CLAIMS

1. A V_H antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is X_1VQLQESGPGLVKPSETLSLTCTVX_2GYSX_3X_4 (SEQ ID: 95) wherein;
X_1 is Q or E
X_2 is S or T
X_3 is I, L or V
X_4 is S or T
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(iii) the sequence of FR2 is WIRQX_5PGKGLX_6WX_7G (SEQ ID NO: 97) wherein
X_5 is S or P
X_6 is Q or E
X_7 is M or I
or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iv) the sequence of CDR2 is HIHX_8SGRPTYX_9PSLX_{10}S (SEQ ID NO: 98) wherein
X_8 is F, Y or W
X_9 is N or D
X_{10} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(v) the sequence of FR3 is RX$_{11}$X$_{12}$ISX$_{13}$X$_{14}$TAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 99) wherein
X_{11} is V or I
X_{12} is T or S
X_{13} is R or K

X_{14} is E or D
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto with the proviso that the residue at position 6 must be R or K;

(vi) the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(vii) the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

2. A V_H antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95%, identical to the sequence

QVQLQESGPGLVKPSETLSLTCTVSGYSX$_3$SWIRQPPGKGLQWIGRVTIS X$_{13}$ETAKNQFSLKLTSMTAADTAVYYCARWGQGTLVTVSS (SEQ ID NO: 102);
wherein X_3 is I, L or V and X_{13} is R or K;
and the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;
the sequence of CDR2 is HIHX$_8$SGRPTYX$_9$PSLX$_{10}$S (SEQ ID NO: 98) wherein
X_8 is F, Y or W
X_9 is N or D
X_{10} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto and;
the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

3. A V_H antibody binding domain as claimed in claim 1 or claim 2 in which the sequence of FR1 is selected from the group consisting of
QVQLQESGPGLVKPSETLSLTCTVSGYSIS, (SEQ ID NO: 103)
QVQLQESGPGLVKPSETLSLTCTVSGYSIT, (SEQ ID NO: 104)
QVQLQESGPGLVKPSETLSLTCTVSGYSLS, (SEQ ID NO: 105)
QVQLQESGPGLVKPSETLSLTCTVSGYSLT, (SEQ ID NO: 106)
QVQLQESGPGLVKPSETLSLTCTVSGYSVS, (SEQ ID NO: 107)
QVQLQESGPGLVKPSETLSLTCTVSGYSVT, (SEQ ID NO: 108)
QVQLQESGPGLVKPSETLSLTCTVTGYSIS, (SEQ ID NO: 109)
QVQLQESGPGLVKPSETLSLTCTVTGYSIT, (SEQ ID NO: 110)

QVQLQESGPGLVKPSETLSLTCTVTGYSLS, (SEQ ID NO: 111)
QVQLQESGPGLVKPSETLSLTCTVTGYSLT, (SEQ ID NO: 112)
QVQLQESGPGLVKPSETLSLTCTVTGYSVS, (SEQ ID NO: 113)
QVQLQESGPGLVKPSETLSLTCTVTGYSVT, (SEQ ID NO: 114)
EVQLQESGPGLVKPSETLSLTCTVSGYSIS, (SEQ ID NO: 115)
EVQLQESGPGLVKPSETLSLTCTVSGYSIT, (SEQ ID NO: 116)
EVQLQESGPGLVKPSETLSLTCTVSGYSLS, (SEQ ID NO: 117)
EVQLQESGPGLVKPSETLSLTCTVSGYSLT, (SEQ ID NO: 118)
EVQLQESGPGLVKPSETLSLTCTVSGYSVS, (SEQ ID NO: 119)
EVQLQESGPGLVKPSETLSLTCTVSGYSVT, (SEQ ID NO: 120)
EVQLQESGPGLVKPSETLSLTCTVTGYSIS, (SEQ ID NO: 121)
EVQLQESGPGLVKPSETLSLTCTVTGYSIT, (SEQ ID NO: 122)
EVQLQESGPGLVKPSETLSLTCTVTGYSLS, (SEQ ID NO: 123)
EVQLQESGPGLVKPSETLSLTCTVTGYSLT, (SEQ ID NO: 124)
EVQLQESGPGLVKPSETLSLTCTVSTGYSVS, (SEQ ID NO: 125) and
EVQLQESGPGLVKPSETLSLTCTVTGYSVT (SEQ ID NO: 126).

