Claims

1. An antibody or functional part thereof or immunoglobulin chain or functional equivalent thereof, which comprises:
- a heavy chain CDR1 sequence comprising a sequence which has at least 70% sequence identity to the sequence RFAMS, and/or
- a heavy chain CDR2 sequence comprising a sequence which has at least 70% sequence identity to the sequence SINNGNNPYYARSVQY, and/or
- a heavy chain CDR3 sequence comprising a sequence which has at least 70% sequence identity to the sequence DHPSSGWPTFDS, and/or
- a light chain CDR1 sequence comprising a sequence which has at least 70% sequence identity to the sequence RASENVGDWLA, and/or
- a light chain CDR2 sequence comprising a sequence which has at least 70% sequence identity to the sequence KTSILES, and/or
- a light chain CDR3 sequence comprising a sequence which has at least 70% sequence identity to the sequence QHYXRFPYT, wherein X is I or M.

2. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 1, having a heavy chain sequence comprising a sequence which has at least 70% sequence identity to the sequence EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS and/or having a light chain sequence which has at least 70% sequence identity to the sequence DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRT V, wherein X is I of M.

3. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 1, having a heavy chain sequence comprising a sequence which has at least 70% sequence identity to the sequence EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS and/or having a light chain sequence which has at least 70% sequence identity to the sequence

DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL
ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRA
, wherein X is I of M.

4. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 1, having a heavy chain sequence comprising a sequence which has at least 70% sequence identity to the sequence EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS and/or having a light chain sequence which has at least 70% sequence identity to the sequence DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRT V, wherein X is I of M.

5. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 1, having a heavy chain sequence comprising a sequence which has at least 70% sequence identity to the sequence EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS and/or having a light chain sequence which has at least 70% sequence identity to the sequence DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRT V, wherein X is I of M.

6. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 1, having a heavy chain sequence comprising a sequence which has at least 70% sequence identity to the sequence EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS and/or having a light chain sequence which has at least 70% sequence identity to the sequence DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRA , wherein X is I of M.

7. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 1, having a heavy chain sequence comprising a sequence which has at least 70% sequence identity to the sequence EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS and/or having a light chain sequence which has at least 70% sequence identity to the sequence DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRT V, wherein X is I of M.

8. An antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claims 1-7, wherein an asparagine has been replaced by another amino acid.

9. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 8, wherein said asparagine is an asparagine at position 53 of the heavy chain, whereby the amino acid numbering is according to Kabat (1991).

10. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 8 or 9, wherein said other amino acid is serine.

11. An antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claims 1-10, wherein at least one amino acid other than cysteine has been replaced with cysteine.

12. An antibody or functional part or immunoglobulin chain or functional equivalent according to claim 11, wherein said at least one amino acid other than cysteine is valine at light chain position 205 and/or valine at light chain position 110, and/or alanine at heavy chain position 114, whereby the amino acid numbering is according to Kabat (1991).

13. An antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claims 1-12, which is a human antibody.

14. An isolated antibody that binds to *in vivo*-grown *S. aureus*.

15. The antibody of claim 14, wherein said antibody is human.

16. An antibody or functional part or immunoglobulin chain or functional equivalent capable of binding an SD-repeat dependent epitope.

17. An antibody or functional part or immunoglobulin chain or functional equivalent capable of binding to *S. aureus* ClfA, ClfB, SdrC, SdrD and SdrE.

18. An antibody or functional part or immunoglobulin chain or functional equivalent which is capable of competing with an antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claims 1-13 for binding to a *Staphylococcus* species.

19. An isolated, synthetic or recombinant nucleic acid sequence with a length of at least 15 nucleotides, or a functional equivalent thereof, encoding at least one CDR sequence of an antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claims 1-13.

20. An isolated, synthetic or recombinant nucleic acid sequence, or a functional equivalent thereof, comprising a sequence which has at least 70% sequence identity to a sequence selected from the group consisting of cgctttgccatgagc, tcgatcaataatgggaataacccatactacgcacggtcggtacaatac, gatcaccctagtagtggctggcccacctttgactcc, cgggccagtgaaaacgttggtgactggttggcc, aagacatctattctagaaagt and caacactatatacgtttcccgtacact.

