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

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Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

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Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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Ala Arg Lys Asn Tyr Gly Gly Ser Tyr Ala Phe Thr Tyr Trp Gly Gln

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Thr Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala

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Ile Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile

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

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

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Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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

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Ser Gly Ser Gly Thr Asp Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala

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Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr

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Ile Gly Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Ser Tyr Asn Gln Lys

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Phe Lys Gly Lys Thr Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala

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Tyr Met Glu Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr

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Cys Thr Arg Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val Trp Gly Thr

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Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

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Tyr Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

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

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Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser

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Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val

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Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr

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Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly

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Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala

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20180308-154537-1

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

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

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser

65

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Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr

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Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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<210> 92

<211> 120

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 92

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

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Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

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

20180308-154537-1

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Ile Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys

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Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr

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Cys Ala Arg Gly Gly Asn Trp Asn Trp Tyr Phe Asp Val Trp Gly Thr

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Gly Thr Thr Val Thr Val Ser Ser

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<210> 93

<211> 112

<212> PRT

<213> Artificial Sequence

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<400> 93

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser

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20180308-154537-1

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

35

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Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

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Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65

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Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

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Ser His Val Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys

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<210> 94

<211> 119

<212> PRT

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<400> 94

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

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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr

20180308-154537-1

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25

30

Ile Ile His Trp Val Lys Gln Lys Ser Gly Gln Gly Leu Glu Trp Ile

35

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

50

55

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

65

70

75

80

Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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Thr Arg His Glu Gly Gly Ser Asn Phe Phe Pro Tyr Trp Gly Gln Gly

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Thr Leu Val Thr Val Ser Ala

115

<210> 95

<211> 107

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 95

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly

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20180308-154537-1

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Asn Ala

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Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

35

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Tyr Trp Ala Ser Thr Arg His Asn Gly Val Pro Asp Arg Phe Thr Gly

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60

Ser Gly Ser Gly Thr Asp Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala

65

70

75

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Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro Tyr

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Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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<210> 96

<211> 121

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<400> 96

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20180308-154537-1

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

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60

Lys Gly Arg Val 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

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Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

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105

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Lys Gly Thr Thr Val Thr Val Ser Ser

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<210> 97

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 97

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

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20180308-154537-1

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala

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30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

65

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Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His

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Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

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<210> 98

<211> 121

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 98

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20180308-154537-1

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

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Lys Gly Arg Val 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

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95

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

105

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Lys Gly Thr Thr Val Thr Val Ser Ser

115

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<210> 99

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 99

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

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20180308-154537-1

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

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45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

65

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75

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Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His

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90

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Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

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<210> 100

<211> 121

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<223> Variable domain

<400> 100

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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45

Ser Gly Ile Asn Trp Ser Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Val 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

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Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

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Lys Gly Thr Thr Val Thr Val Ser Ser

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<210> 101

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 101

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

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20180308-154537-1

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala

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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

35

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45

Gly Lys Thr Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

65

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75

80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Thr His

85

90

95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

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<210> 102

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable domain

<400> 102

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

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25

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

35

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Ser Gly Ile Asn Trp Ser Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Val 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

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Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

105

110

Lys Gly Thr Thr Val Thr Val Ser Ser

115

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<210> 103

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 103

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

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20180308-154537-1

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala

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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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45

Gly Lys Ala Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

65

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75

80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Ala His

85

90

95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

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<210> 104

<211> 121

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 104

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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Ser Gly Ile Asn Trp Ser Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

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60

Lys Gly Arg Val 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

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Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

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Lys Gly Thr Thr Val Thr Val Ser Ser

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<210> 105

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 105

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

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20180308-154537-1

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala

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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

35

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45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

65

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Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His

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Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

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<210> 106

<211> 121

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 106

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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Ser Gly Ile Asn Trp Ala Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

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Lys Gly Arg Val 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

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Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

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Lys Gly Thr Thr Val Thr Val Ser Ser

115

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<210> 107

<211> 108

<212> PRT

<213> Artificial Sequence

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<400> 107

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

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20180308-154537-1

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala

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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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Gly Lys Thr Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

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Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asp His

85

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Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

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<210> 108

<211> 121

<212> PRT

<213> Artificial Sequence

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<400> 108

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20180308-154537-1

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25

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Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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Ser Gly Ile Asn Trp Thr Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

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Lys Gly Arg Val 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

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Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

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Lys Gly Thr Thr Val Thr Val Ser Ser

115

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<210> 109

<211> 108

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 109

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

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20180308-154537-1

Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala

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Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr

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Gly Lys Asp Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser

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Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu

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Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asp His

85

90

95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

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<210> 110

<211> 123

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 110

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

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Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20180308-154537-1

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25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50

55

60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100

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Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser

115

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<210> 111

<211> 107

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 111

Asp Ile Val Met Thr Gln Ser Gln Thr Phe Met Ser Thr Thr Val Gly

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20180308-154537-1

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

20

25

30

Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln Ser Pro Lys Leu Leu Ile

35

40

45

Tyr Ser Ala Ser Asn Arg Phe Thr Gly Val Pro Asp Arg Phe Thr Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Arg Ser

65

70

75

80

Glu Asp Leu Ala Asp Tyr Val Cys Gln Gln Tyr Ser Thr Tyr Pro Leu

85

90

95

Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Arg

100

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<210> 112

<211> 123

<212> PRT

<213> Artificial Sequence

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Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

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Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20180308-154537-1

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

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45

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

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Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser

115

120

<210> 113

<211> 107

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 113

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly

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20180308-154537-1

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Gly

20

25

30

Val Val Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Lys Leu Leu Ile

35

40

45

Tyr Ser Pro Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

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60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Ile Gln Ser

65

70

75

80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Trp

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90

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Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

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<210> 114

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable domain

<400> 114

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

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Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20180308-154537-1

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25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

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

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Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100

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Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser

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120

<210> 115

<211> 107

<212> PRT

<213> Artificial Sequence

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<400> 115

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly

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20180308-154537-1

Asp Arg Val Asn Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

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Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

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45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Met Gln Ser

65

70

75

80

Lys Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Trp

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

100

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<210> 116

<211> 123

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 116

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

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Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20180308-154537-1

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25

30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Val Thr Leu 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 Leu Cys

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Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 117

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable domain

<400> 117

Asp Ile Gln Met Thr Gln Ser Gln Ser Ser Leu Ser Ala Ser Val Gly

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20180308-154537-1

Asp Arg Val Gly Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

20

25

30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Ser Ala Ser Asn Arg Tyr Thr 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

Lys Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Trp

85

90

95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys

100

105

<210> 118

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Variable domain

<400> 118

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

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Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20180308-154537-1

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25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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90

95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser

115

120

<210> 119

<211> 113

<212> PRT

<213> Artificial Sequence

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<223> Variable domain

<400> 119

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly

1

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15

20180308-154537-1

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser

20

25

30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35

40

45

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

50

55

60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65

70

75

80

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

85

90

95

Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile

100

105

110

Lys

<210> 120

<211> 330

<212> PRT

<213> Artificial Sequence

<220>

<223> Constant domain

<400> 120

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

1	5	10	15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr			
20	25	30	
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser			
35	40	45	
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser			
50	55	60	
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr			
65	70	75	80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys			
85	90	95	
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys			
100	105	110	
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro			
115	120	125	
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys			
130	135	140	
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp			
145	150	155	160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu			
165	170	175	
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu			
180	185	190	
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn			
195	200	205	
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly			

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210	215	220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu		
225	230	235
240		
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr		
245	250	255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn		
260	265	270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe		
275	280	285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn		
290	295	300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr		
305	310	315
320		
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys		
325	330	

<210> 121

<211> 329

<212> PRT

<213> Artificial Sequence

<220>

<223> Constant domain

<400> 121

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Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
1			5					10					15		
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
			35					40					45		
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
			50					55					60		
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
65					70					75					80
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
					85					90					95
Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
					100					105					110
Pro	Ala	Pro	Glu	Ala	Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
					115					120					125
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
					130					135					140
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
145						150					155				160
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
						165					170				175
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
						180									190
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
						195									205

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Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly

210

215

220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu

225

230

235

240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

245

250

255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

260

265

270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

275

280

285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290

295

300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

305

310

315

320

Gln Lys Ser Leu Ser Leu Ser Pro Gly

325

<210> 122

<211> 327

<212> PRT

<213> Artificial Sequence

<220>

<223> Constant domain

<400> 122

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
 1 5 10 15
 Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
 65 70 75 80
 Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro
 100 105 110
 Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 115 120 125
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 130 135 140
 Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
 145 150 155 160
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
 165 170 175
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 180 185 190
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu

195	200	205
Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg		
210	215	220
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys		
225	230	235
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp		
245	250	255
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys		
260	265	270
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser		
275	280	285
Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser		
290	295	300
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser		
305	310	315
Leu Ser Leu Ser Leu Gly Lys		320

325

<210> 123

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Constant domain

<400> 123

```

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1           5           10          15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
          20          25          30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
          35          40          45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
          50          55          60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65          70          75          80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
          85          90          95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          100         105

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<210> 124

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 124

Asp Ile 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
 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Gly Gly
 100 105 110
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro
 130 135 140
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp
 145 150 155 160
 Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175
 Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp
 180 185 190
 Ser Val Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser

195

200

205

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

210

215

220

Tyr Cys Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu

225

230

235

240

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser

245

250

<210> 125

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 125

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

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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

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly

100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

115 120 125

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

130 135 140

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

145 150 155 160

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

165 170 175

Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

180 185 190

Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

195 200 205

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

210 215 220

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

225 230 235 240

Lys Gly Thr Thr Val Thr Val Ser Ser

245

<210> 126

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 126

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 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 Asp Ser Ser Gly Thr His
 85 90 95
 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly
 100 105 110
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 115 120 125
 Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly

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130		135		140	
Ser	Leu	Arg	Leu	Ser	Cys
Ala	Ala	Ser	Gly	Phe	Thr
Phe	Asp	Asp	Tyr		
145		150		155	
Gly	Met	Ser	Trp	Val	Arg
Gln	Ala	Pro	Gly	Lys	Gly
Leu	Glu	Trp	Val		
	165		170		175
Ser	Gly	Ile	Asn	Trp	Ser
Gly	Gly	Ser	Thr	Gly	Tyr
Ala	Asp	Ser	Val		
	180		185		190
Lys	Gly	Arg	Val	Thr	Ile
Ser	Arg	Asp	Asn	Ala	Lys
Asn	Ser	Leu	Tyr		
	195		200		205
Leu	Gln	Met	Asn	Ser	Leu
Arg	Ala	Glu	Asp	Thr	Ala
Val	Tyr	Tyr	Cys		
	210		215		220
Ala	Lys	Ile	Leu	Gly	Ala
Gly	Arg	Gly	Trp	Tyr	Phe
Asp	Leu	Trp	Gly		
225		230		235	
Lys	Gly	Thr	Thr	Val	Thr
Val	Ser	Ser			
	245				

<210> 127

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 127

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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	Ala	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	Ala	His
				85					90					95	
Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gly	Gly	Gly
				100				105						110	
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
				115				120						125	
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Glu	Arg	Pro	Gly	Gly
				130				135						140	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr
145				150					155					160	
Gly	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
				165					170					175	
Ser	Gly	Ile	Asn	Trp	Ser	Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val
				180					185					190	
Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
				195					200					205	

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

210

215

220

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

225

230

235

240

Lys Gly Thr Thr Val Thr Val Ser Ser

245

<210> 128

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 128

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	
Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly			
100	105	110	
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
115	120	125	
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly			
130	135	140	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr			
145	150	155	160
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
165	170	175	
Ser Gly Ile Asn Trp Ser Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val			
180	185	190	
Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr			
195	200	205	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			
210	215	220	
Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly			
225	230	235	240
Lys Gly Thr Thr Val Thr Val Ser Ser			
245			

<210> 129

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 129

```

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 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 Asp Ser Ser Gly Asp His
           85           90           95
Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly
           100          105          110
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
           115          120          125
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly
           130          135          140

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

145 150 155 160

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

165 170 175

Ser Gly Ile Asn Trp Ala Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

180 185 190

Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

195 200 205

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

210 215 220

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

225 230 235 240

Lys Gly Thr Thr Val Thr Val Ser Ser

245

<210> 130

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 130

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 Asp 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 Asp His			
85	90	95	
Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly			
100	105	110	
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
115	120	125	
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly			
130	135	140	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr			
145	150	155	160
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val			
165	170	175	
Ser Gly Ile Asn Trp Thr Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val			
180	185	190	
Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr			
195	200	205	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys			

210

215

220

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

225

230

235

240

Lys Gly Thr Thr Val Thr Val Ser Ser

245

<210> 131

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 131

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg 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 Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val

50

55

60

Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr

65

70

75

80

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

85

90

95

Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly

100

105

110

Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly

115

120

125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu

130

135

140

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

145

150

155

160

Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr

165

170

175

Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn

180

185

190

Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly

195

200

205

Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala

210

215

220

Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe

225

230

235

240

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln

245

250

<210> 132

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 132

Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg 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 Cys 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 Val 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 Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly
 100 105 110
 Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu
 130 135 140
 Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg

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145 150 155 160
Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr
 165 170 175
Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn
 180 185 190
Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly
 195 200 205
Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala
 210 215 220
Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe
225 230 235 240
Gly Cys Gly Thr Lys Leu Thr Val Leu Gly Gln
 245 250

<210> 133

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 133

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

1

5

10

15

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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

Val Val Phe Gly Cys Gly Thr Lys Leu Thr Val Leu Gly Gln Gly Gly

100

105

110

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Glu Val Gln Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro

130

135

140

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp

145

150

155

160

Asp Tyr Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu

165

170

175

Trp Val Ser Gly Ile Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp

180

185

190

Ser Val Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser

195

200

205

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr

210

215

220

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Tyr Cys Ala Lys Ile Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu

225 230 235 240

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser

245 250

<210> 134

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 134

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly

1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ile Thr Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

35 40 45

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

50 55 60

Thr Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala

65 70 75 80

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp

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85	90	95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser		
100	105	110
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln		
115	120	125
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser		
130	135	140
Val Lys Leu Ser Cys Lys Ala Phe Asp Tyr Thr Phe Thr Ser Tyr Asp		
145	150	155
Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly		
165	170	175
Trp Ile Asp Pro Gly Ser Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys		
180	185	190
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met		
195	200	205
His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala		
210	215	220
Arg Lys Asn Tyr Gly Gly Ser Tyr Ala Phe Thr Tyr Trp Gly Gln Gly		
225	230	235
Thr Leu Val Thr Val Ala		
245		

<210> 135

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 135

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15
 Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Ala
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Val Leu Ile
 35 40 45
 Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala
 65 70 75 80
 Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys
 115 120 125
 Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Thr Gly Thr Ser
 130 135 140
 Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile
 145 150 155 160

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Ile His Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp Ile Gly

165

170

175

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

180

185

190

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

195

200

205

Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala

210

215

220

Arg His Glu Glu Gly Gly Tyr Ser Ala Trp Phe Pro Tyr Trp Gly Gln

225

230

235

240

Gly Thr Leu Val Thr Val Ser Ala

245

<210> 136

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 136

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1

5

10

15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

20	25	30
Asn Gly Asp Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser		
35	40	45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro		
50	55	60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile		
65	70	75
Ser Arg Val Val Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Arg Gly		
85	90	95
Ser His Ile Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Lys Gly		
100	105	110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly		
115	120	125
Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys		
130	135	140
Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe		
145	150	155
Thr Asp Tyr Tyr Tyr Leu Asn Trp Val Lys Gln Ser His Gly Lys Ser		
165	170	175
Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Asn Asn Gly Asp Thr Ser Tyr		
180	185	190
Asn Gln Lys Phe Lys Gly Lys Thr Thr Leu Thr Val Asp Lys Ser Ser		
195	200	205
Ser Thr Ala Tyr Met Glu Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala		
210	215	220
Val Tyr Tyr Cys Thr Arg Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val		

225 230 235 240

245 250

<213> Artificial Sequence

<223> scFv

85 90 95

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Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly

100

105

110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val

115

120

125

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

130

135

140

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr Tyr Ile

145

150

155

160

Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Lys

165

170

175

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

180

185

190

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln

195

200

205

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser

210

215

220

Thr Gly Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Trp Ser

225

230

235

240

Ala

<210> 138

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 138

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly
 1 5 10 15
 Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Gly Thr Ala
 20 25 30
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 35 40 45
 Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser
 65 70 75 80
 Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
 115 120 125
 Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln Thr
 130 135 140
 Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly
 145 150 155 160
 Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp

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165

170

175

Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu

180

185

190

Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val Phe

195

200

205

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

210

215

220

Ala Arg Arg Arg Leu Gly Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu

225

230

235

240

Val Thr Val Ser Ala

245

<210> 139

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 139

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly

1

5

10

15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Asn Ile Val His Ser

20

25

30

20180308-154537-1

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

35

40

45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

50

55

60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

65

70

75

80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly

85

90

95

Ser His Val Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys

100

105

110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

115

120

125

Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val

130

135

140

Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr

145

150

155

160

Phe Thr Asp Tyr Tyr Tyr Met Asn Trp Val Lys Gln Ser His Gly Lys

165

170

175

Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Arg

180

185

190

Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser

195

200

205

Ser Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser

210

215

220

Ala Val Tyr Tyr Cys Ala Arg Gly Gly Asn Trp Asn Trp Tyr Phe Asp

225

230

235

240

Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser

245

250

<210> 140

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> scFv

<400> 140

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly

1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Asn Ala

20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

35 40 45

Tyr Trp Ala Ser Thr Arg His Asn Gly Val Pro Asp Arg Phe Thr Gly

50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala

65 70 75 80

Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro Tyr

85 90 95

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

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100	105	110	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys			
115	120	125	
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser			
130	135	140	
Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile			
145	150	155	160
Ile His Trp Val Lys Gln Lys Ser Gly Gln Gly Leu Glu Trp Ile Gly			
165	170	175	
Trp Phe Tyr Pro Gly Ser Gly Asn Ile Lys Tyr Asn Glu Lys Phe Lys			
180	185	190	
Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Val Tyr Met			
195	200	205	
Glu Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr			
210	215	220	
Arg His Glu Gly Gly Ser Asn Phe Phe Pro Tyr Trp Gly Gln Gly Thr			
225	230	235	240
Leu Val Thr Val Ser Ala			
245			

<210> 141

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 141

Gly Gly Ser Gly Gly Ser

1 5

<210> 142

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 142

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

1 5 10

<210> 143

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 143

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

1 5 10 15

Gly Gly Gly Ser

20

<210> 144

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker

<400> 144

Gly Gly Gly Ser

1

<210> 145

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 145

Glu Val Gln Leu Gln Gln Ser Val Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160

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Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Lys Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr

450

455

460

Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr

465

470

475

480

Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg

500

505

510

Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr

515

520

525

Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr

530

535

540

Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly

545

550

555

560

Gly Thr Lys Leu Thr Val Leu Gly Gln Gly Gly Gly Gly Ser Gly Gly

565

570

575

20180308-154537-1

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln

580

585

590

Leu Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg

595

600

605

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser

610

615

620

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile

625

630

635

640

Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg

645

650

655

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

660

665

670

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile

675

680

685

Leu Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr

690

695

700

Thr Val Thr Val Ser Ser

705

710

<210> 146

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 146

```

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1           5           10          15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
          20          25          30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35          40          45
Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
        50          55          60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65          70          75          80
Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
          85          90          95
Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
        100         105         110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115         120         125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
        130         135         140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145          150          155          160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
          165          170          175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

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180

185

190

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

195

200

205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

220

<210> 147

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 147

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

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Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

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Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

20180308-154537-1

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gln Gly Gly Gly Gly Ser Gly Gly Gly

565

570

575

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

580

585

590

Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu

595

600

605

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp

610

615

620

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn

625

630

635

640

Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val

645

650

655

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn

660

665

670

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu

675

680

685

Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr

690

695

700

Val Thr Val Ser Ser

705

<210> 148

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 148

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly

1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser

20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35 40 45

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

50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65 70 75 80

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

85 90 95

Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile

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100

105

110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

115

120

125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

130

135

140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu

145

150

155

160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp

165

170

175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr

180

185

190

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

195

200

205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

220

<210> 149

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 149

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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 Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
20 25 30
Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

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Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

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Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625 630 635 640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645 650 655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660 665 670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675 680 685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690 695 700

Val Ser Ser

705

<210> 150

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 150

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly

1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser

20	25	30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln		
35	40	45
Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val		
50	55	60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr		
65	70	75
Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln		
85	90	95
Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile		
100	105	110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp		
115	120	125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn		
130	135	140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu		
145	150	155
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp		
165	170	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr		
180	185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser		
195	200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys		
210	215	220

<210> 151

<211> 705

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 151

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

1 5 10 15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

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

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Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr

340

345

350

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu

355

360

365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp

370

375

380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val

385

390

395

400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp

405

410

415

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His

420

425

430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu

435

440

445

Gly Lys Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln Asp Pro

450

455

460

Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly

465

470

475

480

Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly

485

490

495

Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly

500

505

510

Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu

515

520

525

Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn

530

535

540

20180308-154537-1

Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys

545 550 555 560

Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

565 570 575

Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln Ser Gly

580 585 590

Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala

595 600 605

Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg Gln Ala

610 615 620

Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Asn Gly Gly

625 630 635 640

Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile Ser Arg

645 650 655

Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala

660 665 670

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly Arg

675 680 685

Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr Val Ser

690 695 700

Ser

705

<210> 152

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 152

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
 1 5 10 15
 Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
 100 105 110
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 130 135 140
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu

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145	150	155	160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp			
	165	170	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr			
	180	185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser			
	195	200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
	210	215	220

<210> 153

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 153

Glu Val Gln Leu Gln Gln Ser Val Ala Glu Leu Val Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His			
	20	25	30
Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile			
	35	40	45

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Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

20180308-154537-1

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Glu Val Gln Leu Val Gln

450

455

460

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

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Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser

675

680

685

Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu

690

695

700

Thr Val Leu Gly Gln

705

<210> 154

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 154

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly

1

5

10

15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser

20

25

30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln

35

40

45

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

50

55

60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

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65	70	75	80
Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln			
	85	90	95
Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile			
	100	105	110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp			
	115	120	125
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn			
	130	135	140
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu			
145	150	155	160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp			
	165	170	175
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr			
	180	185	190
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser			
	195	200	205
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
	210	215	220

<210> 155

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 155

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

1 5 10 15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165 170 175

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Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

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Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Glu Val Gln Leu Val Gln
 450 455 460
 Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys
 465 470 475 480
 Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg
 485 490 495
 Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn Trp Asn
 500 505 510
 Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile
 515 520 525
 Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
 530 535 540
 Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala
 545 550 555 560
 Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr
 565 570 575
 Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 580 585 590

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Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Asp Pro Ala

595

600

605

Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp

610

615

620

Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln

625

630

635

640

Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile

645

650

655

Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr

660

665

670

Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser

675

680

685

Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly Thr Lys Leu

690

695

700

Thr Val Leu Gly Gln

705

<210> 156

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 156

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
 1 5 10 15
 Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
 100 105 110
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 130 135 140
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 145 150 155 160
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 165 170 175
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 180 185 190
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser

195

200

205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

220

<210> 157

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 157

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

20180308-154537-1

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

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Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln
450 455 460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys
465 470 475 480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
485 490 495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro
500 505 510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gln Gly Gly Gly Gly Ser Gly Gly Gly

565

570

575

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu

580

585

590

Val Gln Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu

595

600

605

Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp

610

615

620

Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn

625

630

635

640

Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val

645

650

655

Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn

660

665

670

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu

675

680

685

Gly Ala Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr

690

695

700

Val Thr Val Ser Ser

705

<210> 158

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 158

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Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1           5           10           15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
           20           25           30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
           35           40           45
Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
           50           55           60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80
Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
           85           90           95
Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
           100          105          110
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

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115	120	125	
Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn			
130	135	140	
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu			
145	150	155	160
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp			
165	170	175	
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr			
180	185	190	
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser			
195	200	205	
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
210	215	220	

<210> 159

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 159

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

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Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50

55

60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln

450

455

460

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr

465

470

475

480

Cys Lys Ala Ser Gln Asp Val Ile Thr Ala Val Ala Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

500

505

510

His Thr Gly Val Pro Asp Arg Phe Thr Gly Thr Gly Ser Gly Thr Asp

515

520

525

Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr

530

535

540

Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr

545

550

555

560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser

580

585

590

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys

595

600

605

Ala Phe Asp Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln

610

615

620

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp Pro Gly Ser

625

630

635

640

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Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

645

650

655

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met His Leu Ser Ser Leu Thr

660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Lys Asn Tyr Gly Gly

675

680

685

Ser Tyr Ala Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ala

690

695

700

<210> 160

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 160

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35	40	45
Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe		
50	55	60
Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr		
65	70	75
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys		
85	90	95
Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		

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

450		455		460	
Ser	His	Lys	Phe	Met	Ser
	Thr	Ser	Val	Gly	Asp
	Arg	Val	Ser	Ile	Thr
465		470		475	
Cys	Lys	Ala	Ser	Gln	Asp
	Val	Ser	Thr	Ala	Val
	Ala	Trp	Tyr	Gln	Gln
	485		490		495
Lys	Pro	Gly	Gln	Ser	Pro
	Lys	Val	Leu	Ile	Tyr
	Trp	Ala	Ser	Thr	Arg
	500		505		510
His	Thr	Gly	Val	Pro	Asp
	Arg	Phe	Thr	Gly	Ser
	Gly	Ser	Gly	Ser	Gly
	Thr	Asp			
	515		520		525
Tyr	Ile	Leu	Thr	Ile	Ser
	Ser	Ser	Val	Gln	Ala
	Glu	Asp	Leu	Ala	Leu
	Tyr				
	530		535		540
Tyr	Cys	Gln	Gln	His	Tyr
	Ser	Thr	Pro	Tyr	Thr
	Phe	Gly	Gly	Gly	Thr
545		550		555	
Lys	Leu	Glu	Ile	Lys	Gly
	Gly	Gly	Gly	Gly	Ser
	Gly	Gly	Gly	Gly	Ser
	Gly	Ser	Gly		
	565		570		575
Gly	Gly	Gly	Ser	Gly	Gly
	Gly	Gly	Gly	Ser	Lys
	Val	Gln	Leu	Gln	Gln
	Ser				
	580		585		590
Gly	Ala	Glu	Leu	Val	Lys
	Thr	Gly	Thr	Ser	Val
	Lys	Leu	Ser	Cys	Lys
	595		600		605
Ala	Ser	Gly	Tyr	Thr	Phe
	Thr	Glu	Tyr	Ile	Ile
	His	Trp	Val	Lys	Gln
	610		615		620
Arg	Ser	Gly	Gln	Gly	Leu
	Glu	Trp	Ile	Gly	Trp
	Phe	Tyr	Pro	Gly	Ser
625		630		635	
Gly	Ser	Ile	Lys	Tyr	Asn
	Glu	Lys	Phe	Lys	Asp
	Lys	Ala	Thr	Leu	Thr
	645		650		655
Ala	Asp	Lys	Ser	Ser	Ser
	Thr	Val	Tyr	Met	Glu
	Leu	Ser	Arg	Leu	Thr

660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg His Glu Glu Gly Gly

675

680

685

Tyr Ser Ala Trp Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

690

695

700

Ser Ala

705

<210> 161

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 161

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50

55

60

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Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180 185 190

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

195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210 215 220

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

225 230 235 240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260 265 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Val Leu Met Thr Gln

450

455

460

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

465

470

475

480

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

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Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr

690

695

700

Val Thr Val Ser Ser

705

<210> 162

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 162

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50

55

60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85	90	95
Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		

290		295		300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				
	405		410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser				
	420		425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser				
	435		440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ile Val Met Thr Gln				
	450		455	460
Thr Pro Lys Phe Leu Pro Val Ser Ala Gly Asp Arg Val Thr Met Thr				
465		470		475
Cys Lys Ala Ser Gln Asn Val Gly Asn Asn Val Ala Trp Tyr Gln Gln				
	485		490	495
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Ala Ser Asn Arg				

500	505	510
Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp		
515	520	525
Phe Phe Thr Ile Ser Ser Val Gln Val Glu Asp Leu Ala Val Tyr Phe		
530	535	540
Cys Gln Gln His Tyr Ser Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys		
545	550	555
Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly		
565	570	575
Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly		
580	585	590
Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala		
595	600	605
Ser Gly Tyr Ser Phe Thr Asp Tyr Tyr Ile Asn Trp Val Lys Gln Arg		
610	615	620
Pro Gly Gln Gly Leu Glu Trp Ile Gly Lys Ile Gly Pro Gly Ser Gly		
625	630	635
Asn Thr Tyr Tyr Asn Glu Lys Phe Glu Gly Lys Ala Thr Leu Thr Ala		
645	650	655
Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser		
660	665	670
Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Thr Gly Pro Phe Ala Tyr		
675	680	685
Trp Gly Gln Gly Thr Leu Val Thr Trp Ser Ala		
690	695	

<210> 163

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 163

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50 55 60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

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

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Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln

450

455

460

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr

465

470

475

480

Cys Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

500

505

510

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp

515

520

525

Phe Thr Leu Thr Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr

530

535

540

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Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr

545 550 555 560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Thr Leu Lys Glu Ser

580 585 590

Gly Pro Gly Ile Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser

595 600 605

Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile

610 615 620

Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp

625 630 635 640

Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile

645 650 655

Ser Lys Asp Thr Ser Arg Asn Gln Val Phe Leu Lys Ile Thr Ser Val

660 665 670

Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Arg Arg Leu Gly

675 680 685

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

690 695 700

<210> 164

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 164

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe
 50 55 60
 Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		
290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu		
305	310	315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala		
325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro		
340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln		
355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala		

370		375		380	
Val	Glu	Trp	Glu	Ser	Asn
			Gly	Gln	Pro
				Glu	Asn
				Asn	Tyr
				Lys	Thr
				Thr	
385		390		395	400
Pro	Pro	Val	Leu	Asp	Ser
			Asp	Gly	Ser
				Phe	Phe
				Leu	Tyr
				Ser	Lys
				Leu	
	405		410		415
Thr	Val	Asp	Lys	Ser	Arg
			Trp	Gln	Gln
			Gly	Asn	Val
				Phe	Ser
				Cys	Ser
	420		425		430
Val	Met	His	Glu	Ala	Leu
			His	Asn	His
			Tyr	Thr	Gln
			Lys	Ser	Leu
			Ser		
	435		440		445
Leu	Ser	Pro	Gly	Gly	Gly
			Ser	Gly	Gly
			Ser	Asp	Val
				Leu	Met
				Thr	Gln
	450		455		460
Thr	Pro	Leu	Ser	Leu	Pro
			Val	Ser	Leu
			Gly	Asp	Gln
				Ala	Ser
				Ile	Ser
465		470		475	480
Cys	Arg	Ser	Ser	Gln	Asn
			Ile	Val	His
			Ser	Asn	Gly
				Asn	Thr
				Tyr	Leu
	485		490		495
Asp	Trp	Tyr	Leu	Gln	Lys
			Pro	Gly	Gln
			Ser	Pro	Lys
				Leu	Leu
				Ile	Tyr
	500		505		510
Lys	Val	Ser	Asn	Arg	Phe
			Ser	Gly	Val
