
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<212> PRT
<213> Mus musculus

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<223> H-CDR3

<400> 166

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

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

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

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

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

Ala Arg Gly Val Ser Gly Tyr Gly Ala Val Asp His Trp Gly Gln Gly
            100                 105                 110

Thr Ser Val Thr Val Ser Ser
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115

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<212> PRT
<213> Mus musculus

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<223> H-CDR3

<400> 167

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

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

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

Ala Thr Ile Ser Asp Gly Gly His Tyr Thr Tyr Tyr Ser Asp Thr Ile
50 55 60

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

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

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

Val Ser Ser
115

<210> 168
<211> 120
<212> PRT
<213> Mus musculus

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<223> H-CDR2

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<223> H-CDR3

<400> 168

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

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

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

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

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

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

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

Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 169
<211> 115
<212> PRT
<213> Mus musculus

<220>
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<223> Clone XPA.015.173 heavy chain

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<220>
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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(104)
<223> H-CDR3

<400> 169

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

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

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

Ala Thr Ile Ser Asp Gly Gly His Tyr Ile Asp Tyr Pro Asp Asn Val
50 55 60

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

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

Ala Arg Ala Thr Asn Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ala
115

<210> 170
<211> 113
<212> PRT
<213> Mus musculus

<220>
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<223> H-CDR3

<400> 170

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

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

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

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

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

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

Ala Arg Glu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ala

<210> 171
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.023 heavy chain

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<220>
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<220>
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<223> H-CDR3

<400> 171

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

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

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 172
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.068 heavy chain

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<220>
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<222> (51)..(58)
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<220>
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<223> H-CDR3

<400> 172

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

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

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 173
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<220>
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<222> (97)..(109)
<223> H-CDR3

<400> 173

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
            20                  25                  30

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

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 174
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA015.159 heavy chain

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<223> H-CDR2

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<400> 174

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

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

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 175

<211> 120
<212> PRT
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<223> H-CDR3

<400> 175

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

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

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

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 176
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<213> Homo sapiens

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<223> H-CDR2

<220>
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<223> H-CDR3

<400> 176

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
            20                  25                  30

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

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<212> PRT
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<223> H-CDR3

<400> 177

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

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 178
<211> 118
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.094 heavy chain

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<223> H-CDR1

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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(107)
<223> H-CDR3

<400> 178

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

```
1               5                   10                  15

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
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<211> 118
<212> PRT
<213> Homo sapiens

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<222> (51)..(58)
<223> H-CDR2

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<223> H-CDR3

<400> 179

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

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 180
<211> 118
<212> PRT
<213> Homo sapiens

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<222> (51)..(58)
<223> H-CDR2

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<221> MISC_FEATURE
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<223> H-CDR3

<400> 180

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

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210>  181
<211>  118
<212>  PRT
<213>  Homo sapiens


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<223>  Clone XPA.15.075 heavy chain

<220>
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<220>
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<222>  (51)..(58)
<223>  H-CDR2

<220>
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<223>  H-CDR3

<400>  181

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

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Pro 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110
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Leu Val Thr Val Ser Ser
115

<210> 182
<211> 118
<212> PRT
<213> Homo sapiens

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<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(107)
<223> H-CDR3

<400> 182

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

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 183
<211> 121
<212> PRT
<213> Homo sapiens

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<220>
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<222> (51)..(57)
<223> H-CDR2

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<223> H-CDR3

<400> 183

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

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

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

Ser Tyr Ile His Ala Gly Gly Gly Thr His Tyr Ala Asn Ser Val Lys
50 55 60

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

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

Arg Asp Leu His Trp Glu Gly Trp Gly Leu Gly Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 184
<211> 121
<212> PRT
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<223> H-CDR2

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<223> H-CDR3

<400> 184

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

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

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

Ser Tyr Ile His Ala Gly Gly Gly Thr His Tyr Ala Asn Ser Val Lys
50 55 60

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

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

Arg Asp Leu His Trp Glu Gly Trp Gly Leu Gly Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 185
<211> 121
<212> PRT
<213> Homo sapiens

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<223> H-CDR1

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<222> (51)..(57)
<223> H-CDR2

<220>
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<223> H-CDR3

<400> 185

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

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

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

Ser Tyr Ile His Ala Gly Gly Gly Thr His Tyr Ala Asn Ser Val Lys
    50                  55                  60

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

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

Arg Asp Leu His Trp Glu Gly Trp Gly Leu Gly Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 186
<211> 121
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.082 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
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<222> (51)..(57)
<223> H-CDR2

<220>
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<222> (96)..(110)
<223> H-CDR3

<400> 186

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
```