4. A V_H antibody binding domain as claimed in any one of claims 1 to 3 in which the sequence of CDR1 is SGYSWH (SEQ ID NO: 96).

5. A V_H antibody binding domain as claimed in any one of claims 1 to 4 in which the sequence of FR2 is selected from the group consisting of WIRQSPGKGLQWIG (SEQ ID NO: 127), WIRQSPGKGLQWMG (SEQ ID NO: 128), WIRQSPGKGLEWIG (SEQ ID NO: 129), WIRQSPGKGLEWMG (SEQ ID NO: 130), WIRQPPGKGLQWIG (SEQ ID NO: 131), WIRQPPGKGLQWMG (SEQ ID NO: 132), WIRQPPGKGLEWIG (SEQ ID NO: 133), and WIRQPPGKGLEWMG (SEQ ID NO: 134).

6. A V_H antibody binding domain as claimed in any one of claims 1 to 5 in which the sequence of CDR2 is selected from the group consisting of HIHFSGRPTYNPSLSS (SEQ ID NO: 135), HIHFSGRPTYNPSLKS (SEQ ID NO: 136), HIHFSGRPTYNPSLLS (SEQ ID NO: 137), HIHFSGRPTYNPSLHS (SEQ ID NO: 138), HIHFSGRPTYNPSLFS (SEQ ID NO: 139), HIHFSGRPTYNPSLRS (SEQ ID NO: 140), HIHWSGRPTYNPSLSS (SEQ ID NO: 141), HIHWSGRPTYNPSLKS (SEQ ID NO: 142), HIHWSGRPTYNPSLLS (SEQ ID NO: 143), HIHWSGRPTYNPSLHS (SEQ ID NO: 144), HIHWSGRPTYNPSLFS (SEQ ID NO: 145), HIHWSGRPTYNPSLRS (SEQ ID NO: 146), HIHYSGRPTYNPSLSS (SEQ ID NO: 147), HIHYSGRPTYNPSLKS (SEQ ID NO: 148), HIHYSGRPTYNPSLLS (SEQ ID NO: 149), HIHYSGRPTYNPSLHS

(SEQ ID NO: 150), HIHYSGRPTYNPSLFS (SEQ ID NO: 151), HIHYSGRPTYNPSLRS (SEQ ID NO: 152), HIHFSGRPTYDPSLSS (SEQ ID NO: 153), HIHFSGRPTYDPSLKS (SEQ ID NO: 154), HIHFSGRPTYDPSLLS (SEQ ID NO: 155), HIHFSGRPTYDPSLHS (SEQ ID NO: 156), HIHFSGRPTYDPSLFS (SEQ ID NO: 157), HIHFSGRPTYDPSLRS (SEQ ID NO: 158), HIHWSGRPTYDPSLSS (SEQ ID NO: 159), HIHWSGRPTYDPSLKS (SEQ ID NO: 160), HIHWSGRPTYDPSLLS (SEQ ID NO: 161), HIHWSGRPTYDPSLHS (SEQ ID NO: 162), HIHWSGRPTYDPSLFS (SEQ ID NO: 163), HIHWSGRPTYDPSLRS (SEQ ID NO: 164), HIHYSGRPTYDPSLSS (SEQ ID NO: 165), HIHYSGRPTYDPSLKS (SEQ ID NO: 166), HIHYSGRPTYDPSLLS (SEQ ID NO: 167), HIHYSGRPTYDPSLHS (SEQ ID NO: 168), HIHYSGRPTYDPSLFS (SEQ ID NO: 169), and HIHYSGRPTYDPSLRS (SEQ ID NO: 170).