			Pro	Asp	Arg
				Phe	Ser
				Gly	Ser
	515		520		525
Gly	Ser	Gly	Thr	Asp	Phe
			Thr	Leu	Lys
			Ile	Ser	Arg
				Val	Glu
				Ala	Glu
	530		535		540
Asp	Leu	Gly	Val	Tyr	Tyr
			Cys	Phe	Gln
			Gly	Ser	His
				Val	Pro
				Pro	Thr
545		550		555	560
Phe	Gly	Ala	Gly	Thr	Lys
			Leu	Glu	Leu
			Lys	Gly	Gly
			Gly	Gly	Gly
				Ser	Gly
	565		570		575
Gly	Gly	Gly	Ser	Gly	Gly
			Gly	Gly	Gly
			Ser	Gly	Gly
				Ser	Glu
				Val	

580		585		590											
Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	Val
	595						600						605		
Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr	Tyr	Tyr
	610						615						620		
Met	Asn	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	Glu	Trp	Ile	Gly
	625						630						635		640
Tyr	Ile	Tyr	Pro	Asn	Asn	Gly	Gly	Thr	Arg	Tyr	Asn	Gln	Lys	Phe	Lys
				645					650					655	
Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met
				660					665					670	
Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys	Ala
				675					680					685	
Arg	Gly	Gly	Asn	Trp	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Thr	Gly	Thr
				690					695					700	
Thr	Val	Thr	Val	Ser	Ser										
	705													710	

<210> 165

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 165

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe
 50 55 60
 Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240
 Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 290 295 300
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln
 450 455 460
 Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr
 465 470 475 480
 Cys Lys Ala Ser Gln Asp Val Ser Asn Ala Val Ala Trp Tyr Gln Gln
 485 490 495
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 500 505 510
 His Asn Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 515 520 525
 Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr
 530 535 540
 Tyr Cys Gln Gln His Tyr Arg Thr Pro Tyr Thr Phe Gly Gly Gly Thr
 545 550 555 560
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser
 580 585 590
 Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 595 600 605

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Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln

610

615

620

Lys Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser

625

630

635

640

Gly Asn Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

645

650

655

Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr

660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg His Glu Gly Gly Ser

675

680

685

Asn Phe Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

690

695

700

<210> 166

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 166

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1	5	10	15
Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His			
20	25	30	
Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile			
35	40	45	
Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe			
50	55	60	
Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr			
65	70	75	80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys			
85	90	95	
Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr			
100	105	110	
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly			
115	120	125	
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly			
130	135	140	
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val			
145	150	155	160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe			
165	170	175	
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val			
180	185	190	
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val			
195	200	205	
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys			

210	215	220	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala			
225	230	235	240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr			
	245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val			
	260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val			
	275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser			
	290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
	355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
	370	375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			

420		425		430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser				
435		440		445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln				
450		455		460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys				
465		470		475
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys				
	485		490	
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro				
	500		505	
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala				
	515		520	
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr				
	530		535	
Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly				
545		550		555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser				
	565		570	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln				
	580		585	
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys				
	595		600	
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg				
	610		615	
Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn Trp Asn				

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625 630 635 640
Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile
 645 650 655
Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
 660 665 670
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala
 675 680 685
Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr
 690 695 700
Val Ser Ser
705

<210> 167

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 167

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30

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Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50

55

60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

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Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

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Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

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Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 168

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 168

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50		55		60											
Lys	Ala	Lys	Ser	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr
65		70		75		80									
Met	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
		85		90		95									
Ala	Arg	Trp	Ser	Trp	His	Phe	Gly	Ser	Asn	Tyr	Tyr	Gly	Leu	Asp	Tyr
		100		105		110									
Trp	Gly	Gln	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
		115		120		125									
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
		130		135		140									
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145		150		155		160									
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
		165		170		175									
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
		180		185		190									
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195		200		205									
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
		210		215		220									
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
225		230		235		240									
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
		245		250		255									
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val

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

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

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 169

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 169

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50

55

60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65

70

75

80

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Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

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Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

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Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Ala Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Ala His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 170

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 170

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50 55 60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100		105		110
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly				
115		120		125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly				
130		135		140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val				
145		150		155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe				
	165		170	
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val				
	180		185	
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
	195		200	
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
	210		215	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				

305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
	355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
	370	375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
	420	425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
	435	440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln			
	450	455	460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys			
465	470	475	480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys			
	485	490	495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro			
	500	505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala			

515	520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr		
530	535	540
Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly		
545	550	555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
565	570	575
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln		
580	585	590
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys		
595	600	605
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg		
610	615	620
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser		
625	630	635
Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile		
645	650	655
Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu		
660	665	670
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala		
675	680	685
Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr		
690	695	700
Val Ser Ser		
705		

<210> 171

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 171

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe

50 55 60

Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

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

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Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Thr Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

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Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly

545 550 555 560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565 570 575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580 585 590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595 600 605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610 615 620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ala

625 630 635 640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645 650 655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660 665 670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675 680 685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690 695 700

Val Ser Ser

705

<210> 172

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 172

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Asp Gln Gly Leu Asp Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Asp Ile Thr Gln Tyr Asn Glu Asn Phe
 50 55 60
 Lys Ala Lys Ser Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Ser Trp His Phe Gly Ser Asn Tyr Tyr Gly Leu Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145	150	155	160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe			
	165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val			
	180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val			
	195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys			
	210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala			
225	230	235	240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr			
	245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val			
	260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val			
	275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser			
	290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			

355		360		365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
370		375		380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				
	405		410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser				
	420		425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser				
	435		440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln				
	450		455	460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys				
465		470		475
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys				
	485		490	495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asp Asn Arg Pro				
	500		505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala				
	515		520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr				
	530		535	540
Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly				
545		550		555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser				

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565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Thr

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 173

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 173

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Asp Ile Val Met Thr Gln Ser Gln Thr Phe Met Ser Thr Thr Val Gly
1           5           10           15
Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
           20           25           30
Leu Ala Trp Tyr Gln Gln Lys Pro Arg Gln Ser Pro Lys Leu Leu Ile
           35           40           45
Tyr Ser Ala Ser Asn Arg Phe Thr Gly Val Pro Asp Arg Phe Thr Gly
           50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Arg Ser
65           70           75           80
Glu Asp Leu Ala Asp Tyr Val Cys Gln Gln Tyr Ser Thr Tyr Pro Leu
           85           90           95
Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Arg Arg Thr Val Ala Ala
           100          105          110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
           115          120          125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
           130          135          140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145          150          155          160
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
           165          170          175

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Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

180

185

190

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

195

200

205

Phe Asn Arg Gly Glu Cys

210

<210> 174

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 174

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
		85				90							95		
Ala	Arg	Trp	Gly	Tyr	Tyr	Phe	Gly	Ser	Thr	Ser	Tyr	Tyr	Phe	Asp	Phe
		100					105						110		
Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
		115					120						125		
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
		130				135					140				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145				150					155					160	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
		165					170						175		
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
		180					185						190		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195					200						205		
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
		210				215					220				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
225				230					235					240	
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
		245					250						255		
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		260					265						270		
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val

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

485	490	495
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg		
500	505	510
His Thr Gly Val Pro Asp Arg Phe Thr Gly Thr Gly Ser Gly Thr Asp		
515	520	525
Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr		
530	535	540
Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr		
545	550	555
Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly		
565	570	575
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser		
580	585	590
Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys		
595	600	605
Ala Phe Asp Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln		
610	615	620
Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp Pro Gly Ser		
625	630	635
Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr		
645	650	655
Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met His Leu Ser Ser Leu Thr		
660	665	670
Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Lys Asn Tyr Gly Gly		
675	680	685
Ser Tyr Ala Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ala		

690

695

700

<210> 175

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 175

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

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

85 90 95

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Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

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Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln
450 455 460
Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr
465 470 475 480
Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln
485 490 495
Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg
500 505 510

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp

515

520

525

Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr

530

535

540

Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr Thr Phe Gly Gly Gly Thr

545

550

555

560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser

580

585

590

Gly Ala Glu Leu Val Lys Thr Gly Thr Ser Val Lys Leu Ser Cys Lys

595

600

605

Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln

610

615

620

Arg Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser

625

630

635

640

Gly Ser Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

645

650

655

Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr

660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg His Glu Glu Gly Gly

675

680

685

Tyr Ser Ala Trp Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

690

695

700

Ser Ala

705

<210> 176

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 176

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

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

325	330	335	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
340	345	350	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
355	360	365	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
370	375	380	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
405	410	415	
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
420	425	430	
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
435	440	445	
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Val Leu Met Thr Gln			
450	455	460	
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser			
465	470	475	480
Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu			
485	490	495	
Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr			
500	505	510	
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser			
515	520	525	
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Val Ala Glu			

530 535 540
 Asp Leu Gly Val Tyr Tyr Cys Phe Arg Gly Ser His Ile Pro Pro Thr
 545 550 555 560
 Phe Gly Ala Gly Thr Lys Leu Glu Lys Gly Gly Gly Gly Ser Gly Gly
 565 570 575
 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 580 585 590
 Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys
 595 600 605
 Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr Leu
 610 615 620
 Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr
 625 630 635 640
 Ile Tyr Pro Asn Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly
 645 650 655
 Lys Thr Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu
 660 665 670
 Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Arg
 675 680 685
 Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr
 690 695 700
 Val Thr Val Ser Ser
 705

<210> 177

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 177

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

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Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
210 215 220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225 230 235 240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ile Val Met Thr Gln
 450 455 460
 Thr Pro Lys Phe Leu Pro Val Ser Ala Gly Asp Arg Val Thr Met Thr
 465 470 475 480
 Cys Lys Ala Ser Gln Asn Val Gly Asn Asn Val Ala Trp Tyr Gln Gln
 485 490 495
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Ala Ser Asn Arg
 500 505 510
 Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 515 520 525
 Phe Phe Thr Ile Ser Ser Val Gln Val Glu Asp Leu Ala Val Tyr Phe
 530 535 540
 Cys Gln Gln His Tyr Ser Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys
 545 550 555 560

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Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

565

570

575

Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly

580

585

590

Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala

595

600

605

Ser Gly Tyr Ser Phe Thr Asp Tyr Tyr Ile Asn Trp Val Lys Gln Arg

610

615

620

Pro Gly Gln Gly Leu Glu Trp Ile Gly Lys Ile Gly Pro Gly Ser Gly

625

630

635

640

Asn Thr Tyr Tyr Asn Glu Lys Phe Glu Gly Lys Ala Thr Leu Thr Ala

645

650

655

Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser

660

665

670

Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Thr Gly Pro Phe Ala Tyr

675

680

685

Trp Gly Gln Gly Thr Leu Val Thr Trp Ser Ala

690

695

<210> 178

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 178

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180		185		190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				

385	390	395	400
Pro	Pro	Val	Leu
Asp	Ser	Asp	Gly
Ser	Phe	Phe	Leu
Tyr	Ser	Lys	Leu
405	410	415	
Thr	Val	Asp	Lys
Ser	Arg	Trp	Gln
Gln	Gln	Gly	Asn
Val	Phe	Ser	Cys
Ser			
420	425	430	
Val	Met	His	Glu
Ala	Leu	His	Asn
His	Tyr	Thr	Gln
Lys	Ser	Leu	Ser
435	440	445	
Leu	Ser	Pro	Gly
Gly	Gly	Ser	Gly
Gly	Ser	Asp	Ile
Val	Met	Thr	Gln
450	455	460	
Ser	His	Lys	Phe
Met	Ser	Thr	Ser
Val	Gly	Asp	Arg
Val	Ser	Ile	Thr
465	470	475	480
Cys	Lys	Ala	Ser
Gln	Asp	Val	Gly
Thr	Ala	Val	Ala
Trp	Tyr	Gln	Gln
485	490	495	
Lys	Pro	Gly	Gln
Ser	Pro	Lys	Leu
Leu	Ile	Tyr	Trp
Ala	Ser	Thr	Arg
500	505	510	
His	Thr	Gly	Val
Pro	Asp	Arg	Phe
Thr	Gly	Ser	Gly
Ser	Gly	Ser	Gly
Thr	Asp		
515	520	525	
Phe	Thr	Leu	Thr
Ile	Ser	Asn	Val
Gln	Ser	Glu	Asp
Leu	Ala	Asp	Tyr
530	535	540	
Phe	Cys	Gln	Gln
Tyr	Ser	Ser	Tyr
Pro	Tyr	Thr	Phe
Gly	Gly	Gly	Gly
Thr			
545	550	555	560
Lys	Leu	Glu	Ile
Lys	Gly	Gly	Gly
Gly	Gly	Ser	Gly
Gly	Gly	Gly	Gly
Ser	Gly		
565	570	575	
Gly	Gly	Gly	Ser
Gly	Gly	Gly	Gly
Ser	Gln	Val	Thr
Leu	Lys	Glu	Ser
580	585	590	
Gly	Pro	Gly	Ile
Leu	Gln	Pro	Ser
Gln	Thr	Leu	Ser
Leu	Thr	Cys	Ser

595 600 605
 Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile
 610 615 620
 Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp
 625 630 635 640
 Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile
 645 650 655
 Ser Lys Asp Thr Ser Arg Asn Gln Val Phe Leu Lys Ile Thr Ser Val
 660 665 670
 Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Arg Arg Leu Gly
 675 680 685
 Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
 690 695 700

<210> 179

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 179

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

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Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

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

85

90

95

Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Val Leu Met Thr Gln
 450 455 460
 Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 465 470 475 480
 Cys Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu
 485 490 495
 Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
 500 505 510
 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 515 520 525
 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
 530 535 540
 Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Pro Thr
 545 550 555 560
 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly
 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val
 580 585 590
 Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
 595 600 605
 Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr
 610 615 620
 Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly
 625 630 635 640

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Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe Lys

645

650

655

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met

660

665

670

Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala

675

680

685

Arg Gly Gly Asn Trp Asn Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr

690

695

700

Thr Val Thr Val Ser Ser

705

710

<210> 180

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 180

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35	40	45													
Gly	Tyr	Ile	Tyr	Pro	Arg	Asp	Ala	Ile	Thr	Lys	Tyr	Asn	Glu	Lys	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	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
			85						90					95	
Ala	Arg	Trp	Gly	Tyr	Tyr	Phe	Gly	Ser	Thr	Ser	Tyr	Tyr	Phe	Asp	Phe
		100						105						110	
Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
		115						120						125	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
		130				135					140				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145					150					155				160	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
			165						170					175	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
		180							185					190	
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195						200					205		
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
	210					215						220			
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
225					230					235				240	
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr

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

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

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660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg His Glu Gly Gly Ser

675

680

685

Asn Phe Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

690

695

700

<210> 181

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 181

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys Phe

50

55

60

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Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe

100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180 185 190

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

195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210 215 220

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

225 230 235 240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260 265 270

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

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

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Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 182

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 182

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

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

85	90	95
Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe		
100	105	110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		

290		295		300	
Thr	Tyr	Arg	Val	Val	Ser
			Val	Leu	Thr
				Val	Leu
				His	Gln
				Asp	Trp
				Leu	
305		310		315	320
Asn	Gly	Lys	Glu	Tyr	Lys
			Cys	Lys	Val
				Ser	Asn
				Lys	Ala
				Leu	Pro
				Ala	
	325		330		335
Pro	Ile	Glu	Lys	Thr	Ile
			Ser	Lys	Ala
				Lys	Gly
				Gln	Pro
				Arg	Glu
				Pro	
	340		345		350
Gln	Val	Tyr	Thr	Leu	Pro
			Pro	Ser	Arg
				Glu	Glu
				Met	Thr
				Lys	Asn
				Gln	
	355		360		365
Val	Ser	Leu	Thr	Cys	Leu
			Val	Lys	Gly
				Phe	Tyr
				Pro	Ser
				Asp	Ile
				Ala	
	370		375		380
Val	Glu	Trp	Glu	Ser	Asn
			Gly	Gln	Pro
				Glu	Asn
				Asn	Tyr
				Lys	Thr
				Thr	
385		390		395	400
Pro	Pro	Val	Leu	Asp	Ser
			Asp	Gly	Ser
				Phe	Phe
				Leu	Tyr
				Ser	Lys
				Leu	
	405		410		415
Thr	Val	Asp	Lys	Ser	Arg
			Trp	Gln	Gln
				Gly	Asn
				Val	Phe
				Ser	Cys
				Ser	
	420		425		430
Val	Met	His	Glu	Ala	Leu
			His	Asn	His
				Tyr	Thr
				Gln	Lys
				Ser	Leu
				Ser	
	435		440		445
Leu	Ser	Pro	Gly	Gly	Gly
			Ser	Gly	Gly
				Ser	Ser
				Ser	Ser
				Glu	Leu
				Thr	Gln
	450		455		460
Asp	Pro	Ala	Val	Ser	Val
			Ala	Leu	Gly
				Gln	Thr
				Val	Arg
				Ile	Thr
				Cys	
465		470		475	480
Gln	Gly	Asp	Ser	Leu	Arg
			Ser	Tyr	Tyr
				Ala	Ser
				Trp	Tyr
				Gln	Gln
				Lys	
	485		490		495
Pro	Gly	Gln	Ala	Pro	Val
			Leu	Val	Ile
				Tyr	Gly
				Lys	Asn
				Asn	Arg
				Pro	

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

705

<210> 183

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 183

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

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

85 90 95

Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe

100 105 110

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

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Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Thr Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

20180308-154537-1

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Thr His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 184

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 184

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

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

340		345		350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
355		360		365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
370		375		380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				
	405		410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser				
	420		425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser				
	435		440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln				
	450		455	460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys				
465		470		475
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys				
	485		490	495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Ala Asn Arg Pro				
	500		505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala				
	515		520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr				
	530		535	540
Cys Asn Ser Arg Asp Ser Ser Gly Ala His Val Val Phe Gly Gly Gly				

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545 550 555 560
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 565 570 575
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln
 580 585 590
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys
 595 600 605
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg
 610 615 620
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser
625 630 635 640
Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile
 645 650 655
Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu
 660 665 670
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala
 675 680 685
Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr
 690 695 700
Val Ser Ser
705

<210> 185

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 185

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160

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Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240
 Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 290 295 300
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

20180308-154537-1

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 186

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 186

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Ala Ile Thr Lys Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180		185		190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				

385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
	420	425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
	435	440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln			
	450	455	460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys			
465	470	475	480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys			
	485	490	495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Thr Asn Arg Pro			
	500	505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala			
	515	520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr			
	530	535	540
Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly			
545	550	555	560
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
	565	570	575
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln			
	580	585	590
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys			

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595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ala

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 187

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 187

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Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

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

85 90 95

Ala Arg Trp Gly Tyr Tyr Phe Gly Ser Thr Ser Tyr Tyr Phe Asp Phe

100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180 185 190

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

195 200 205

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Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asp Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

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Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Thr

625 630 635 640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645 650 655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660 665 670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675 680 685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690 695 700

Val Ser Ser

705

<210> 188

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 188

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly

1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Gly

20	25	30
Val Val Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Lys Leu Leu Ile		
35	40	45
Tyr Ser Pro Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly		
50	55	60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Ile Gln Ser		
65	70	75
Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Thr Tyr Pro Trp		
85	90	95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala		
100	105	110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly		
115	120	125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala		
130	135	140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln		
145	150	155
Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser		
165	170	175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr		
180	185	190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser		
195	200	205
Phe Asn Arg Gly Glu Cys		
210		

<210> 189

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 189

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

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

85 90 95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

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

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Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln

450

455

460

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr

465

470

475

480

Cys Lys Ala Ser Gln Asp Val Ile Thr Ala Val Ala Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

500

505

510

His Thr Gly Val Pro Asp Arg Phe Thr Gly Thr Gly Ser Gly Thr Asp

515

520

525

Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr

530

535

540

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Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr

545 550 555 560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser

580 585 590

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys

595 600 605

Ala Phe Asp Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln

610 615 620

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp Pro Gly Ser

625 630 635 640

Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

645 650 655

Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met His Leu Ser Ser Leu Thr

660 665 670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Lys Asn Tyr Gly Gly

675 680 685

Ser Tyr Ala Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ala

690 695 700

<210> 190

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 190

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

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

85 90 95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145	150	155	160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe			
	165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val			
	180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val			
	195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys			
	210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala			
225	230	235	240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr			
	245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val			
	260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val			
	275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser			
	290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			

355		360		365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
370		375		380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				
	405		410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser				
	420		425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser				
	435		440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln				
	450		455	460
Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr				
465		470		475
Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln				
	485		490	495
Lys Pro Gly Gln Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg				
	500		505	510
His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp				
	515		520	525
Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr				
	530		535	540
Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr Thr Phe Gly Gly Gly Thr				
545		550		555
Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly				

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565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser

580

585

590

Gly Ala Glu Leu Val Lys Thr Gly Thr Ser Val Lys Leu Ser Cys Lys

595

600

605

Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln

610

615

620

Arg Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser

625

630

635

640

Gly Ser Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

645

650

655

Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr

660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg His Glu Glu Gly Gly

675

680

685

Tyr Ser Ala Trp Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

690

695

700

Ser Ala

705

<210> 191

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 191

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175

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Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
385					390					395					400
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
				405					410					415	
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
			420					425						430	
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
		435					440					445			
Leu	Ser	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Asp	Val	Leu	Met	Thr	Gln
	450					455					460				
Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser
465					470					475					480
Cys	Arg	Ser	Ser	Gln	Ser	Ile	Val	His	Ser	Asn	Gly	Asp	Thr	Tyr	Leu
				485					490					495	
Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr
		500					505					510			
Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser
		515					520					525			
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Val	Ala	Glu
	530					535					540				
Asp	Leu	Gly	Val	Tyr	Tyr	Cys	Phe	Arg	Gly	Ser	His	Ile	Pro	Pro	Thr
545					550					555					560
Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly
				565					570				575		
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln
		580					585					590			

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

595

600

605

Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr Leu

610

615

620

Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr

625

630

635

640

Ile Tyr Pro Asn Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly

645

650

655

Lys Thr Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu

660

665

670

Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Arg

675

680

685

Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr

690

695

700

Val Thr Val Ser Ser

705

<210> 192

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 192

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val

195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				

405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser		
420	425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser		
435	440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ile Val Met Thr Gln		
450	455	460
Thr Pro Lys Phe Leu Pro Val Ser Ala Gly Asp Arg Val Thr Met Thr		
465	470	475
Cys Lys Ala Ser Gln Asn Val Gly Asn Asn Val Ala Trp Tyr Gln Gln		
485	490	495
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Ala Ser Asn Arg		
500	505	510
Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp		
515	520	525
Phe Phe Thr Ile Ser Ser Val Gln Val Glu Asp Leu Ala Val Tyr Phe		
530	535	540
Cys Gln Gln His Tyr Ser Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys		
545	550	555
Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly		
565	570	575
Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly		
580	585	590
Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala		
595	600	605
Ser Gly Tyr Ser Phe Thr Asp Tyr Tyr Ile Asn Trp Val Lys Gln Arg		

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610 615 620
Pro Gly Gln Gly Leu Glu Trp Ile Gly Lys Ile Gly Pro Gly Ser Gly
625 630 635 640
Asn Thr Tyr Tyr Asn Glu Lys Phe Glu Gly Lys Ala Thr Leu Thr Ala
 645 650 655
Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 660 665 670
Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Thr Gly Pro Phe Ala Tyr
 675 680 685
Trp Gly Gln Gly Thr Leu Val Thr Trp Ser Ala
690 695

<210> 193

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 193

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30

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Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

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

85

90

95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

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Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

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

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Ser Lys Asp Thr Ser Arg Asn Gln Val Phe Leu Lys Ile Thr Ser Val

660

665

670

Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Arg Arg Leu Gly

675

680

685

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

690

695

700

<210> 194

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 194

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys
		85				90								95	
Ala	Arg	Trp	Gly	Tyr	Phe	Tyr	Gly	Ser	Arg	Ser	Tyr	Tyr	Phe	Asp	Tyr
		100					105						110		
Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
		115					120						125		
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
		130				135					140				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145				150					155					160	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
		165					170						175		
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
		180					185						190		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195					200						205		
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
		210				215					220				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
225				230					235					240	
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
		245					250						255		
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		260					265						270		
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val

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

485		490		495
Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr				
500		505		510
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser				
515		520		525
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu				
530		535		540
Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Pro Thr				
545		550		555
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly				
565		570		575
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val				
580		585		590
Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val				
595		600		605
Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr				
610		615		620
Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly				
625		630		635
Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe Lys				
645		650		655
Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met				
660		665		670
Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala				
675		680		685
Arg Gly Gly Asn Trp Asn Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr				

690

695

700

Thr Val Thr Val Ser Ser

705

710

<210> 195

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 195

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

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

85

90

95

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Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln
 450 455 460
 Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr
 465 470 475 480
 Cys Lys Ala Ser Gln Asp Val Ser Asn Ala Val Ala Trp Tyr Gln Gln
 485 490 495
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 500 505 510

His Asn Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 515 520 525
 Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr
 530 535 540
 Tyr Cys Gln Gln His Tyr Arg Thr Pro Tyr Thr Phe Gly Gly Gly Thr
 545 550 555 560
 Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 565 570 575
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser
 580 585 590
 Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys
 595 600 605
 Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln
 610 615 620
 Lys Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser
 625 630 635 640
 Gly Asn Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr
 645 650 655
 Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr
 660 665 670
 Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg His Glu Gly Gly Ser
 675 680 685
 Asn Phe Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
 690 695 700

<210> 196

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 196

Gln	Val	Gln	Leu	Gln	Gln	Ser	Asp	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala
1			5						10					15	
Ser	Val	Lys	Ile	Ser	Cys	Lys	Val	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	His
			20						25					30	
Thr	Ile	His	Trp	Met	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile
		35					40						45		
Gly	Tyr	Ile	Tyr	Pro	Arg	Asp	Val	Ile	Thr	Gln	Tyr	Asn	Glu	Lys	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	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Leu	Cys
			85							90					95
Ala	Arg	Trp	Gly	Tyr	Phe	Tyr	Gly	Ser	Arg	Ser	Tyr	Tyr	Phe	Asp	Tyr
			100						105						110
Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly

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

325	330	335	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
340	345	350	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
355	360	365	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
370	375	380	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
405	410	415	
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
420	425	430	
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
435	440	445	