20 25 30

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

Ser Tyr Ile His Ala Gly Gly Gly Thr His Tyr Ala Asn Ser Val Lys
50 55 60

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

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

Arg Asp Leu His Trp Glu Gly Trp Gly Leu Gly Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 187
<211> 129
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.088 heavy chain

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<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(118)
<223> H-CDR3

<400> 187

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

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

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

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

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

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

Ser

<210> 188
<211> 129
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.100 heavy chain

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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(118)
<223> H-CDR3

<400> 188

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

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

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

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

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

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

Ser
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<210> 189
<211> 129
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.163 heavy chain

<220>
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<220>
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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(118)
<223> H-CDR3

<400> 189

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

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

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

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

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

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

Ser

<210> 190
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<222> (51)..(58)
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<220>
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<223> H-CDR3

<400> 190

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Gln Val Gly Gly Gly Pro Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser

115

<210> 191
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.059 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(107)
<223> H-CDR3

<400> 191

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

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

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

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

Lys Gly Arg Ser Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Gln Val Gly Gly Gly Pro Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 192
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.022 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(106)
<223> H-CDR3

<400> 192

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


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


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


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


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


Val Thr Val Ser Ser
        115
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<210> 193
<211> 117
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.021 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> H-CDR1

<220>
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<222> (51)..(57)
<223> H-CDR2

<220>
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<222> (96)..(106)
<223> H-CDR3

<400> 193

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
            20                  25                  30

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

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

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

Val Thr Val Ser Ser
        115
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<210> 194
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.026 heavy chain

<220>
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<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(109)
<223> H-CDR3

<400> 194

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

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

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

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

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 195
<211> 118
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<213> Homo sapiens

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<223> H-CDR2

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<223> H-CDR3

<400> 195

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

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

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

Ser Ser Ile Ser Ser Ser Ser Arg Tyr Ala Asp Val Ala Asn Ser Val
    50                  55                  60

Val Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Glu Trp Leu Asp His Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


<210>  196
<211>  116
<212>  PRT
<213>  Homo sapiens


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<223>  Clone XPA.15.064 heavy chain

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<223>  H-CDR2

<220>
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<222>  (97)..(105)
<223>  H-CDR3

<400>  196

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

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

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

Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

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

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

Ala Ser Gln Ser Thr Ala Phe Asp Ile Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115
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<210> 197
<211> 118
<212> PRT
<213> Homo sapiens

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<223> H-CDR2

<220>
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<223> H-CDR3

<400> 197

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

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

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

Ala Val Ile Ser Lys Asp Gly Ser Ser Thr Asp Tyr Ala His Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Arg Asp Trp Ile Pro Gly Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115

<210>  198
<211>  126
<212>  PRT
<213>  Homo sapiens

<220>
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<223>  H-CDR2

<220>
<221>  MISC_FEATURE
<222>  (97)..(115)
<223>  H-CDR3

<400>  198

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

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

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

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

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

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

Thr Thr Asp Leu Gly Arg Tyr Tyr Asp Ile Leu Thr Gly Tyr Tyr Ala
            100                 105                 110

Pro Asn Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

<210>  199
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<211> 119
<212> PRT
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<220>
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<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
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<223> H-CDR3

<400> 199

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

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

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

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp His Ser Ser Ser Trp Ala Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 200
<211> 129
<212> PRT
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<220>
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<220>
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<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(118)
<223> H-CDR3

<400> 200

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Lys Gly Tyr Cys Ser Ser Thr Ser Cys Tyr Phe Asp Tyr
            100                 105                 110

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

Ser
```

<210> 201
<211> 119
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> H-CDR1

<220>
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<222> (51)..(57)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (96)..(108)
<223> H-CDR3

<400> 201

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

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

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

Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

Arg Ile Asn Trp Asn Asp Gly Gly Asn Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 202
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.121 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(56)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (95)..(108)
<223> H-CDR3

<400> 202

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

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

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

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

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

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

His Ala Asp Gln Trp Pro Gly Ser Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 203
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.122 heavy chain

<220>
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<223> H-CDR1

<220>
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<222> (51)..(56)
<223> H-CDR2

<220>
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<222> (95)..(105)
<223> H-CDR3

<400> 203

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

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