21. A nucleic acid sequence or functional equivalent according to claim 20, wherein said nucleic acid sequence or functional equivalent comprises a sequence which has at least 70% sequence identity to at least part of a nucleotide sequence as depicted in Figure 1, said part having at least 15 nucleotides and encoding at least one CDR region.

22. An isolated, synthetic or recombinant nucleic acid sequence, or a functional equivalent thereof, comprising a sequence encoding an amino acid sequence which has at least 70% sequence identity to the sequence RFAMS, and/or at least 70% sequence identity to the sequence SINNGNNPYYARSVQY, and/or at least 70% sequence identity to the sequence DHPSSGWPTFDS, and/or at least 70% sequence identity to the sequence RASENVGDWLA, and/or at least 70% sequence identity to the sequence KTSILES, and/or at least 70% sequence identity to the sequence QHYXRFPYT, wherein X is I or M, and/or at least 70% sequence identity to the sequence EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINN GNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWP TFDSWGPGTLVTVSS, and/or at least 70% sequence identity to the sequence

DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSIL
ESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRT
V, wherein X is I or M.

23. An antibody or functional part or an immunoglobulin chain or functional equivalent thereof or a nucleic acid sequence or functional equivalent thereof according to any one of claims 1-22, for use as a medicament and/or prophylactic agent.

24. An antibody or functional part or an immunoglobulin chain or functional equivalent thereof or a nucleic acid sequence or functional equivalent thereof according to any one of claims 1-22, for use as a medicament and/or prophylactic agent for at least in part treating and/or preventing a Gram-positive bacterium-related disorder.

25. Use of an antibody or functional part or an immunoglobulin chain or functional equivalent thereof or a nucleic acid sequence or functional equivalent thereof according to any one of claims 1-22 for the preparation of a medicament and/or prophylactic agent for at least in part treating and/or preventing a Gram-positive bacterium-related disorder.

26. A pharmaceutical composition comprising an antibody or functional part or an immunoglobulin chain or functional equivalent thereof or a nucleic acid sequence or functional equivalent thereof according to any one of claims 1-22 and a pharmaceutical acceptable carrier, diluent or excipient.

27. An isolated or recombinant antibody producing cell capable of producing an antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claims 1-18.

28. A method for producing an antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claim 1-18, comprising providing a cell with a nucleic acid sequence or functional equivalent according to any one of claims 19-22 and allowing said cell to translate said nucleic acid sequence or functional equivalent according to any one of claims 19-22, thereby producing said antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claim 1-18.

29. A method according to claim 28, further comprising harvesting, purifying and/or isolating said antibody or functional part or immunoglobulin chain or functional equivalent according to any one of claim 1-18.

30. Use of an antibody or functional part or an immunoglobulin chain or functional equivalent thereof or a nucleic acid sequence or functional equivalent thereof according to any one of claims 1-18 for diagnosis of a *Staphylococcus* infection.

31. Use of an antibody or functional part or an immunoglobulin chain or functional equivalent thereof or a nucleic acid sequence or functional equivalent thereof according to any one of claims 1-18 for detecting *S. aureus* and/or *S. epidermidis*.

32. An antibody or functional part thereof or an immunoglobulin chain or functional equivalent thereof according to any one of claims 1-18 for use in the diagnosis of a *Staphylococcus* infection.

33. A method for isolating *S. aureus* and/or *S. epidermidis* bacteria from a solution using an antibody or functional part or an immunoglobulin chain or functional equivalent thereof according to any one of claims 1-18.

WHAT IS CLAIMED IS:

1. An isolated antibody or a functional part comprising:

a heavy chain variable domain comprising

(a) a heavy chain CDR1 sequence RFAMS (SEQ ID NO:1), and

(b) a heavy chain CDR2 sequence SINNGNNPYYARSVQY (SEQ ID NO:2) or SINSGNNPYYARSVQY (SEQ ID NO:60), and

(c) a heavy chain CDR3 sequence DHPSSGWPTFDS (SEQ ID NO:3); and

a light chain variable domain comprising

(d) a light chain CDR1 sequence RASENVGDWLA (SEQ ID NO:4), and

(e) a light chain CDR2 sequence KTSILES (SEQ ID NO:5), and

(f) a light chain CDR3 sequence QHYXRFPYT (SEQ ID NO:6), wherein X is I or M.