7. A V_H antibody binding domain as claimed in any one of claims 1 to 6 in which the sequence of FR3 is selected from the group consisting of RVTISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 171), RVTISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 172), RVTISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 173), RVTISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 174), RVSISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 175), RVSISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 176), RVSISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 177), RVSISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 178), RITISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 179), RITISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 180), RITISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 181), RITISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 182), RISISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 183), RISISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 184), RISISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 185), and RISISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 186).

8. A V_H antibody binding domain as claimed in any one of claims 1 to 7 in which the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100).

9. A V_H antibody binding domain as claimed in any one of claims 1 to 8 in which the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101).

10. A V_H antibody binding domain as claimed in any one of claims 1 to 9 further comprising a constant domain.

11. A V_H antibody binding domain as claimed in claim 10 in which the constant domain has the sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK
SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
QGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK
SCDKTHTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNG
KEYKCKVSNKALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT
CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

12. A V_L antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is EX_{13}VLTQSPGTLSLSX_{14}GERATLSC (SEQ ID NO: 187) wherein,
X_{13} is I or N,
X_{14} is A or P,

or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iii) the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189) or a sequence at least 90% similar, preferably at least 90% identical, thereto

(iv) the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(v) the sequence of FR3 is GIPDRFSGSGSGX$_{15}$DFTLTISRVEPEDFAVYYC (SEQ ID NO: 191) wherein,
X$_{15}$ is T or N
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(vi) the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(vii) the sequence of FR4 is FGQGTKLEIKR (SEQ ID NO: 193) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

13. A V_L antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95%, identical to the sequence EIVLTQSPGTLSLSPGERATLSCWYQQKPGQAPRLLIYGIPDRFSGSGSGTDF TLTISRVEPEDFAVYYCFGQGTKLEIKR (SEQ ID NO: 194);
and the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence at least 90% similar, preferably at least 90% identical, thereto;
the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190) or a sequence at least 80% similar, preferably at least 80% identical, thereto and;
the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto.

14. A V_L antibody binding domain as claimed in claim 12 or claim 13 in which the sequence of FR1 is selected from the group EIVLTQSPGTLSLSPGERATLSC (SEQ ID NO: 195), EIVLTQSPGTLSLSAGERATLSC (SEQ ID NO: 196),

ENVLTQSPGTLSLSPGERATLSC (SEQ ID NO: 197), and
ENVLTQSPGTLSLSAGERATLSC (SEQ ID NO: 198).

15. A V_L antibody binding domain as claimed in any one of claims 12 to 14 in which the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188).

16. A V_L antibody binding domain as claimed in any one of claims 12 to 15 in which the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189).

17. A V_L antibody binding domain as claimed in any one of claims 12 to 16 in which the sequence of the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190).

18. A V_L antibody binding domain as claimed in any one of claims 12 to 17 in which the sequence of the sequence of FR3 is
GIPDRFSGSGSGTDFTLTISRVEPEDFAVYYC (SEQ ID NO: 199) or
GIPDRFSGSGSGNDFTLTISRVEPEDFAVYYC (SEQ ID NO: 200).

19. A V_L antibody binding domain as claimed in any one of claims 12 to 18 in which the sequence of the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192).

20. A V_L antibody binding domain as claimed in any one of claims 12 to 19 in which the sequence of the sequence of FR4 is FGQGTKLEIKR (SEQ ID NO: 193).

21. A V_L antibody binding domain as claimed in any one of claims 12 to 20 further comprising a constant domain.

22. A V_L antibody binding domain as claimed in claim 21 in which the constant domain has the sequence
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC (SEQ ID NO: 93).

23. An antibody comprising a V_H binding domain as claimed in any one of claims 1 to 9 and a V_L binding domain as claimed in any one of claims 12 to 20.