```
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
    50                  55                  60

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

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

Gly Gly Val Gly Asp Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115


<210>  204
<211>  123
<212>  PRT
<213>  Homo sapiens


<220>
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<223>  Clone XPA.15.127 heavy chain

<220>
<221>  MISC_FEATURE
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<223>  H-CDR1

<220>
<221>  MISC_FEATURE
<222>  (51)..(58)
<223>  H-CDR2

<220>
<221>  MISC_FEATURE
<222>  (97)..(112)
<223>  H-CDR3

<400>  204

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

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

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ser Asp Val Glu Gly Gly Tyr Phe His Asn Ser Gly Pro Asp His
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 205
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.015.125 heavy chain

<220>
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<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(109)
<223> H-CDR3

<400> 205

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

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

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Pro Val Gly Ile Ser Gly Asn Tyr Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  206
<211>  120
<212>  PRT
<213>  Homo sapiens


<220>
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<223>  Clone XPA.15.133 heavy chain

<220>
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<222>  (26)..(33)
<223>  H-CDR1

<220>
<221>  MISC_FEATURE
<222>  (51)..(58)
<223>  H-CDR2

<220>
<221>  MISC_FEATURE
<222>  (97)..(109)
<223>  H-CDR3

<400>  206

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

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

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

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

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

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

Ala Ala Asp Leu Gly Ile Gly Ser Gly Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120

<210>  207
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<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.135 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(109)
<223> H-CDR3

<400> 207

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Pro Gly Gly Ile Tyr Asp Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 208
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.139 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(107)
<223> H-CDR3

<400> 208

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

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

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

Ser Gly Ile Ser Gly Ser Gly Gly Tyr Ile His Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr 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 Glu Gly Ser Gly Trp Leu Val Asp Gln Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 209
<211> 121
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.138 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(110)
<223> H-CDR3

<400> 209

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

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

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

Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Arg Trp Tyr Lys Asp Ser Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 210
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.143 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
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<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(107)
<223> H-CDR3

<400> 210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1 5 10 15

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

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

Ala His Ile Asn Gln Asp Gly Ser Glu Lys Tyr Tyr Val Glu Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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

Gly Lys Leu Arg Gly Gly Ala Tyr Asn Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 211
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.145 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(107)
<223> H-CDR3

<400> 211

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

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

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

```
Ser Val Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

Leu Val Thr Val Ser Ser
        115
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<210> 212
<211> 123
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.140 heavy chain

<220>
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<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(112)
<223> H-CDR3

<400> 212

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

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

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

Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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

Val Arg Glu Ala Trp Arg Glu Asn Asn Asp Trp Tyr Glu Leu Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 213
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.167 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (97)..(109)
<223> H-CDR3

<400> 213

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 214
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.169 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> H-CDR1

<220>
<221> MISC_FEATURE
<222> (51)..(56)
<223> H-CDR2

<220>
<221> MISC_FEATURE
<222> (95)..(109)
<223> H-CDR3

<400> 214

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

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

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

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

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

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

Glu Val Glu Tyr Ser Ser Ser Trp Gly Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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<223> H-CDR3

<400> 215

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

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

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

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

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

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

Arg Glu Ser Thr Arg Leu Arg Gly Ser Tyr Tyr Tyr Gly Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<223> H-CDR3

<400> 216

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

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

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

Ser Val Ile Tyr Ser Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

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

Arg Gln Val Arg Asp Gly Asp Tyr Gly Asp Trp Phe Asp Pro Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<223> H-CDR3

<400> 217

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ser Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115
```

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<211> 117
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<223> H-CDR3