2. The antibody or functional part of claim 1, wherein the light chain CDR3 sequence is QHYIRFPYT.

3. The antibody or functional part of claim 1, wherein the light chain CDR3 sequence is QHYMRFPYT.

4. The antibody or functional part of claim 1, wherein the heavy chain variable domain comprises:

(a) framework 1 (FW1) which has the sequence of EVQLLESGGGLVQPGGSLRLSCAASGFTLS (SEQ ID NO: 38) or EVQLVESGGGLVQPGGSLRLSCAASGFTLS (SEQ ID NO: 61);

(b) framework 2 (FW2) which has the sequence of WVRQAPGRGLEWVA (SEQ ID NO: 40);

(c) framework 3 (FW3) which has the sequence of RFTVSRDVSQNTVSLQMNNLRAEDSATYFCAK (SEQ ID NO: 42); and

(d) framework 4 (FW4) which has the sequence of WGPGTLVTVSS (SEQ ID NO: 44).

5. The antibody or functional part of claim 1 or claim 4, wherein the light chain variable domain comprises:

(a) framework 1 (FW1) which has the sequence of DIQLTQSPSALPASVGDRVSITC (SEQ ID NO: 48);

(b) framework 2 (FW2) which has the sequence of WYRQKPGKAPNLLIY (SEQ ID NO: 50);

(c) framework 3 (FW3) which has the sequence of GVPSRFSGSGSGTEFTLTISSLQPDDFATYYC (SEQ ID NO: 52); and

(d) framework 4 (FW4) which has the sequence of FGQGTKLEIKRTV (SEQ ID NO: 54) or the sequence of FGQGTKVEIKRTV (SEQ ID NO: 59).

6. The antibody or functional part of claim 1, wherein the heavy chain variable domain comprises a sequence which has at least 90% sequence identity to the sequence EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:7).

7. The antibody or functional part of claim 6, wherein the heavy chain variable domain comprises a sequence of EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:7).

8. The antibody or functional part of claim 6, wherein the heavy chain variable domain comprises a sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINSGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:62).

9. The antibody or functional part of claim 1, wherein the light chain variable domain comprises a sequence which has at least 90% sequence identity to the sequence DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRTV, wherein X is I or M (SEQ ID NO:11).

10. The antibody or functional part of claim 9, wherein the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRTV, wherein X is I or M (SEQ ID NO:11).

11. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:7) and

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRTV, wherein X is I or M (SEQ ID NO:11).

12. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN

PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:9)

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRTV, wherein X is I or M (SEQ ID NO:8).

13. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:9)

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRA,wherein X is I or M (SEQ ID NO:10).

14. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:9) and

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRTV, wherein X is I or M (SEQ ID NO:11).

15. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises g a sequence of EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:7) and

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRTV, wherein X is I or M (SEQ ID NO:8).

16. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLLESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINNGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:7) and

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKLEIKRA, wherein X is I or M (SEQ ID NO:10).

17. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASINSGNN PYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTFDSWGP GTLVTVSS (SEQ ID NO:62); and

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRTV, wherein X is M (SEQ ID NO:11).

18. The antibody or functional part of claim 17, further comprising

(a) a heavy chain constant domain comprising the sequence of: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP (SEQ ID NO:63); and

(b) a light chain constant domain comprising the sequence of: AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:64).

19. The antibody or functional part of claim 18, wherein the valine at light chain position 205 is replaced by a cysteine, wherein the amino acid position is as shown in Figure 9B.

20. The antibody or functional part of claim 17, further comprising

(a) a heavy chain constant domain comprising the sequence of: ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP (SEQ ID NO:63) and;

(b) a light chain constant domain comprising the sequence of: AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPCTKSFNRGEC (SEQ ID NO:65).

21. The antibody of claim 17, further comprising

(a) a heavy chain constant domain comprising the sequence of: CSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP (SEQ ID NO:66) and;

(b) a light chain constant domain comprising the sequence of: AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPCTKSFNRGEC (SEQ ID NO:65).

22. The antibody or functional part of claim 17, further comprising

(a) a heavy chain constant domain comprising the sequence of: CSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP (SEQ ID NO:66) and;

(b) a light chain constant domain comprising the sequence of: AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:64).