24. An antibody as claimed in claim 23 in which the V_H binding domain and/or the V_L binding domain further comprise a constant domain.

25. An antibody as claimed in claim 24 in which the constant domain of the V_H binding domain has the following sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

26. An antibody as claimed in claim 24 or claim 25 in which the constant domain of the V_L binding domain has the sequence
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC (SEQ ID NO: 93).

27. A V_H antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is
EVQLQQWGAGLLKPSETLSLTCAVYGYS$X_{18}X_{19}$ (SEQ ID NO: 201)
wherein;
X_{18} is I, L or V
X_{19} is S or T

or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(iii) the sequence of FR2 is WIRQPPGKGLEWX_{20}G (SEQ ID NO: 202) wherein
X_{20} is M or I
or a sequence at least 90% similar, preferably identical, thereto;

(iv) the sequence of CDR2 is HIHX_{21}SGRPTYX_{22}PSLX_{23}S (SEQ ID NO: 98) wherein
X_{21} is F, Y or W
X_{22} is N or D
X_{23} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(v) the sequence of FR3 is
R$X_{24}X_{25}$ISX_{26}DTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 203) wherein
X_{24} is V or I
X_{25} is S or T
X_{26} is R or K
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto with the proviso that the residue at position 6 must be R or K;

(vi) the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(vii) the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

28. A V_H antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95%, identical to the sequence
EVQLQQWGAGLLKPSETLSLTCAVYGYSX_{18}SWIRQPPGKGLEWIGRVTIS X_{26}DTSKNQFSLKLSSVTAADTAVYYCARWGQGTLVTVSS

(SEQ ID NO: 204);
wherein X_{18} is I, L or V and X_{26} is R or K
and the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;
the sequence of CDR2 is HIHX$_{21}$SGRPTYX$_{22}$PSLX$_{23}$S (SEQ ID NO: 98) wherein
X_{21} is F, Y or W
X_{22} is N or D
X_{23} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto and;
the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

29. A V_H antibody binding domain as claimed in claim 27 or claim 28 in which the sequence of FR1 is selected from the group consisting of EVQLQQWGAGLLKPSETLSLTCAVYGYSIS (SEQ ID NO: 205), EVQLQQWGAGLLKPSETLSLTCAVYGYSIT (SEQ ID NO: 206), EVQLQQWGAGLLKPSETLSLTCAVYGYSLS (SEQ ID NO: 207), EVQLQQWGAGLLKPSETLSLTCAVYGYSLT (SEQ ID NO: 208), EVQLQQWGAGLLKPSETLSLTCAVYGYSVS (SEQ ID NO: 209), and EVQLQQWGAGLLKPSETLSLTCAVYGYSVT (SEQ ID NO: 210).

30. A V_H antibody binding domain as claimed in any one of claims 27 to 29 in which the sequence of CDR1 is SGYSWH (SEQ ID NO: 96).

31. A V_H antibody binding domain as claimed in any one of claims 27 to 30 in which the sequence of FR2 is WIRQPPGKGLEWIG (SEQ ID NO: 133) or WIRQPPGKGLEWMG (SEQ ID NO: 134).

32. A V_H antibody binding domain as claimed in any one of claims 27 to 31 in which the sequence of CDR2 is selected from the group consisting of HIHFSGRPTYNPSLSS (SEQ ID NO: 135), HIHFSGRPTYNPSLKS (SEQ ID NO: 136), HIHFSGRPTYNPSLLS (SEQ ID NO: 137), HIHFSGRPTYNPSLHS (SEQ ID NO: 138), HIHFSGRPTYNPSLFS (SEQ ID NO: 139), HIHFSGRPTYNPSLRS (SEQ ID NO: 140), HIHWSGRPTYNPSLSS (SEQ ID NO: 141), HIHWSGRPTYNPSLKS (SEQ ID NO: 142), HIHWSGRPTYNPSLLS (SEQ ID NO: 143), HIHWSGRPTYNPSLHS (SEQ ID NO: 144), HIHWSGRPTYNPSLFS (SEQ ID NO: 145), HIHWSGRPTYNPSLRS (SEQ ID NO: 146), HIHYSGRPTYNPSLSS (SEQ ID NO: 147), HIHYSGRPTYNPSLKS (SEQ ID NO: 148), HIHYSGRPTYNPSLLS (SEQ ID NO: 149),