<400> 218

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
```

20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
85 90 95

Leu Asp Trp Ser Ser Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 219
<211> 120
<212> PRT
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<223> H-CDR2

<220>
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<223> H-CDR3

<400> 219

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Gly Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Asn Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Gly Ser Gly Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<223> H-CDR2

<220>
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<223> H-CDR3

<400> 220

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Ser Trp Glu Leu Leu Gly Tyr Asp Ala Phe Asp Ile Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 221
<211> 121
<212> PRT
<213> Homo sapiens

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<223> H-CDR1

<220>
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<222> (51)..(58)
<223> H-CDR2

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<223> H-CDR3

<400> 221

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Arg Tyr Ser Ser Gly Trp Tyr Trp Ser Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<212> PRT
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<220>
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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(107)
<223> H-CDR3

<400> 222

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Ser Gly Ser Gly Gly Tyr Thr Ser Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Lys Asp Ser Ser Asp Trp Tyr Ile Asn Ser Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
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<211> 120
<212> PRT
<213> Homo sapiens

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<220>
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<223> H-CDR1

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<222> (51)..(58)
<223> H-CDR2

<220>
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<222> (97)..(109)
<223> H-CDR3

<400> 223

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asn Phe
20 25 30

Ala Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Pro Ser Gly Ala Tyr Pro Thr Pro Phe Asp Asn Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 224
<211> 118
<212> PRT
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<222> (51)..(58)

<223> H-CDR2

<220>
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<222> (97)..(107)
<223> H-CDR3

<400> 224

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Gly Ile Trp Ser Ala Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

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<211> 120
<212> PRT
<213> Homo sapiens

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<220>
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<222> (97)..(109)
<223> H-CDR3

<400> 225

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Asp Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Glu Leu Pro Ala Phe Trp Ser Ala Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Phe
        115                 120
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<210> 226
<211> 124
<212> PRT
<213> Homo sapiens

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<220>
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<222> (51)..(58)
<223> HCDR2

<220>
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<222> (97)..(113)
<223> HCDR3

<400> 226

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Ala
1               5                   10                  15

Thr Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Gly Asp Tyr
            20                  25                  30

His Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
```

35 40 45

Gly Leu Val Asp Pro Glu Asn Gly Glu Thr Glu Tyr Gly Glu Lys Phe
50 55 60

Gln Asp Arg Ile Thr Met Ala Ala Asp Thr Ser Thr Asp 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 Ser Pro Ser Ser Ser Gly Tyr Phe Arg Val Asp Gly Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 227
<211> 121
<212> PRT
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<220>
<221> MISC_FEATURE
<222> (97)..(110)
<223> HCDR3

<400> 227

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gly Lys Leu Tyr Ser Arg Asp Tyr Trp Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<211> 119
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.195 heavy chain

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<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(108)
<223> HCDR3

<400> 228

```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Arg Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Val 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 Thr His His Ala Ser Gly Arg Gly Leu Asp Pro Trp Gly Gln Gly
            100                 105                 110
```

Thr Leu Val Thr Val Ser Ser
115

<210> 229
<211> 124
<212> PRT
<213> Homo sapiens

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<222> (51)..(58)
<223> HCDR2

<220>
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<222> (99)..(113)
<223> HCDR3

<400> 229

Gln Val Gln Val Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ser Ser Ser Ser Trp Pro Val Tyr Phe Tyr Tyr Met Asp
100 105 110

Val Trp Gly Lys Gly Ser Thr Val Thr Val Ser Ser
115 120

<210> 230
<211> 124
<212> PRT
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<223> Clone XPA.15.197 heavy chain

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<222> (51)..(58)
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<220>
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<223> HCDR3

<400> 230

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Ser Ser Ser Ser Trp Pro Val Tyr Phe Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 231
<211> 121
<212> PRT
<213> Homo sapiens

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<223> Clone XPA.15.198 heavy chain

<220>
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<222> (26)..(33)

<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(110)
<223> HCDR3

<400> 231

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Gln Gly Trp Leu Arg Phe Tyr Gly Met Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 232
<211> 117
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.199 heavy chain

<220>
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<220>
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<222> (51)..(57)
<223> HCDR2

<220>
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<222> (96)..(106)
<223> HCDR3

<400> 232

Gln Val Gln Leu Val Gln Ser Gly Ser Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Ser
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Ala Gly Thr Ser Tyr Ala Gln Lys Phe Gln
50 55 60

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
65 70 75 80

Glu Leu Ser Ser Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Val Gly Trp Leu Pro Gly Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 233
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.200 heavy chain

<220>
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<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
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<223> HCDR3

<400> 233

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Tyr Gly Tyr Arg Phe Ser Asp Asn
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Arg Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln 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 His Ala Pro Leu Ala Val Ala Gly Met Ala Leu Gly Asp Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 234
<211> 122
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.202 heavy chain

<220>
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<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(57)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (96)..(111)
<223> HCDR3

<400> 234

Gln Leu Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Ser Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Tyr Ser Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Asp Ile Ser His Thr Gly Ser Thr Asp Tyr Asn Pro Ser Leu Lys