23. An isolated antibody or a functional part thereof comprising:

(a) a heavy chain comprising a sequence of SEQ ID NO: 55 and

(b) a light chain comprising a sequence of SEQ ID NO: 57.

24. An isolated antibody or a functional part thereof comprising:

(a) a heavy chain comprising a sequence of SEQ ID NO: 56 and

(b) a light chain comprising a sequence of SEQ ID NO: 58.

25. The antibody or functional part of claim 23, wherein an asparagine at position 53 in the heavy chain has been replaced by another amino acid, wherein the amino acid position is as shown in Figure 9A.

26. The antibody or functional part of claim 25, wherein said asparagine at position 53 is replaced with a serine, wherein an alanine at position 114 of the heavy chain is replaced with a cysteine, and wherein an arginine at position 222 of the heavy chain is replaced with a lysine, wherein the amino acid position is as shown in Figure 9A.

27. The antibody or functional part of claim 23, wherein a valine at a light chain position 205 is replaced with cysteine, an alanine at light chain position 110 is replaced with valine, and a leucine at light chain position 104 is replaced with a valine, wherein the amino acid position is as shown in Figure 9B.

28. The antibody or functional part of claim 1 comprising:

(a) the heavy chain variable domain comprising the sequence of SEQ ID NO:62 and a heavy chain constant domain comprising the sequence of SEQ ID NO:63; and

(b) the light chain comprising a sequence of SEQ ID NO:58.

29. The antibody or functional part of claim 1 comprising:

(a) the heavy chain comprising a sequence of SEQ ID NO: 56; and

(b) the light chain variable domain comprising the sequence of SEQ ID NO:11 and a light chain constant domain comprising the sequence of SEQ ID NO:64;

30. The antibody or functional part of claim 1, wherein

(a) the heavy chain variable domain comprises a sequence of EVQLVESGGGLVQPGGSLRLSCAASGFTLSRFAMSWVRQAPGRGLEWVASIN NGNNPYYARSVQYRFTVSRDVSQNTVSLQMNNLRAEDSATYFCAKDHPSSGWPTF DSWGPGTLVTVSS (SEQ ID NO:9), wherein the asparagine at position 53 (numbering according to Kabat) is replaced by serine, and

(b) the light chain variable domain comprises a sequence of DIQLTQSPSALPASVGDRVSITCRASENVGDWLAWYRQKPGKAPNLLIYKTSILESGV PSRFSGSGSGTEFTLTISSLQPDDFATYYCQHYXRFPYTFGQGTKVEIKRTV, wherein X is I or M (SEQ ID NO:11).

31. The antibody or the functional part of claim 30, wherein the antibody further comprises a heavy chain constant domain comprising a sequence of SEQ ID NO:66 or SEQ ID NO:63.

32. The antibody or the functional part of claim 30 or 31, wherein the antibody further comprises a light chain constant domain comprising a sequence of SEQ ID NO:65 or SEQ ID NO:64.

33. The antibody of any one of claims 1-32, wherein the antibody is coupled to a cytotoxic agent.

34. The antibody of claim 33, wherein the cytotoxic agent is an antibiotic.

35. The antibody of claim 33 or 34, wherein the cytotoxic agent is conjugated to a cysteine at light chain position 205, wherein the amino acid position is as shown in Figure 9B.

36. An isolated antibody or a functional part thereof capable of binding a serine-aspartate (SD) repeat-dependent epitope on a SD repeat (SDR) protein expressed by a *Staphylococcus* species, wherein the antibody or the functional part is coupled to a cytotoxic agent to form an antibody-drug conjugate.

37. The antibody or the functional part of claim 36, wherein the SDR protein is located on the cell surface of a *Staphylococcus* species.

38. The antibody or the functional part of claim 36, wherein the SDR protein is anchored to the peptidoglycan cell wall of a *Staphylococcus* species.

39. The antibody or the functional part of any one of claims 36-38, wherein the epitope further comprises a sugar or sugar residues.