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln			
450	455	460	
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys			
465	470	475	480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys			
485	490	495	
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro			
500	505	510	
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala			
515	520	525	
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr			

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530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly

545 550 555 560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625 630 635 640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 197

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 197

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

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Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
210 215 220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225 230 235 240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

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Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

20180308-154537-1

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 198

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 198

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		
290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu		
305	310	315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala		
325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro		
340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln		
355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala		

370		375		380	
Val	Glu	Trp	Glu	Ser	Asn
			Gly	Gln	Pro
				Glu	Asn
				Asn	Tyr
				Lys	Thr
				Thr	
385		390		395	400
Pro	Pro	Val	Leu	Asp	Ser
			Asp	Gly	Ser
				Phe	Phe
				Leu	Tyr
				Ser	Lys
				Leu	
	405		410		415
Thr	Val	Asp	Lys	Ser	Arg
			Trp	Gln	Gln
			Gly	Asn	Val
				Phe	Ser
				Cys	Ser
	420		425		430
Val	Met	His	Glu	Ala	Leu
			His	Asn	His
			Tyr	Thr	Gln
			Lys	Ser	Leu
			Ser		
	435		440		445
Leu	Ser	Pro	Gly	Gly	Gly
			Ser	Gly	Gly
			Ser	Ser	Ser
			Glu	Leu	Thr
			Gln		
	450		455		460
Asp	Pro	Ala	Val	Ser	Val
			Ala	Leu	Gly
			Gln	Thr	Val
			Arg	Ile	Thr
			Cys		
465		470		475	480
Gln	Gly	Asp	Ser	Leu	Arg
			Ser	Tyr	Tyr
			Ala	Ser	Trp
			Tyr	Gln	Gln
			Lys		
	485		490		495
Pro	Gly	Gln	Ala	Pro	Val
			Leu	Val	Ile
			Tyr	Gly	Lys
			Thr	Asn	Arg
			Pro		
	500		505		510
Ser	Gly	Ile	Pro	Asp	Arg
			Phe	Ser	Gly
			Ser	Ser	Ser
			Gly	Asn	Thr
			Ala		
	515		520		525
Ser	Leu	Thr	Ile	Thr	Gly
			Ala	Gln	Ala
			Glu	Asp	Glu
			Ala	Asp	Tyr
			Tyr		
	530		535		540
Cys	Asn	Ser	Arg	Asp	Ser
			Ser	Ser	Gly
			Thr	His	Val
			Val	Val	Phe
			Gly	Gly	Gly
	545		550		555
Thr	Lys	Leu	Thr	Val	Leu
			Gly	Gly	Gly
			Gly	Gly	Ser
			Gly	Gly	Gly
			Gly	Gly	Gly
			Ser	Glu	Val
			Gln	Leu	Val
			Gln		
	565		570		575
Gly	Gly	Gly	Gly	Ser	Glu
			Val	Gln	Leu
			Val	Gln	

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 199

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 199

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240
 Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 290 295 300
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln
 450 455 460
 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys
 465 470 475 480
 Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
 485 490 495
 Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Ala Asn Arg Pro
 500 505 510
 Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala
 515 520 525
 Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
 530 535 540
 Cys Asn Ser Arg Asp Ser Ser Gly Ala His Val Val Phe Gly Gly Gly
 545 550 555 560
 Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 565 570 575
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln
 580 585 590
 Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys
 595 600 605

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Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 200

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 200

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1	5	10	15
Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His			
20	25	30	
Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile			
35	40	45	
Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys			
85	90	95	
Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr			
100	105	110	
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly			
115	120	125	
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly			
130	135	140	
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val			
145	150	155	160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe			
165	170	175	
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val			
180	185	190	
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val			
195	200	205	
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys			

210	215	220	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala			
225	230	235	240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr			
	245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val			
	260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val			
	275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser			
	290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
	355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
	370	375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			

420	425	430	
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
435	440	445	
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln			
450	455	460	
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys			
465	470	475	480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys			
485	490	495	
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro			
500	505	510	
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala			
515	520	525	
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr			
530	535	540	
Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly			
545	550	555	560
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser			
565	570	575	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln			
580	585	590	
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys			
595	600	605	
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg			
610	615	620	
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser			

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625 630 635 640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645 650 655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660 665 670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675 680 685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690 695 700

Val Ser Ser

705

<210> 201

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 201

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

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Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys 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 Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240

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Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

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

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Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 202

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 202

Gln Val Gln Leu Gln Gln Ser Asp Ala Glu Leu Val Lys Pro Gly Ala

1

5

10

15

Ser Val Lys Ile Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50		55		60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr				
65		70		75
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Leu Cys				
	85		90	95
Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr				
	100		105	110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly				
	115		120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly				
	130		135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val				
145		150		155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe				
	165		170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val				
	180		185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
	195		200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
	210		215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				

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

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465				470				475				480			
Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	Trp	Tyr	Gln	Gln	Lys
				485				490				495			
Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr	Gly	Lys	Asp	Asn	Arg	Pro
500								505				510			
Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Thr	Ala
515								520				525			
Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr
530								535				540			
Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asp	His	Val	Val	Phe	Gly	Gly	Gly
545								550				555			
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
				565								570			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Gln
				580								585			
Ser	Gly	Gly	Gly	Val	Glu	Arg	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
595								600				605			
Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly	Met	Ser	Trp	Val	Arg
610								615				620			
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile	Asn	Trp	Thr
625								630				635			
Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Val	Thr	Ile
				645								650			
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu
660								665				670			
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Ile	Leu	Gly	Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 203

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 203

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Thr Val Gly

1

5

10

15

Asp Arg Val Asn Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala

20

25

30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

35

40

45

Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly

50

55

60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Asn Met Gln Ser

65

70

75

80

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Lys Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Trp

85

90

95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala

100

105

110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly

115

120

125

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

130

135

140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145

150

155

160

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

165

170

175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

180

185

190

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

195

200

205

Phe Asn Arg Gly Glu Cys

210

<210> 204

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 204

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 Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Val Thr Leu 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 Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180		185		190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				

385	390	395	400
Pro	Pro	Val	Leu
Asp	Ser	Asp	Gly
Ser	Phe	Phe	Leu
Tyr	Ser	Lys	Leu
405	410	415	
Thr	Val	Asp	Lys
Ser	Arg	Trp	Gln
Gln	Gln	Gly	Asn
Val	Phe	Ser	Cys
Ser			
420	425	430	
Val	Met	His	Glu
Ala	Leu	His	Asn
His	Tyr	Thr	Gln
Lys	Ser	Leu	Ser
435	440	445	
Leu	Ser	Pro	Gly
Gly	Gly	Ser	Gly
Gly	Ser	Asp	Ile
Val	Met	Thr	Gln
450	455	460	
Ser	His	Lys	Phe
Met	Ser	Thr	Ser
Val	Gly	Asp	Arg
Val	Ser	Ile	Thr
465	470	475	480
Cys	Lys	Ala	Ser
Gln	Asp	Val	Ile
Thr	Ala	Val	Ala
Trp	Tyr	Gln	Gln
485	490	495	
Lys	Pro	Gly	Gln
Ser	Pro	Lys	Leu
Leu	Ile	Tyr	Trp
Ala	Ser	Thr	Arg
500	505	510	
His	Thr	Gly	Val
Pro	Asp	Arg	Phe
Thr	Gly	Thr	Gly
Ser	Gly	Thr	Asp
515	520	525	
Tyr	Thr	Leu	Thr
Ile	Ser	Ser	Val
Gln	Ala	Glu	Asp
Leu	Ala	Leu	Tyr
530	535	540	
Tyr	Cys	Gln	Gln
His	Tyr	Ser	Thr
Pro	Trp	Thr	Phe
Gly	Gly	Gly	Gly
Thr			
545	550	555	560
Lys	Leu	Glu	Ile
Lys	Gly	Gly	Gly
Gly	Gly	Ser	Gly
Gly	Gly	Gly	Gly
Ser	Gly	Ser	Gly
565	570	575	
Gly	Gly	Ser	Gly
Gly	Gly	Gly	Gly
Ser	Gln	Val	Gln
Leu	Gln	Gln	Ser
580	585	590	
Gly	Ala	Glu	Leu
Val	Lys	Pro	Gly
Ala	Ser	Val	Lys
Leu	Ser	Cys	Lys

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595		600		605											
Ala	Phe	Asp	Tyr	Thr	Phe	Thr	Ser	Tyr	Asp	Ile	Asn	Trp	Val	Lys	Gln
610					615						620				
Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Trp	Ile	Asp	Pro	Gly	Ser
625					630						635				640
Gly	Asn	Thr	Lys	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr
					645						650				655
Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	Tyr	Met	His	Leu	Ser	Ser	Leu	Thr
					660						665				670
Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Lys	Asn	Tyr	Gly	Gly
					675						680				685
Ser	Tyr	Ala	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ala
690											695				700

<210> 205

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 205

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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	Val	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	His
			20					25						30	
Thr	Ile	His	Trp	Met	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
		35					40					45			
Gly	Tyr	Ile	Tyr	Pro	Arg	Asp	Val	Ile	Thr	Gln	Tyr	Asn	Glu	Lys	Phe
	50					55						60			
Lys	Gly	Lys	Val	Thr	Leu	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	Leu	Cys
				85						90				95	
Ala	Arg	Trp	Gly	Tyr	Phe	Tyr	Gly	Ser	Arg	Ser	Tyr	Tyr	Phe	Asp	Tyr
			100						105					110	
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
			115						120					125	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
		130							135					140	
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145					150					155					160
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
				165						170				175	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
			180							185				190	
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195							200					205	

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Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

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Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln

450

455

460

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr

465

470

475

480

Cys Lys Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln

485

490

495

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

500

505

510

His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp

515

520

525

Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr

530

535

540

Tyr Cys Gln Gln His Tyr Ser Thr Pro Tyr Thr Phe Gly Gly Gly Thr

545

550

555

560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser

580

585

590

Gly Ala Glu Leu Val Lys Thr Gly Thr Ser Val Lys Leu Ser Cys Lys

595

600

605

Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln

610

615

620

20180308-154537-1

Arg Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser

625 630 635 640

Gly Ser Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

645 650 655

Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr

660 665 670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg His Glu Glu Gly Gly

675 680 685

Tyr Ser Ala Trp Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

690 695 700

Ser Ala

705

<210> 206

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 206

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20	25	30
Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile		
35	40	45
Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe		
50	55	60
Lys Gly Lys Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr		
65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Leu Cys		
85	90	95
Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		

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

435		440		445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Val Leu Met Thr Gln				
450		455		460
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser				
465		470		475
				480
Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu				
	485		490	495
Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr				
	500		505	510
Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser				
	515		520	525
Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Val Ala Glu				
	530		535	540
Asp Leu Gly Val Tyr Tyr Cys Phe Arg Gly Ser His Ile Pro Pro Thr				
545		550		555
				560
Phe Gly Ala Gly Thr Lys Leu Glu Lys Gly Gly Gly Gly Ser Gly Gly				
	565		570	575
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln				
	580		585	590
Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val Lys				
	595		600	605
Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr Leu				
	610		615	620
Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr				
625		630		635
				640
Ile Tyr Pro Asn Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly				

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645

650

655

Lys Thr Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu

660

665

670

Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Arg

675

680

685

Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr

690

695

700

Val Thr Val Ser Ser

705

<210> 207

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 207

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

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Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Val Thr Leu 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 Leu Cys

85

90

95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

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Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ile Val Met Thr Gln

450

455

460

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

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Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Thr Gly Pro Phe Ala Tyr

675

680

685

Trp Gly Gln Gly Thr Leu Val Thr Trp Ser Ala

690

695

<210> 208

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 208

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Val Thr Leu 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 Leu Cys

85	90	95
Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
160		
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
240		
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		

290		295		300	
Thr	Tyr	Arg	Val	Val	Ser
			Val	Leu	Thr
				Val	Leu
				His	Gln
				Asp	Trp
				Leu	
305		310		315	320
Asn	Gly	Lys	Glu	Tyr	Lys
			Cys	Lys	Val
				Ser	Asn
				Lys	Ala
				Leu	Pro
				Ala	
	325		330		335
Pro	Ile	Glu	Lys	Thr	Ile
			Ser	Lys	Ala
				Lys	Gly
				Gln	Pro
				Arg	Glu
				Pro	
	340		345		350
Gln	Val	Tyr	Thr	Leu	Pro
			Pro	Ser	Arg
				Glu	Glu
				Met	Thr
				Lys	Asn
				Gln	
	355		360		365
Val	Ser	Leu	Thr	Cys	Leu
			Val	Lys	Gly
				Phe	Tyr
				Pro	Ser
				Asp	Ile
				Ala	
	370		375		380
Val	Glu	Trp	Glu	Ser	Asn
			Gly	Gln	Pro
				Glu	Asn
				Asn	Tyr
				Lys	Thr
				Thr	
385		390		395	400
Pro	Pro	Val	Leu	Asp	Ser
			Asp	Gly	Ser
				Phe	Phe
				Leu	Tyr
				Ser	Lys
				Leu	
	405		410		415
Thr	Val	Asp	Lys	Ser	Arg
			Trp	Gln	Gln
				Gly	Asn
				Val	Phe
				Ser	Cys
				Ser	
	420		425		430
Val	Met	His	Glu	Ala	Leu
			His	Asn	His
				Tyr	Thr
				Gln	Lys
				Ser	Leu
				Ser	
	435		440		445
Leu	Ser	Pro	Gly	Gly	Gly
			Ser	Gly	Gly
				Ser	Asp
				Ile	Val
				Met	Thr
				Gln	
	450		455		460
Ser	His	Lys	Phe	Met	Ser
			Thr	Ser	Val
				Gly	Asp
				Arg	Val
				Ser	Ile
				Thr	
465		470		475	480
Cys	Lys	Ala	Ser	Gln	Asp
			Val	Gly	Thr
				Ala	Val
				Ala	Trp
				Tyr	Gln
				Gln	
	485		490		495
Lys	Pro	Gly	Gln	Ser	Pro
			Lys	Leu	Leu
				Ile	Tyr
				Trp	Ala
				Ser	Thr
				Arg	

500	505	510
His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp		
515	520	525
Phe Thr Leu Thr Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr		
530	535	540
Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr		
545	550	555
Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly		
565	570	575
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Thr Leu Lys Glu Ser		
580	585	590
Gly Pro Gly Ile Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser		
595	600	605
Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile		
610	615	620
Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp		
625	630	635
Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile		
645	650	655
Ser Lys Asp Thr Ser Arg Asn Gln Val Phe Leu Lys Ile Thr Ser Val		
660	665	670
Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Arg Arg Leu Gly		
675	680	685
Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala		
690	695	700

<210> 209

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 209

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Val Thr Leu 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 Leu Cys

85 90 95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115 120 125

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

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Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Val Leu Met Thr Gln

450

455

460

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

465

470

475

480

Cys Arg Ser Ser Gln Asn Ile Val His Ser Asn Gly Asn Thr Tyr Leu

485

490

495

Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr

500

505

510

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser

515

520

525

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu

530

535

540

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Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Pro Thr

545 550 555 560

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly

565 570 575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val

580 585 590

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

595 600 605

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr

610 615 620

Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly

625 630 635 640

Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe Lys

645 650 655

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met

660 665 670

Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala

675 680 685

Arg Gly Gly Asn Trp Asn Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr

690 695 700

Thr Val Thr Val Ser Ser

705 710

<210> 210

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 210

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 Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Val Thr Leu 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 Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145	150	155	160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe			
	165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val			
	180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val			
	195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys			
	210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala			
225	230	235	240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr			
	245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val			
	260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val			
	275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser			
	290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu			
305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			

355		360		365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
370		375		380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				
	405		410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser				
	420		425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser				
	435		440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln				
	450		455	460
Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr				
465		470		475
Cys Lys Ala Ser Gln Asp Val Ser Asn Ala Val Ala Trp Tyr Gln Gln				
	485		490	495
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg				
	500		505	510
His Asn Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp				
	515		520	525
Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr				
	530		535	540
Tyr Cys Gln Gln His Tyr Arg Thr Pro Tyr Thr Phe Gly Gly Gly Thr				
545		550		555
Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly				

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565	570	575
Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser		
580	585	590
Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys		
595	600	605
Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln		
610	615	620
Lys Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser		
625	630	635
Gly Asn Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr		
645	650	655
Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr		
660	665	670
Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg His Glu Gly Gly Ser		
675	680	685
Asn Phe Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala		
690	695	700

<210> 211

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 211

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 Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Val Thr Leu 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 Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175

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Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln
 450 455 460
 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys
 465 470 475 480
 Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
 485 490 495
 Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro
 500 505 510
 Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala
 515 520 525
 Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
 530 535 540
 Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly
 545 550 555 560
 Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 565 570 575
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln
 580 585 590

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Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 212

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 212

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 Val Ser Gly Tyr Thr Phe Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Val Thr Leu 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 Leu Cys
 85 90 95
 Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val

195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
385		390		395
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu				

405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser		
420	425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser		
435	440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln		
450	455	460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys		
465	470	475
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys		
485	490	495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro		
500	505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala		
515	520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr		
530	535	540
Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly		
545	550	555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
565	570	575
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln		
580	585	590
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys		
595	600	605
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg		

610 615 620

1 5 10 15

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Ser	Val	Lys	Val	Ser	Cys	Lys	Val	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	His
			20					25						30	
Thr	Ile	His	Trp	Met	Lys	Gln	Arg	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile
			35				40						45		
Gly	Tyr	Ile	Tyr	Pro	Arg	Asp	Val	Ile	Thr	Gln	Tyr	Asn	Glu	Lys	Phe
			50				55						60		
Lys	Gly	Lys	Val	Thr	Leu	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	Leu	Cys
					85				90					95	
Ala	Arg	Trp	Gly	Tyr	Phe	Tyr	Gly	Ser	Arg	Ser	Tyr	Tyr	Phe	Asp	Tyr
			100					105						110	
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
			115					120						125	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
			130					135						140	
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145					150					155				160	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
					165					170				175	
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
					180					185				190	
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
			195					200						205	
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
			210					215						220	

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

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Thr Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Thr His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

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Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 214

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 214

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35	40	45
Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe		
50	55	60
Lys Gly Lys Val Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr		
65	70	75
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Leu Cys		
85	90	95
Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		

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

450		455		460	
Asp	Pro	Ala	Val	Ser	Val
		Ala	Leu	Gly	Gln
				Thr	Val
				Arg	Ile
				Thr	Cys
465		470		475	480
Gln	Gly	Asp	Ser	Leu	Arg
				Ser	Tyr
				Tyr	Ala
				Ser	Trp
				Tyr	Gln
				Gln	Lys
		485		490	495
Pro	Gly	Gln	Ala	Pro	Val
				Leu	Val
				Ile	Tyr
				Gly	Lys
				Ala	Asn
				Arg	Pro
		500		505	510
Ser	Gly	Ile	Pro	Asp	Arg
				Phe	Ser
				Gly	Ser
				Ser	Ser
				Gly	Asn
				Thr	Ala
		515		520	525
Ser	Leu	Thr	Ile	Thr	Gly
				Ala	Gln
				Ala	Glu
				Asp	Glu
				Ala	Asp
				Tyr	Tyr
		530		535	540
Cys	Asn	Ser	Arg	Asp	Ser
				Ser	Gly
				Ala	His
				Val	Val
				Phe	Gly
				Gly	Gly
				Gly	Gly
545		550		555	560
Thr	Lys	Leu	Thr	Val	Leu
				Gly	Gly
				Gly	Gly
				Gly	Gly
				Ser	Gly
				Gly	Gly
				Gly	Gly
				Ser	Glu
				Val	Gln
				Leu	Val
				Gln	
		580		585	590
Ser	Gly	Gly	Gly	Val	Glu
				Arg	Pro
				Gly	Gly
				Ser	Leu
				Arg	Leu
				Ser	Cys
		595		600	605
Ala	Ala	Ser	Gly	Phe	Thr
				Phe	Asp
				Asp	Tyr
				Gly	Met
				Ser	Trp
				Val	Arg
		610		615	620
Gln	Ala	Pro	Gly	Lys	Gly
				Leu	Glu
				Trp	Val
				Ser	Gly
				Ile	Asn
				Trp	Ser
625		630		635	640
Gly	Gly	Ser	Thr	Gly	Tyr
				Ala	Asp
				Ser	Val
				Lys	Gly
				Arg	Val
				Thr	Ile
		645		650	655
Ser	Arg	Asp	Asn	Ala	Lys
				Asn	Ser
				Leu	Tyr
				Leu	Gln
				Met	Asn
				Ser	Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 215

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 215

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50

55

60

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Lys	Gly	Lys	Val	Thr	Leu	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	Leu	Cys
					85					90					95
Ala	Arg	Trp	Gly	Tyr	Phe	Tyr	Gly	Ser	Arg	Ser	Tyr	Tyr	Phe	Asp	Tyr
					100					105					110
Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
					115					120					125
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
					130					135					140
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145					150					155					160
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
					165					170					175
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
					180					185					190
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
					195					200					205
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
					210					215					220
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
225					230					235					240
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
					245					250					255
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
					260					265					270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

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Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 216

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 216

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Val Thr Leu 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 Leu Cys

85	90	95
Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		

290		295		300	
Thr	Tyr	Arg	Val	Val	Ser
			Val	Leu	Thr
				Val	Leu
				His	Gln
				Asp	Trp
				Leu	
305		310		315	320
Asn	Gly	Lys	Glu	Tyr	Lys
			Cys	Lys	Val
				Ser	Asn
				Lys	Ala
				Leu	Pro
				Ala	
	325		330		335
Pro	Ile	Glu	Lys	Thr	Ile
			Ser	Lys	Ala
				Lys	Gly
				Gln	Pro
				Arg	Glu
				Pro	
	340		345		350
Gln	Val	Tyr	Thr	Leu	Pro
			Pro	Ser	Arg
				Glu	Glu
				Met	Thr
				Lys	Asn
				Gln	
	355		360		365
Val	Ser	Leu	Thr	Cys	Leu
			Val	Lys	Gly
				Phe	Tyr
				Pro	Ser
				Asp	Ile
				Ala	
	370		375		380
Val	Glu	Trp	Glu	Ser	Asn
			Gly	Gln	Pro
				Glu	Asn
				Asn	Tyr
				Lys	Thr
				Thr	
385		390		395	400
Pro	Pro	Val	Leu	Asp	Ser
			Asp	Gly	Ser
				Phe	Phe
				Leu	Tyr
				Ser	Lys
				Leu	
	405		410		415
Thr	Val	Asp	Lys	Ser	Arg
			Trp	Gln	Gln
				Gly	Asn
				Val	Phe
				Ser	Cys
				Ser	
	420		425		430
Val	Met	His	Glu	Ala	Leu
			His	Asn	His
				Tyr	Thr
				Gln	Lys
				Ser	Leu
				Ser	
	435		440		445
Leu	Ser	Pro	Gly	Gly	Gly
			Ser	Gly	Gly
				Ser	Ser
				Ser	Ser
				Glu	Leu
				Thr	Gln
	450		455		460
Asp	Pro	Ala	Val	Ser	Val
			Ala	Leu	Gly
				Gln	Thr
				Val	Arg
				Ile	Thr
				Cys	
465		470		475	480
Gln	Gly	Asp	Ser	Leu	Arg
			Ser	Tyr	Tyr
				Ala	Ser
				Trp	Tyr
				Gln	Gln
				Lys	
	485		490		495
Pro	Gly	Gln	Ala	Pro	Val
			Leu	Val	Ile
				Tyr	Gly
				Lys	Thr
				Asn	Arg
				Pro	

500	505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala		
515	520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr		
530	535	540
Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly		
545	550	555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
565	570	575
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln		
580	585	590
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys		
595	600	605
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg		
610	615	620
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ala		
625	630	635
Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile		
645	650	655
Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu		
660	665	670
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala		
675	680	685
Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr		
690	695	700
Val Ser Ser		

705

<210> 217

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 217

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Val Thr Leu 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 Leu Cys

85 90 95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100 105 110

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

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
325	330	335	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
340	345	350	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
355	360	365	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
370	375	380	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
405	410	415	
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
420	425	430	
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
435	440	445	
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln			
450	455	460	
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys			
465	470	475	480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys			
485	490	495	
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asp Asn Arg Pro			
500	505	510	
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala			
515	520	525	

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Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Thr

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 218

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain

<400> 218

Asp Ile Gln Met Thr Gln Ser Gln Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Gly Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala
 20 25 30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
Tyr Ser Ala Ser Asn Arg Tyr Thr 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
Lys Asp Phe Ala Thr Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Trp
 85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala

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130

135

140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln

145

150

155

160

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

165

170

175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr

180

185

190

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

195

200

205

Phe Asn Arg Gly Glu Cys

210

<210> 219

<211> 704

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 219

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

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Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

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Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln

450

455

460

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr

465

470

475

480

Cys Lys Ala Ser Gln Asp Val Ile Thr Ala Val Ala Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

500

505

510

His Thr Gly Val Pro Asp Arg Phe Thr Gly Thr Gly Ser Gly Thr Asp

515

520

525

Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr

530

535

540

Tyr Cys Gln Gln His Tyr Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr

545

550

555

560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln Ser

580

585

590

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys

595

600

605

Ala Phe Asp Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Lys Gln

610

615

620

Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp Pro Gly Ser

625

630

635

640

Gly Asn Thr Lys Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr

645

650

655

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Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met His Leu Ser Ser Leu Thr

660

665

670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Lys Asn Tyr Gly Gly

675

680

685

Ser Tyr Ala Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ala

690

695

700

<210> 220

<211> 706

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 220

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50		55		60	
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr					
65		70		75	80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys					
	85		90		95
Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr					
	100		105		110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly					
	115		120		125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly					
	130		135		140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val					
145		150		155	160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe					
	165		170		175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val					
	180		185		190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val					
	195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys					
	210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala					
225		230		235	240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr					
	245		250		255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val					

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

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

675

680

685

Tyr Ser Ala Trp Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

690

695

700

Ser Ala

705

<210> 221

<211> 709

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 221

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

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Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

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Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Val Leu Met Thr Gln
450 455 460
Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
465 470 475 480
Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asp Thr Tyr Leu
485 490 495

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Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr

500

505

510

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser

515

520

525

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Val Ala Glu

530

535

540

Asp Leu Gly Val Tyr Tyr Cys Phe Arg Gly Ser His Ile Pro Pro Thr

545

550

555

560

Phe Gly Ala Gly Thr Lys Leu Glu Lys Gly Gly Gly Gly Ser Gly Gly

565

570

575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln

580

585

590

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

595

600

605

Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr Leu

610

615

620

Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr

625

630

635

640

Ile Tyr Pro Asn Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys Gly

645

650

655

Lys Thr Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu

660

665

670

Phe Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Thr Arg

675

680

685

Gly Ser Asn Trp Ile Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr

690

695

700

Val Thr Val Ser Ser

705

<210> 222

<211> 699

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 222

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

1 5 10 15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20 25 30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65 70 75 80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85 90 95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100		105		110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly				
115		120		125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly				
130		135		140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val				
145		150		155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe				
	165		170	
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val				
	180		185	
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
	195		200	
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
	210		215	
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				

305	310	315	320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala			
	325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
	340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
	355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
	370	375	380
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
	405	410	415
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
	420	425	430
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
	435	440	445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ile Val Met Thr Gln			
	450	455	460
Thr Pro Lys Phe Leu Pro Val Ser Ala Gly Asp Arg Val Thr Met Thr			
465	470	475	480
Cys Lys Ala Ser Gln Asn Val Gly Asn Asn Val Ala Trp Tyr Gln Gln			
	485	490	495
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Ser Tyr Ala Ser Asn Arg			
	500	505	510
Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp			

515 520 525
 Phe Phe Thr Ile Ser Ser Val Gln Val Glu Asp Leu Ala Val Tyr Phe
 530 535 540
 Cys Gln Gln His Tyr Ser Ser Pro Leu Thr Phe Gly Ala Gly Thr Lys
 545 550 555 560
 Leu Glu Leu Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 565 570 575
 Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly
 580 585 590
 Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala
 595 600 605
 Ser Gly Tyr Ser Phe Thr Asp Tyr Tyr Ile Asn Trp Val Lys Gln Arg
 610 615 620
 Pro Gly Gln Gly Leu Glu Trp Ile Gly Lys Ile Gly Pro Gly Ser Gly
 625 630 635 640
 Asn Thr Tyr Tyr Asn Glu Lys Phe Glu Gly Lys Ala Thr Leu Thr Ala
 645 650 655
 Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser
 660 665 670
 Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Thr Gly Pro Phe Ala Tyr
 675 680 685
 Trp Gly Gln Gly Thr Leu Val Thr Trp Ser Ala
 690 695

<210> 223

<211> 703

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 223

Glu Val Gln Leu Gln Gln Ser Val Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

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Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
210 215 220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225 230 235 240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln
 450 455 460
 Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr
 465 470 475 480
 Cys Lys Ala Ser Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln
 485 490 495
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
 500 505 510
 His Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
 515 520 525
 Phe Thr Leu Thr Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr
 530 535 540
 Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr
 545 550 555 560

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Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Thr Leu Lys Glu Ser

580

585

590

Gly Pro Gly Ile Leu Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser

595

600

605

Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile

610

615

620

Arg Gln Pro Ser Gly Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp

625

630

635

640

Asp Asp Asp Lys Arg Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile

645

650

655

Ser Lys Asp Thr Ser Arg Asn Gln Val Phe Leu Lys Ile Thr Ser Val

660

665

670

Asp Thr Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Arg Arg Leu Gly

675

680

685

Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

690

695

700

<210> 224

<211> 710

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 224

Glu Val Gln Leu Gln Gln Ser Val Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
 165 170 175
 Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180		185		190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val				
195		200		205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys				
210		215		220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala				
225		230		235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr				
	245		250	
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val				
	260		265	
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val				
	275		280	
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser				
	290		295	
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu				
305		310		315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala				
	325		330	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro				
	340		345	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln				
	355		360	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala				
	370		375	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				

385	390	395	400
Pro	Pro	Val	Leu
Asp	Ser	Asp	Gly
Ser	Phe	Phe	Leu
Tyr	Ser	Lys	Leu
405	410	415	
Thr	Val	Asp	Lys
Ser	Arg	Trp	Gln
Gln	Gln	Gly	Asn
Val	Phe	Ser	Cys
Ser			
420	425	430	
Val	Met	His	Glu
Ala	Leu	His	Asn
His	Tyr	Thr	Gln
Lys	Ser	Leu	Ser
435	440	445	
Leu	Ser	Pro	Gly
Gly	Gly	Ser	Gly
Gly	Ser	Asp	Val
Leu	Met	Thr	Gln
450	455	460	
Thr	Pro	Leu	Ser
Leu	Pro	Val	Ser
Leu	Gly	Asp	Gln
Ala	Ser	Ile	Ser
465	470	475	480
Cys	Arg	Ser	Ser
Gln	Asn	Ile	Val
His	Ser	Asn	Gly
Asn	Thr	Tyr	Leu
485	490	495	
Asp	Trp	Tyr	Leu
Gln	Lys	Pro	Gly
Gln	Ser	Pro	Lys
Leu	Leu	Ile	Tyr
500	505	510	
Lys	Val	Ser	Asn
Arg	Phe	Ser	Gly
Val	Pro	Asp	Arg
Phe	Ser	Gly	Ser
515	520	525	
Gly	Ser	Gly	Thr
Asp	Phe	Thr	Leu
Lys	Ile	Ser	Arg
Val	Glu	Ala	Glu
530	535	540	
Asp	Leu	Gly	Val
Tyr	Tyr	Cys	Phe
Gln	Gly	Ser	His
Val	Pro	Pro	Thr
545	550	555	560
Phe	Gly	Ala	Gly
Thr	Lys	Leu	Glu
Leu	Lys	Gly	Gly
Gly	Gly	Gly	Ser
Gly			
565	570	575	
Gly	Gly	Gly	Ser
Gly	Gly	Gly	Gly
Ser	Glu	Val	
580	585	590	
Gln	Leu	Gln	Gln
Ser	Gly	Pro	Glu
Leu	Val	Lys	Pro
Gly	Ala	Ser	Val

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595

600

605

Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Tyr

610

615

620

Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly

625

630

635

640

Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Arg Tyr Asn Gln Lys Phe Lys

645

650

655

Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met

660

665

670

Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala

675

680

685

Arg Gly Gly Asn Trp Asn Trp Tyr Phe Asp Val Trp Gly Thr Gly Thr

690

695

700

Thr Val Thr Val Ser Ser

705

710

<210> 225

<211> 704

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Heavy chain

<400> 225

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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 Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
20 25 30
Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
100 105 110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