50 55 60

Thr Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Ala Pro Lys Gly Gly Ser Gly Leu Tyr Leu Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 235
<211> 126
<212> PRT
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<220>
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<223> Clone XPA.15.203 heavy chain

<220>
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<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(115)
<223> HCDR3

<400> 235

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Asp Ser Tyr Ser Ser Gly Trp Tyr Ser His Gly Pro Glu Tyr
            100                 105                 110

Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125

<210>  236
<211>  122
<212>  PRT
<213>  Homo sapiens

<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.204 heavy chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(33)
<223>  HCDR1

<220>
<221>  MISC_FEATURE
<222>  (51)..(58)
<223>  HCDR2

<220>
<221>  MISC_FEATURE
<222>  (97)..(111)
<223>  HCDR3

<400>  236

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Arg Ile Ile Pro Ile Phe Gly Ile Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Pro Asp Tyr Asp Phe Trp Asn Asp Ala Phe Asp Ile Trp
            100                 105                 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 237
<211> 126
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.205 heavy chain

<220>
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<222> (26)..(33)
<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(115)
<223> HCDR3

<400> 237

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Ser His Tyr Tyr Asp Phe Trp Ser Gly Tyr Gln Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 238
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> Clone XPA.15.206 heavy chain

<220>
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<222> (26)..(33)
<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(106)
<223> HCDR3

<400> 238

```
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Ala Gly Asn Gly Asn Thr Arg Tyr Ser Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala 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 Tyr Thr Ser Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
```

<210> 239
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.207 heavy chain

<220>
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<222> (26)..(33)
<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
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<222> (97)..(105)
<223> HCDR3

<400> 239

```
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Arg Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Val Arg Asp Asn His Gly Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 240
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.208 heavy chain

<220>
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<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(116)
<223> HCDR3

<400> 240

```
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Thr Lys Gly Ser Asp Phe Trp Ser Gly Tyr Tyr Tyr Tyr Tyr Tyr
            100                 105                 110

Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  241
<211>  122
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.209 heavy chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(33)
<223>  HCDR1

<220>
<221>  MISC_FEATURE
<222>  (51)..(58)
<223>  HCDR2

<220>
<221>  MISC_FEATURE
<222>  (97)..(111)
<223>  HCDR3

<400>  241

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Thr Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Gln Gly Tyr Gly Tyr Arg Phe Thr Asp Asn
            20                  25                  30
```

```
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Arg Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Glu Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Glu Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg His Ala Pro Leu Ala Val Ala Gly Met Ala Leu Gly Asp Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 242
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.210 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(122)
<223> HCDR3

<400> 242

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Leu Pro Pro Lys Pro Tyr Tyr Asp Phe Trp Ser Gly Tyr
100 105 110

Trp Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
115 120 125

Val Thr Val Ser Ser
130

<210> 243
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.211 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(57)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (96)..(109)
<223> HCDR3

<400> 243

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

```
Arg Gly Pro Ser Gly Trp Tyr Ile Arg Glu Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  244
<211>  121
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.212 heavy chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(35)
<223>  HCDR1

<220>
<221>  MISC_FEATURE
<222>  (53)..(61)
<223>  HCDR2

<220>
<221>  MISC_FEATURE
<222>  (100)..(110)
<223>  HCDR3

<400>  244

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15


Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
            20                  25                  30


Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35                  40                  45


Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Thr Asp Tyr Ala
    50                  55                  60


Leu Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80


Gln Phe Ser Leu His Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95


Tyr Tyr Cys Ala Arg Glu Gly Trp Leu Gly Tyr Phe Asp Phe Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 245
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.213 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(106)
<223> HCDR3

<400> 245

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Phe Ser Phe Pro Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Leu Val
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Thr Ser Ile Ser Thr Val Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Gln Thr Thr Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Phe Asn Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
```

<210> 246
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> Clone XPA.15.214 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(105)
<223> HCDR3

<400> 246

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln 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 His Glu Leu Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115
```

<210> 247
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.215 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE

<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(111)
<223> HCDR3

<400> 247

```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ala Ser Tyr Gly Gly Asn Ser Glu Gly Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 248
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.216 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(117)
<223> HCDR3

<400> 248

```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 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 Ala Ser Gly Asp Tyr Asp Phe Trp Ser Gly Tyr Tyr Gly Ala
            100                 105                 110

Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  249
<211>  131
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.217 heavy chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(33)
<223>  HCDR1

<220>
<221>  MISC_FEATURE
<222>  (51)..(62)
<223>  HCDR2

<220>
<221>  MISC_FEATURE
<222>  (101)..(120)
<223>  HCDR3

<400>  249

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Gln Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Asn Ser Tyr
            20                  25                  30
```