40. The antibody or the functional part of any one of claims 36-39, wherein the cytotoxic agent is an antibiotic.

41. The antibody or the functional part of any one of claims 36-40, wherein the antibody or the functional part competes for binding to the SD repeat-dependent epitope with an antibody comprising:

(a) a heavy chain CDR1 sequence RFAMS (SEQ ID NO:1), and
(b) a heavy chain CDR2 sequence SINNGNNPYYARSVQY (SEQ ID NO:2) or SINSGNNPYYARSVQY (SEQ ID NO:60), and
(c) a heavy chain CDR3 sequence DHPSSGWPTFDS (SEQ ID NO:3), and
(d) a light chain CDR1 sequence RASENVGDWLA (SEQ ID NO:4), and
(e) a light chain CDR2 sequence KTSILES (SEQ ID NO:5), and
(f) a light chain CDR3 sequence QHYXRFPYT (SEQ ID NO:6), wherein X is I or M.

42. The antibody or the functional part of any one of claims 36-41, wherein the *Staphylococcus* species is *S. aureus.*

43. The antibody or the functional part of claim 42, wherein the SDR protein is selected from the group consisting of ClfA (SdrA), ClfB (SdrB), SdrC, SdrD and SdrE.

44. The antibody or the functional part of any one of claims 36-41, wherein the *Staphylococcus* species is *S. epidermidis.*

45. The antibody or the functional part of claim 44, wherein the SDR protein is selected from the group consisting of SdrF, SdrG and SdrH.

46. The antibody or the functional part of any one of claims 36-41, wherein the *Staphylococcus* species is *S. saprophyticus.*

47. The antibody or the functional part of claim 46, wherein the SDR protein is SdrI.

48. The antibody or the functional part of any one of claims 36-41, wherein the *Staphylococcus* species is *S. capitis.*

49. The antibody or the functional part of claim 48, wherein the SDR protein is SdrX.

50. The antibody or the functional part of any one of claims 36-41, wherein the *Staphylococcus* species is *S. caprae.*

51. The antibody or the functional part of claim 50, wherein the SDR protein is selected from the group consisting of SdrY and SdrZ.

52. The antibody or the functional part of any one of claims 36-41, wherein the antibody or the functional part binds to cell wall lysates from *S. aureus* and/or *S. epidermidis.*

53. The antibody or the functional part of any one of claims 1-52, wherein the antibody or the functional part binds to a gram positive bacterium.

54. The antibody or the functional part of claim 53, wherein the gram positive bacterium is a *Staphylococcus* species.

55. The antibody or the functional part of claim 54, wherein the *Staphylococcus* species is *S. aureus, S. epidermidis, S. caprae, S. saprophyticus, S. capitis,* or methicillin-resistant *S. aureus* (MRSA).

56. An isolated antibody or a functional part thereof which is capable of competing with the antibody according to any one of claims 1-35, for binding to a *Staphylococcus* species.

57. The antibody or functional part of any one of claims 1-56, wherein the functional part of an antibody is selected from the group consisting of a single domain antibody, a single chain antibody, a nanobody, an unibody, a single chain variable fragment (scFv), a Fab fragment and a $F(ab')_2$ fragment.

58. A composition comprising the antibody or functional part of any one of claims 1-57.

59. An isolated, synthetic or recombinant nucleic acid encoding for any one of the antibodies or the functional part thereof according to claims 1-57.

60. A producer cell comprising the isolated, synthetic or recombinant nucleic acid sequence or a functional equivalent thereof, according to claim 59.

61. A method for producing an antibody or a functional part thereof comprising providing a cell with a nucleic acid according to claim 59 and allowing said cell to translate said nucleic acid thereby producing said antibody.

62. The method according to claim 61, further comprising harvesting, purifying and/or isolating said antibody or functional part thereof.

63. An antibody or a functional part thereof according to any one of claims 1-57 or a nucleic acid according to claim 59, for use as a medicament and/or prophylactic agent.

64. An antibody or a functional part thereof according to any one of claims 1-57 or a nucleic acid according to claim 59, for use as a medicament and/or prophylactic agent for treating and/or preventing a Gram-positive bacterium-related disorder.

65. Use of an antibody or functional part thereof according to any one of claims 1-57 or a nucleic acid according to claim 59, for the preparation of a medicament and/or prophylactic agent for treating and/or preventing a Gram-positive bacterium-related disorder.

66. Use of an antibody or functional part thereof according to any one of claims 1-57 or a nucleic acid according to claim 59 for in vitro diagnosis of a *Staphylococcus* infection.