 210 215 220
 Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240
 Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 245 250 255
 Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 260 265 270
 Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
 275 280 285
 Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
 290 295 300
 Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415

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Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Val Met Thr Gln

450

455

460

Ser His Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr

465

470

475

480

Cys Lys Ala Ser Gln Asp Val Ser Asn Ala Val Ala Trp Tyr Gln Gln

485

490

495

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg

500

505

510

His Asn Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp

515

520

525

Tyr Ile Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu Tyr

530

535

540

Tyr Cys Gln Gln His Tyr Arg Thr Pro Tyr Thr Phe Gly Gly Gly Thr

545

550

555

560

Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly

565

570

575

Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Val Gln Leu Gln Gln Ser

580

585

590

Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys Leu Ser Cys Lys

595

600

605

Ala Ser Gly Tyr Thr Phe Thr Glu Tyr Ile Ile His Trp Val Lys Gln

610

615

620

20180308-154537-1

Lys Ser Gly Gln Gly Leu Glu Trp Ile Gly Trp Phe Tyr Pro Gly Ser

625 630 635 640

Gly Asn Ile Lys Tyr Asn Glu Lys Phe Lys Asp Lys Ala Thr Leu Thr

645 650 655

Ala Asp Lys Ser Ser Ser Thr Val Tyr Met Glu Leu Ser Arg Leu Thr

660 665 670

Ser Glu Asp Ser Ala Val Tyr Phe Cys Thr Arg His Glu Gly Gly Ser

675 680 685

Asn Phe Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

690 695 700

<210> 226

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 226

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

1 5 10 15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20	25	30
Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile		
35	40	45
Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe		
50	55	60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr		
65	70	75
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys		
85	90	95
Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr		
100	105	110
Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly		
115	120	125
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly		
130	135	140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val		
145	150	155
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe		
165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		

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

435		440		445
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Asp Ile Glu Leu Thr Gln				
450		455		460
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys				
465		470		475
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys				
	485		490	
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro				
	500		505	
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala				
	515		520	
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr				
	530		535	
Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Cys Gly				
545		550		555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser				
	565		570	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln				
	580		585	
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys				
	595		600	
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg				
	610		615	
Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser Gly Ile Asn Trp Asn				
625		630		635
Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile				

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645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 227

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 227

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

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Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

20180308-154537-1

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

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

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Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 228

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 228

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65		70		75		80									
Met	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
		85				90							95		
Ala	Arg	Trp	Gly	Tyr	Ser	Tyr	Arg	Asn	Tyr	Ala	Tyr	Tyr	Tyr	Asp	Tyr
		100						105					110		
Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
		115						120					125		
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
		130				135					140				
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
145				150						155				160	
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
		165						170					175		
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
		180						185					190		
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
		195						200					205		
Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
		210				215					220				
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
225				230						235				240	
Ala	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
		245						250					255		
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
		260						265					270		
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val

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

485	490	495
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Thr Asn Arg Pro		
500	505	510
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala		
515	520	525
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr		
530	535	540
Cys Asn Ser Arg Asp Ser Ser Gly Thr His Val Val Phe Gly Gly Gly		
545	550	555
Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		
565	570	575
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln		
580	585	590
Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys		
595	600	605
Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg		
610	615	620
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser		
625	630	635
Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile		
645	650	655
Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu		
660	665	670
Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala		
675	680	685
Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr		

690

695

700

Val Ser Ser

705

<210> 229

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 229

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

1

5

10

15

Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His

20

25

30

Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

65

70

75

80

Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

85

90

95

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Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 305 310 315 320
 Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
 325 330 335
 Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 340 345 350
 Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
 355 360 365
 Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 370 375 380
 Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 385 390 395 400
 Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 405 410 415
 Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 420 425 430
 Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 435 440 445
 Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln
 450 455 460
 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys
 465 470 475 480
 Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys
 485 490 495
 Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Ala Asn Arg Pro
 500 505 510

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Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Ala His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 230

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 230

Glu	Val	Gln	Leu	Gln	Gln	Ser	Val	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala
1			5						10					15	
Ser	Val	Lys	Met	Ser	Cys	Lys	Val	Ser	Gly	Tyr	Thr	Leu	Thr	Asp	His
			20						25					30	
Thr	Ile	His	Trp	Met	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile
		35					40						45		
Gly	Tyr	Ile	Tyr	Pro	Arg	Asp	Gly	Ile	Thr	Gly	Tyr	Asn	Glu	Lys	Phe
		50					55						60		
Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Thr	Ser	Ser	Ser	Thr	Ala	Tyr
65					70					75					80
Met	Gln	Leu	Asn	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	Cys
					85					90					95
Ala	Arg	Trp	Gly	Tyr	Ser	Tyr	Arg	Asn	Tyr	Ala	Tyr	Tyr	Tyr	Asp	Tyr
					100					105					110
Trp	Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly

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

325	330	335	
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro			
340	345	350	
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln			
355	360	365	
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala			
370	375	380	
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr			
385	390	395	400
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu			
405	410	415	
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser			
420	425	430	
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser			
435	440	445	
Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln			
450	455	460	
Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys			
465	470	475	480
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys			
485	490	495	
Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro			
500	505	510	
Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala			
515	520	525	
Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr			

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530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545 550 555 560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ser

625 630 635 640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

$\langle 210 \rangle$ 231

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 231

Glu Val Gln Leu Gln Gln Ser Val Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140

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Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
210 215 220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225 230 235 240
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
275 280 285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
290 295 300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305 310 315 320
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
325 330 335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
340 345 350

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Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Thr Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asp His Val Val Phe Gly Gly Gly

545

550

555

560

20180308-154537-1

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Ala

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 232

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain

<400> 232

Glu Val Gln Leu Gln Gln Ser Val Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Asp His
 20 25 30
 Thr Ile His Trp Met Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Pro Arg Asp Gly Ile Thr Gly Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Trp Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly
 115 120 125
 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
 130 135 140
 Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
 145 150 155 160
 Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165	170	175
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val		
180	185	190
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val		
195	200	205
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys		
210	215	220
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala		
225	230	235
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr		
245	250	255
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
260	265	270
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val		
275	280	285
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser		
290	295	300
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu		
305	310	315
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala		
325	330	335
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro		
340	345	350
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln		
355	360	365
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala		

370		375		380	
Val	Glu	Trp	Glu	Ser	Asn
			Gly	Gln	Pro
				Glu	Asn
				Asn	Tyr
				Lys	Thr
				Thr	
385		390		395	400
Pro	Pro	Val	Leu	Asp	Ser
			Asp	Gly	Ser
				Phe	Phe
				Leu	Tyr
				Ser	Lys
				Leu	
	405		410		415
Thr	Val	Asp	Lys	Ser	Arg
			Trp	Gln	Gln
			Gly	Asn	Val
				Phe	Ser
				Cys	Ser
	420		425		430
Val	Met	His	Glu	Ala	Leu
			His	Asn	His
			Tyr	Thr	Gln
			Lys	Ser	Leu
			Ser		
	435		440		445
Leu	Ser	Pro	Gly	Gly	Gly
			Ser	Gly	Gly
			Ser	Ser	Ser
			Glu	Leu	Thr
			Gln		
	450		455		460
Asp	Pro	Ala	Val	Ser	Val
			Ala	Leu	Gly
			Gln	Thr	Val
			Arg	Ile	Thr
			Cys		
465		470		475	480
Gln	Gly	Asp	Ser	Leu	Arg
			Ser	Tyr	Tyr
			Ala	Ser	Trp
			Tyr	Gln	Gln
			Lys		
	485		490		495
Pro	Gly	Gln	Ala	Pro	Val
			Leu	Val	Ile
			Tyr	Gly	Lys
			Asp	Asn	Arg
			Pro		
	500		505		510
Ser	Gly	Ile	Pro	Asp	Arg
			Phe	Ser	Gly
			Ser	Ser	Ser
			Gly	Asn	Thr
			Ala		
	515		520		525
Ser	Leu	Thr	Ile	Thr	Gly
			Ala	Gln	Ala
			Glu	Asp	Glu
			Ala	Asp	Tyr
			Tyr		
	530		535		540
Cys	Asn	Ser	Arg	Asp	Ser
			Ser	Gly	Asp
			His	Val	Val
			Phe	Gly	Gly
			Gly		
545		550		555	560
Thr	Lys	Leu	Thr	Val	Leu
			Gly	Gly	Gly
			Gly	Gly	Ser
			Gly	Gly	Gly
			Gly	Gly	Gly
			Ser	Glu	Val
			Gln	Leu	Val
			Gln		
	565		570		575
Gly	Gly	Gly	Gly	Ser	Glu
			Val	Gln	Leu
			Val	Gln	

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Thr

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

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<211> 220

<212> PRT

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<220>

<223> Light chain

<400> 233

Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
 1 5 10 15
 Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
 20 25 30
 Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80
 Ile Thr Ser Val Lys Ser Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Tyr Pro Trp Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile
 100 105 110
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 130 135 140
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 145 150 155 160
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 165 170 175
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 180 185 190

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

195

200

205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

220

<210> 234

<211> 45

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ctaatacgac tcactatagg gcaagcagtg gtatcaacgc agagt

45

<210> 235

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 235

ctaatacgac tcactatagg gc

22

<210> 236

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 236

ctgctcactg gatggtggga agatgg

26

<210> 237

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 237

ggggccagtg gatagacaga tggggg

26

<210> 238

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 238

cgtatcgcct ccctcgcgcc atcagacgag tgcgtctaatacgcactcact atagggc

57

<210> 239

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 239

cgtatcgcct ccctcgcgcc atcagacgct cgacactaat acgactcact atagggc 57

<210> 240

<211> 57

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<210> 241

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<223> Primer

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<210> 244

<211> 57

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<213> Artificial Sequence

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<223> Primer

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cgtatcgcct ccctcgcgcc atcagcgtgt ctctactaata acgactcact atagggc 57

<210> 245

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 245

cgtatcgcct ccctcgcgcc atcagctcgc gtgtcctaatac gactcact atagggc 57

<210> 246

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 246

ctatgcgcct tgccagcccg ctcagacgag tgcgtctgct cactggatgg tgggaagatg 60

g 61

<210> 247

<211> 61

<212> DNA

<213> Artificial Sequence

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<223> Primer

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ctatgCGcct tgccagcccg CTCagacgct CGacactgct cactggatgg tgggaagatg 60

g 61

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<223> Primer

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g 61

<210> 249

<211> 61

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g 61

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g 61

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g 61

<210> 252

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<212> DNA

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<223> Primer

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g 61

<210> 253

<211> 61

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<223> Primer

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g 61

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<210> 255

<211> 57

<212> DNA

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<211> 57

<212> DNA

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<212> DNA

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<210> 258

<211> 57

<212> DNA

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<211> 57

<212> DNA

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<210> 261

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<210> 262

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<212> DNA

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<223> Primer

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ctatg'gcgcct tgccagcccg ctcagacgag tgcgtggggc cagtggatag acagatgggg 60

g 61

<210> 263

<211> 61

<212> DNA

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<223> Primer

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g 61

<210> 264

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<400> 264

ctatgcgctt tgccagcccg ctgagagacg cactcggggc cagtggatag acagatgggg 60

g 61

<210> 265

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<223> Primer

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g

61

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ctatgcgccct tgccagcccg ctcagatcag acacgggggc cagtggatag acagatgggg 60

g

61

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ctatgcgccct tgccagcccg ctcagatata gcgagggggc cagtggatag acagatgggg 60

g 61

<210> 268

<211> 61

<212> DNA

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<223> Primer

<400> 268

ctatgcgccct tgccagcccg ctcagcgtgt ctctaggggc cagtggatag acagatgggg 60

g 61

<210> 269

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g 61

<210> 270

<211> 329

<212> PRT

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<223> Primer

<400> 270

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

1 5 10 15

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

20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser

35	40	45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser		
50	55	60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
65	70	75
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys		
85	90	95
Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys		
100	105	110
Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro		
115	120	125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys		
130	135	140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp		
145	150	155
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu		
165	170	175
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu		
180	185	190
Ala Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn		
195	200	205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly		
210	215	220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu		
225	230	235
Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr		

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245

250

255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn

260

265

270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

275

280

285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

290

295

300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr

305

310

315

320

Gln Lys Ser Leu Ser Leu Ser Pro Gly

325

<210> 271

<211> 707

<212> PRT

<213> Artificial Sequence

<220>

<223> Primer

<400> 271

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 Val Ser Gly Tyr Thr Phe Thr Asp His

20

25

30

20180308-154537-1

Thr Ile His Trp Met Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile

35

40

45

Gly Tyr Ile Tyr Pro Arg Asp Val Ile Thr Gln Tyr Asn Glu Lys Phe

50

55

60

Lys Gly Lys Val Thr Leu 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 Leu Cys

85

90

95

Ala Arg Trp Gly Tyr Phe Tyr Gly Ser Arg Ser Tyr Tyr Phe Asp Tyr

100

105

110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly

115

120

125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly

130

135

140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val

145

150

155

160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe

165

170

175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

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

195

200

205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys

210

215

220

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

225

230

235

240

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Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr

245

250

255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val

260

265

270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val

275

280

285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser

290

295

300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu Ala Gln Asp Trp Leu

305

310

315

320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala

325

330

335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro

340

345

350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln

355

360

365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala

370

375

380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr

385

390

395

400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu

405

410

415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser

420

425

430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser

435

440

445

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Leu Ser Pro Gly Gly Gly Ser Gly Gly Ser Ser Ser Glu Leu Thr Gln

450

455

460

Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys

465

470

475

480

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys

485

490

495

Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro

500

505

510

Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala

515

520

525

Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr

530

535

540

Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val Phe Gly Gly Gly

545

550

555

560

Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

565

570

575

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Gln

580

585

590

Ser Gly Gly Gly Val Glu Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys

595

600

605

Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg

610

615

620

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Asn Trp Asn

625

630

635

640

Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val Lys Gly Arg Val Thr Ile

645

650

655

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Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu

660

665

670

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala

675

680

685

Gly Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr Val Thr

690

695

700

Val Ser Ser

705

<210> 272

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR

<400> 272

Gly Tyr Ser Tyr Arg Asn Tyr Ala Tyr Tyr Tyr Asp Tyr

1

5

10