Thr Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Gly Thr Asn Tyr Phe Ala Asn Tyr
50 55 60

Ala Leu Lys Phe Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr
65 70 75 80

Gly Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala
85 90 95

Val Tyr Tyr Cys Ala Arg Val Arg Asp Ser Trp Ser His Glu Asp Tyr
100 105 110

Ser Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr
115 120 125

Val Ser Ser
130

<210> 250
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.218 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(118)
<223> HCDR3

<400> 250

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser 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 Glu Arg Val Phe Pro Asp Tyr Tyr Asp Ser Ile Ala Ser Asn
100 105 110

Tyr Pro Leu Asp Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
115 120 125

Ser

<210> 251
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.219 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(107)
<223> HCDR3

<400> 251

Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly 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 Leu Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ile Leu Gly Val Glu Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 252
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.220 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(108)
<223> HCDR3

<400> 252

```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln 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 Leu Gly Ser Gly Ser Tyr Ser Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110
```

Thr Leu Val Thr Val Ser Ser
115

<210> 253
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.221 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(110)
<223> HCDR3

<400> 253

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Met
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Trp Asn Ser Ala Asn Ile Val Tyr Ala Asp Ser Val
50 55 60

Arg Gly 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 Asp Asp Met Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Gly Asp Thr Thr Met Ile Tyr Tyr Ala Met Ala Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 254
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.222 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(55)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(108)
<223> HCDR3

<400> 254

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Ile 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 Leu Gly Arg Gly Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 255
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.223 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)

<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(106)
<223> HCDR3

<400> 255

```
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln 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 Trp Gly Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110

Val Thr Val Ser Ser
        115
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<400> 256

Glu Val Gln Leu Val Glu Ser Gly Gly Ser Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
20 25 30

Tyr Met Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr 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 Lys Asp Asp Tyr Asp Phe Trp Ser Gly Tyr Tyr Asp Pro Tyr Tyr
100 105 110

Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<400> 257

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Met
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Trp Asn Ser Ala Asn Ile Val Tyr Ala Asp Ser Val
50 55 60

Arg Gly 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 Asp Asp Met Ala Leu Tyr Tyr Cys
85 90 95

Val Lys Gly Asp Thr Thr Met Ile Tyr Tyr Ala Met Ala Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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<400> 258

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe

50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ser Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Arg Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Leu Gly Ser Gly Trp Tyr Gly Asn Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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<400> 259

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln 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 Trp Asp Ala Gly Tyr Ser Pro Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115

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<400>  260

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Gly Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Val Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Gly Arg Ile Ser Thr Pro Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110

Met Val Thr Val Ser Ser
        115
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<223> HCDR3

<400> 261

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys 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 Val Gly Ala Ala Ala Ala Trp Phe Asp Pro Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
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<222> (97)..(105)
<223> HCDR3

<400> 262

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Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln 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 Trp Asp Ala Gly Tyr Ser Pro Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser
        115
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<400> 263

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Ser Ser Ser
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Arg 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 Val Gly Ala Ser Gly Trp Thr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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<212> PRT
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<223> HCDR3

<400> 264

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Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ser Tyr
            20                  25                  30

Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Ser Tyr Asp Gly Asn Asp Lys Gln Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Arg Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asp Ser Leu Arg Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
                85                  90                  95

Thr Arg Glu Gly Asn Gly Arg Glu Ile Asp Tyr Trp Gly Pro Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115


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<220>
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<223>  HCDR3

<400>  265

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Arg Pro Gly Ala
1               5                  10                  15

Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe His Ser Tyr
            20                  25                  30
```

```
Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln Gly Leu Glu Trp Val
        35                  40                  45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Asp Phe Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asn Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Val Asn Trp Asn Tyr Gly Gly Thr Ser Asp Ser Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<223> HCDR3

<400> 266

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
            20                  25                  30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys 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 Val Gly Val Ala Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

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<223> HCDR3

<400> 267

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Cys
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 Glu Glu Ala Tyr Gly Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

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<400> 268

Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln 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 Trp Gly Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser Ser
115

<210> 269
<211> 121
<212> PRT

<213> Homo sapiens

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<223> HCDR3

<400> 269

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Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Arg Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Trp Asn Gly Gly Phe Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Ser Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Gly Ala Ser Tyr Asp Ser Tyr Ala Ala Met Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<212> PRT
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<223> HCDR3

<400> 270

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Lys Asp Pro Arg Val Val His Arg Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

Thr Met Val Thr Val Ser Ser
        115
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<211> 125
<212> PRT
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<220>
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<223> HCDR3

<400> 271

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
20 25 30

Tyr Trp Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Tyr Ser Gly Lys Thr Asn Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Thr Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Ser Phe Tyr Phe Glu Ser Ser Arg Ser Trp Asn Asp Leu Phe
100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 272
<211> 125
<212> PRT
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<220>
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<223> HCDR3

<400> 272

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
            20                  25                  30

Tyr Trp Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Asn Ile Tyr Tyr Ser Gly Lys Thr Asn Tyr Asn Pro Ser Leu Gly
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Ser Phe Tyr Phe Glu Ser Ser Arg Ser Trp Asn Asp Leu Phe
            100                 105                 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120                 125
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<210> 273
<211> 118
<212> PRT
<213> Homo sapiens

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<223> HCDR3

<400> 273

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Ala Arg Gly Val Val Ile Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 274
<211> 125
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<222> (51)..(57)
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<220>
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<223> HCDR3

<400> 274

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Asn Ile Tyr Tyr Ser Gly Lys Thr Asn Tyr Asn Pro Ser Leu Glu
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala

85 90 95

Arg Asp Ser Phe Tyr Phe Glu Ser Ser Arg Ser Trp Asn Asp Leu Phe
100 105 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 275
<211> 118
<212> PRT
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<220>
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<223> HCDR3

<400> 275

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Asn Ile Asn Gln Asp Gly Ser Glu Lys His Tyr Val Asp Ser Val
50 55 60

Lys Gly 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 Gly Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Gly Ala Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 276
<211> 124
<212> PRT
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<220>
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<220>
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<222> (51)..(58)
<223> HCDR2

<220>
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<223> HCDR3

<400> 276

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Gln Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly 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 Asp Gln Gly Gly Glu Leu Leu Gly Phe Thr Gly Tyr Phe Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<211> 118
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<400> 277