67. The use of claim 66, wherein the *Staphylococcus* infection is a *S. aureus* infection.

68. The use of claim 67, wherein the *S. aureus* infection is a MRSA infection.

69. Use of an antibody or functional part thereof according to any one of claims 1-57 or a nucleic acid according to claim 59 for detecting *S. aureus* and/or *S. epidermidis* in a sample obtained from an individual or from any other source suspected to be infected with a *Staphylococcus* bacteria.

70. An antibody or functional part thereof according to any one of claims 1-57, for use in the diagnosis of a *Staphylococcus* infection.

71. A method for isolating *S. aureus* and/or *S. epidermidis* bacteria from a solution using an antibody or functional part thereof according to any one of claims 1-57.

SEQUENCE LISTING

<110> Genentech, Inc.
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MARIATHASAN, Sanjeev
KAJIHARA, Kimberly
XIA, Yi

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<141> 2010-07-15

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<151> 2009-07-15

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            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
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Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
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Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50                  55                  60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65                  70                  75                  80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85                  90                  95
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Gly Thr Leu Val Thr Val Ser Ser
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Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
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35 40 45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
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tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ctt agc cgc ttt 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
20 25 30

gcc atg agc tgg gtc cgc cag gct cca gga agg gga ctg gaa tgg gtc 144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
35 40 45

gca tcg atc aat aat ggg aat aac cca tac tac gca cgg tcg gta caa 192
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tac cgc ttc acc gtc tcc cgg gac gtc tcc cag aac act gtg tct ctg 240
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65 70 75 80

cag atg aac aac ctg aga gcc gaa gac tcg gcc aca tat ttc tgt gct 288
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
85 90 95

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35 40 45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
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65 70 75 80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala

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20 25 30

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gac aga gtc agc atc act tgt cgg gcc agt gaa aac gtt ggt gac tgg 96
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
20 25 30

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

tat aag aca tct att cta gaa agt ggg gtc cca tca agg ttc agc ggc 192
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt ggg tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag cct 240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Ile Arg Phe Pro Tyr

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                85                  90                  95

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

<210> 53
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<220>
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<400> 53
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Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
1 5 10

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<400> 54
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
1 5 10

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<220>
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<220>
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<400> 55
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50                  55                  60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65                  70                  75                  80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85                  90                  95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro
225                 230
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<210> 56
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<220>
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<220>
<223> rF1 A114C

<400> 56

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 1               5                  10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Asn Ser Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50                  55                  60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65                  70                  75                  80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85                  90                  95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
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                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro
225                 230


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<220>
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<220>
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<400> 57
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20                  25                  30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Met Arg Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro
            100                 105                 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205
Asn Arg Gly Glu Cys
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<220>
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<400> 58
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Met Arg Phe Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val 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 Cys Thr Lys Ser
        195   200   205
Phe Asn Arg Gly Glu Cys
    210

<210> 59
<211> 13
<212> PRT
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<220>
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<400> 59

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
 1   5   10

SEQUENCE LISTING

<110> BEAUMONT, Tim
KWAKKENBOS, Mark Jeroen
BROWN, Eric J.
MORISAKI, John Hiroshi
HAZENBOS, Wouter L.W.
MARIATHASAN, Sanjeev
KAJIHARA, Kimberly
XIA, Yi

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<151> 2010-07-15

<150> US 61/225,878
<151> 2009-07-15

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<400> 1
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<220>
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<400> 2
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1 5 10 15

<210> 3
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<220>
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<400> 3
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 1   5   10

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<400> 4
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<400> 5
Lys Thr Ser Ile Leu Glu Ser
 1   5

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<220>
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<223> Xaa = M or I

<400> 6
Gln His Tyr Xaa Arg Phe Pro Tyr Thr
 1   5

<210> 7
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<220>
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<400> 7
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

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<220>
<223> F1 Antibody Variant Light Chain

<220>
<221> VARIANT
<222> 92
<223> Xaa = M or I

<400> 8
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Xaa Arg Phe Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
            100   105   110

<210> 9
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<220>
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<220>
<223> F1 Antibody Variant Heavy Chain

<400> 9
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

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

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<220>
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<222> 92
<223> Xaa = M or I

<400> 11
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Xaa Arg Phe Pro Tyr
                85   90   95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
            100   105   110

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<220>
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<220>
<223> F1 Heavy Chain CDR1