```
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Met Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser Asp Tyr
            20                  25                  30

Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Pro Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Gly Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

Ala Arg Ala Arg Gly Val Trp Met Phe Asp Asn Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
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<220>
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<223> HCDR3

<400> 278

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Leu Ile Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Ala Arg Gly Val Val Ile Ile Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

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<223> HCDR3

<400> 279

```
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Glu Trp Gly Phe Gly Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser
        115
```

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<211> 117
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<220>
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<223> HCDR3

<400> 280

```
Gln Met Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1               5                  10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30
```

```
Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln 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 Trp Gly Pro Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
            100                 105                 110

Val Thr Val Ser Ser
        115
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<211> 121
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<223> HCDR3

<400> 281

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Lys Asp Arg Val Gly Ala Ala Asn Gly Trp Phe Asp Pro Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 282
<211> 120
<212> PRT
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<223> Clone XPA.15.250 heavy chain

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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(109)
<223> HCDR3

<400> 282

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Asn Tyr
            20                  25                  30

Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Asp Ile Lys Gly Asp Gly Ser Arg Gln His Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ser Leu Phe
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Thr Asp Pro Pro Trp Asp Arg Asp Ala Phe Asp Leu Trp Gly Gln
```

100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 283
<211> 118
<212> PRT
<213> Homo sapiens

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<220>
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<223> HCDR1

<220>
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<220>
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<223> HCDR3

<400> 283

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gly Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Asn Ile Lys Gln Asp Gly Ser Glu Gln Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly 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 Ile Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Met Asp Tyr Ile Phe Asp Ile Trp Gly Arg Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 284
<211> 120

<212> PRT
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<220>
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<223> HCDR3

<400> 284

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Val Pro Asp Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Gly Ile Ser Leu Arg Gly Ser Asp Asn Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Asn Leu Arg Pro Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Phe Arg Trp Pro Val Thr Pro Phe Asp His Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<211> 121
<212> PRT
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<220>

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<223> HCDR3

<400> 285

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys 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 Pro Asp Tyr Ser Asn Tyr Gly Gly Ala Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 286
<211> 119
<212> PRT
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<223> Clone XPA.15.284 heavy chain

<220>
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<220>
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<222> (52)..(58)
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<222> (97)..(108)
<223> HCDR3