<400> 12
cgctttgcca tgagc 15

<210> 13
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<212> DNA
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<220>
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<220>
<223> F1 Heavy Chain CDR2

<400> 13
tcgatcaata atgggaataa cccatactac gcacggtcgg tacaatac 48

<210> 14
<211> 36
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<220>
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<220>
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<400> 14
gatcacccta gtagtggctg gcccaccttt gactcc 36

<210> 15
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<212> DNA
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<220>
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<400> 15
cgggccagtg aaaacgttgg tgactggttg gcc 33

<210> 16
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<212> DNA
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<220>
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<220>
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<400> 16
aagacatcta ttctagaaag t 21

<210> 17
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<212> DNA
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<220>
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<220>
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<400> 17
caacactata tacgtttccc gtacact 27

<210> 18
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<212> DNA
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<220>
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<220>
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<400> 18
atggctgagg tgcagctggt ggagtctg 28

<210> 19
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<220>
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<220>
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<400> 19
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<210> 20
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<212> DNA
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<400> 20
cggctcgacc gatatccagc tgacccagag 30

<210> 21
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<400> 21
gatttccagc ttggtaccct ggccg 25

<210> 22
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<220>
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<400> 22
ggtggccagc atcaacagcg gcaacaaccc ctactacg 38

<210> 23
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<400> 23
cgtagtaggg gttgttgccg ctgttgatgc tggccacc 38

<210> 24
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<220>
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<400> 24

Asn Asn Gly Asn Asn
1 5

<210> 25
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<220>
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<400> 25
aac 3

<210> 26
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<210> 27
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<400> 27
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<210> 28
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<400> 28
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<210> 29
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<212> DNA
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<210> 30
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<220>
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<400> 30
gatgggccct tggtgctgca actcgagact gtgaccag 38

<210> 31
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<400> 31
Leu Pro Xaa Thr Gly
1 5

<210> 32
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<220>
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<400> 33
Ser Asp Ser Asp Ser
 1   5

<210> 34
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<400> 34
Ser Asp Ser Asp Ser Asp
 1   5

<210> 35
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<220>
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gag gtg caa ctg ttg gag tcg ggg ggg ggc ttg gtg cag ccg ggg ggg 48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ctt agc cgc ttt 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30

gcc atg agc tgg gtc cgc cag gct cca gga agg gga ctg gaa tgg gtc 144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45

gca tcg atc aat aat ggg aat aac cca tac tac gca cgg tcg gta caa 192
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60

tac cgc ttc acc gtc tcc cgg gac gtc tcc cag aac act gtg tct ctg 240
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80

cag atg aac aac ctg aga gcc gaa gac tcg gcc aca tat ttc tgt gct 288
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95

aaa gat cac cct agt agt ggc tgg ccc acc ttt gac tcc tgg ggc ccg 336
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110

gga acc ctg gtc acc gtc tcc tcg   360
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 36
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<400> 36
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 37
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<222> (1)..(90)

<400> 37
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ctt agc   90
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
            20   25   30

<210> 38
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<400> 38
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
            20   25   30

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Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Ala
1 5 10

<210> 40
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<400> 40
Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val Ala
1 5 10

<210> 41
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<220>
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Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu Gln
1 5 10 15

atg aac aac ctg aga gcc gaa gac tcg gcc aca tat ttc tgt gct aaa 96
Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala Lys
20 25 30

<210> 42
<211> 32
<212> PRT
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<400> 42
Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu Gln
 1   5   10   15
Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala Lys
            20   25   30

<210> 43
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<220>
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<400> 43
tgg ggc ccg gga acc ctg gtc acc gtc tcc tcg   33
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 44
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 44
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
 1   5   10

<210> 45
<211> 330
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> F1 Light Chain

<220>
<221> CDS
<222> (1)..(330)

<400> 45
gac atc cag ttg acc cag tct cct tcc gcc ctg cct gca tct gtg gga   48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
1   5   10   15

gac aga gtc agc atc act tgt cgg gcc agt gaa aac gtt ggt gac tgg   96
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20   25   30

ttg gcc tgg tat cgg cag aaa ccg ggg aaa gcc cct aat ctt ctc atc   144
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35   40   45

```
tat aag aca tct att cta gaa agt ggg gtc cca tca agg ttc agc ggc      192
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag cct      240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

gat gat ttt gca act tat tac tgt caa cac tat ata cgt ttc ccg tac      288
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Ile Arg Phe Pro Tyr
                85                  90                  95

act ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg              330
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
            100                 105                 110


<210> 46
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 46
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
            20                  25                  30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
        35                  40                  45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Ile Arg Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
            100                 105                 110


<210> 47
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> F1 Light Chain FW1

<220>
<221> CDS
<222> (1)..(69)

<400>  47
gac atc cag ttg acc cag tct cct tcc gcc ctg cct gca tct gtg gga       48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
1               5                  10                  15

gac aga gtc agc atc act tgt                                          69
Asp Arg Val Ser Ile Thr Cys
            20


<210> 48
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<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Ser Ile Thr Cys
            20

<210> 49
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> F1 Light Chain FW2

<220>
<221> CDS
<222> (1)..(45)

<400> 49
tgg tat cgg cag aaa ccg ggg aaa gcc cct aat ctt ctc atc tat   45
Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr
1   5   10   15

<210> 50
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 50
Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile Tyr
 1   5   10   15

<210> 51
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> F1 Light Chain FW3

<220>
<221> CDS
<222> (1)..(96)

<400> 51
ggg gtc cca tca agg ttc agc ggc agt ggg tct ggg aca gaa ttc act   48
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1   5   10   15

ctc acc atc agc agc ctg cag cct gat gat ttt gca act tat tac tgt 96
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 52
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 52
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15
Leu Thr Ile Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 53
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> F1 Light Chain FW4

<220>
<221> CDS
<222> (1)..(39)

<400> 53
ttt ggc cag ggg acc aag ctg gag atc aaa cga act gtg 39
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
1 5 10

<210> 54
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 54
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val
1 5 10

<210> 55
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 55
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe

```
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45
Ala Ser Ile Asn Asn Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50                  55                  60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65                  70                  75                  80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85                  90                  95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    130                 135                 140
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160
Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        195                 200                 205
Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
Lys Thr His Thr Cys Pro
225                 230
```

<210> 56
<211> 230
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 A114C

<400> 56

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

210 215 220
Lys Thr His Thr Cys Pro
225 230

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

<220>
<223> Synthetic construct

<220>
<223> rF1 Light Chain

<400> 57
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
20 25 30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Met Arg Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

<210> 58
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 V205C

<400> 58
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ala Leu Pro Ala Ser Val Gly
1 5 10 15
Asp Arg Val Ser Ile Thr Cys Arg Ala Ser Glu Asn Val Gly Asp Trp
20 25 30
Leu Ala Trp Tyr Arg Gln Lys Pro Gly Lys Ala Pro Asn Leu Leu Ile
35 40 45
Tyr Lys Thr Ser Ile Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

```
65                  70                  75                  80
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Met Arg Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val 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 Cys Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
```

<210> 59
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 59

```
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
 1               5                   10
```

<210> 60
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 A114C

<400> 60

```
Ser Ile Asn Ser Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln Tyr
 1               5                   10                  15
```

<210> 61
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 61

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1               5                   10                  15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser
            20                  25                  30
```

<210> 62
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 A114C

<400> 62
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Arg Phe
            20   25   30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
        35   40   45
Ala Ser Ile Asn Ser Gly Asn Asn Pro Tyr Tyr Ala Arg Ser Val Gln
    50   55   60
Tyr Arg Phe Thr Val Ser Arg Asp Val Ser Gln Asn Thr Val Ser Leu
65   70   75   80
Gln Met Asn Asn Leu Arg Ala Glu Asp Ser Ala Thr Tyr Phe Cys Ala
                85   90   95
Lys Asp His Pro Ser Ser Gly Trp Pro Thr Phe Asp Ser Trp Gly Pro
            100   105   110
Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 63
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 63
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
            100   105   110

<210> 64
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Light Chain

<400> 64
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
 1   5   10   15
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
            20   25   30
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
        35   40   45
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
    50   55   60
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
65   70   75   80
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
                85   90   95
Lys Ser Phe Asn Arg Gly Glu Cys
            100

<210> 65
<211> 104
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Light Chain

<400> 65

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

<210> 66
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<220>
<223> rF1 Heavy Chain

<400> 66

Cys 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
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
100 105 110