<400> 286

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ser Ser Ser
20 25 30

Asn Trp Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Val Thr Ile Ser Val Asp Lys 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 Val Gly Ala Ala Ala Ala Trp Phe Asp Pro Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 287
<211> 125
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (97)..(115)
<223> HCDR3

<400> 287

Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
            20                  25                  30

Tyr Trp Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Asn Ile Tyr Tyr Ser Gly Lys Thr Asn Tyr Asn Pro Ser Leu Glu
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Asp Ser Phe Tyr Phe Glu Ser Ser Arg Ser Trp Asn Asp Leu Phe
            100                 105                 110

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120                 125
```

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<211> 120
<212> PRT
<213> Homo sapiens

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<220>
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<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
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<223> HCDR3

<400> 288

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ala Thr Gly Ile Gly Gly Tyr His Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Gln
        115                 120
```

<210> 289
<211> 120
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<223> HCDR3

<400> 289

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Asn Ser Gly Gly Thr Thr Phe Tyr Ala Asp Ala Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Asp Arg Arg Phe Leu Glu Trp Thr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Gln
        115                 120
```

<210> 290
<211> 117
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> HCDR1

<220>
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<222> (51)..(57)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (96)..(106)
<223> HCDR3

<400> 290

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
            20                  25                  30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Gly Thr Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Lys Ser Arg Trp Leu Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Gln
```

115

<210> 291
<211> 123
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(112)
<223> HCDR3

<400> 291

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
20 25 30

Tyr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Lys Glu Ile Pro Gly Arg Trp Leu Gln Leu Gly Gly Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Arg Leu
115 120

<210> 292
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.062 heavy chain

<220>
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<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
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<222> (97)..(109)
<223> HCDR3

<400> 292

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30

Val Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Phe Tyr Pro Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Val Gly Leu Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

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<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.085 heavy chain

<220>
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<223> HCDR1

<220>
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<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(107)
<223> HCDR3

<400> 293

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Phe
115

<210> 294
<211> 118
<212> PRT
<213> Homo sapiens

<220>
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<223> Clone XPA.15.099 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(107)
<223> HCDR3

<400> 294

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Gly Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 His Lys Gly Leu Gln Pro Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Gln
        115
```

<210> 295
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Clone XPA.15.141 heavy chain

<220>
<221> MISC_FEATURE
<222> (26)..(33)
<223> HCDR1

<220>
<221> MISC_FEATURE
<222> (51)..(58)
<223> HCDR2

<220>
<221> MISC_FEATURE
<222> (97)..(106)
<223> HCDR3

<400> 295

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
            20                  25                  30
```

```
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Val Ser Trp Asn Gly Ser Arg Thr His Tyr Ala Tyr Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Arg Ser Pro Leu Lys Asp Gly Phe Asp Ile Trp Gly Leu Gly
            100                 105                 110

Thr Leu Val Thr Val Thr Gln
        115


<210>  296
<211>  123
<212>  PRT
<213>  Homo sapiens


<220>
<221>  MISC_FEATURE
<223>  Clone XPA.15.142 heavy chain

<220>
<221>  MISC_FEATURE
<222>  (26)..(33)
<223>  HCDR1

<220>
<221>  MISC_FEATURE
<222>  (51)..(58)
<223>  HCDR2

<220>
<221>  MISC_FEATURE
<222>  (97)..(112)
<223>  HCDR3

<400>  296

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Phe
            20                  25                  30

Ala Val His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60
```

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ser Asp Val Glu Gly Gly Tyr Phe His Asn Ser Gly Pro Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asn Tyr
            20                  25                  30

Asn Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Val Ser Trp Asn Gly Ser Arg Thr His Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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
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Ala Arg Glu Arg Gly Ser Trp Asp Thr Thr Gly Tyr Tyr Asn Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Val Ser Ala Thr Gly Pro His Thr Tyr Tyr Ala Asp Ser Ala
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Gln Val Gly Gly Gly Pro Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser

115

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Val Gly Ser Ser Gly Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ala
            20                  25                  30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr 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 Ala Pro Thr Val Pro Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
            20                  25                  30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ser Ile Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Arg Lys Gly
    50                  55                  60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65                  70                  75                  80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
                85                  90                  95

Leu Asp Trp Ser Ser Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
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1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
            20                  25                  30
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Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Ser Ser Ser Ser Trp Pro Val Tyr Phe Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Ser Thr Val Thr Val Ser Ser
        115                 120
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