HIHYSGRPTYNPSLHS (SEQ ID NO: 150), HIHYSGRPTYNPSLFS (SEQ ID NO: 151), HIHYSGRPTYNPSLRS (SEQ ID NO: 152), HIHFSGRPTYDPSLSS (SEQ ID NO: 153), HIHFSGRPTYDPSLKS (SEQ ID NO: 154), HIHFSGRPTYDPSLLS (SEQ ID NO: 155), HIHFSGRPTYDPSLHS (SEQ ID NO: 156), HIHFSGRPTYDPSLFS (SEQ ID NO: 157), HIHFSGRPTYDPSLRS (SEQ ID NO: 158), HIHWSGRPTYDPSLSS (SEQ ID NO: 159), HIHWSGRPTYDPSLKS (SEQ ID NO: 160), HIHWSGRPTYDPSLLS (SEQ ID NO: 161), HIHWSGRPTYDPSLHS (SEQ ID NO: 162), HIHWSGRPTYDPSLFS (SEQ ID NO: 163), HIHWSGRPTYDPSLRS (SEQ ID NO: 164), HIHYSGRPTYDPSLSS (SEQ ID NO: 165), HIHYSGRPTYDPSLKS (SEQ ID NO: 166), HIHYSGRPTYDPSLLS (SEQ ID NO: 167), HIHYSGRPTYDPSLHS (SEQ ID NO: 168), HIHYSGRPTYDPSLFS (SEQ ID NO: 169), and HIHYSGRPTYDPSLRS (SEQ ID NO: 170).

33. A V_H antibody binding domain as claimed in any one of claims 27 to 32 in which the sequence of FR3 is selected from the group consisting of RVTISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 218), RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 219), RVSISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 220), RVSISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 221), RITISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 222), RITISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 223), RISISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 224), RISISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 225),.

34. A V_H antibody binding domain as claimed in any one of claims 27 to 33 in which the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100).

35. A V_H antibody binding domain as claimed in any one of claims 27 to 34 in which the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101).

36. A V_H antibody binding domain as claimed in any one of claims 27 to 35 further comprising a constant domain.

37. A V_H antibody binding domain as claimed in claim 36 in which the constant domain has the sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE

VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC
DKTHTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYK
CKVSNKALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

38. A V_L antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is EX23VLTQSPATLSLSPGERATLSC (SEQ ID NO: 211) wherein,
X23 is I or N,
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iii) the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iv) the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(v) the sequence of FR3 is GIPDRFSGSGSGX24DFTLTISRLEPEDFAVYYC (SEQ ID NO: 212) wherein,
X24 is T or N
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(vi) the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(vii) the sequence of FR4 is FGGGTKVEIKR (SEQ ID NO: 193) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

39. A V_L antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95% identical to the sequence EIVLTQSPATLSLSPGERATLSCWYQQKPGQAPRLLIYGIPDRFSGSGSGTDF TLTISRLEPEDFAVYYCFGGGTKVEIKR (SEQ ID NO: 213);
and the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence at least 90% similar, preferably at least 90% identical, thereto;
the sequence of CDR2 is DTSNLAS (SEQ ID NO: 140) or a sequence at least 80% similar, preferably at least 80% identical, thereto and;
the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto.

40. A V_L antibody binding domain as claimed in claim 38 or claim 39 in which the sequence of FR1 is selected from the group EIVLTQSPATLSLSPGERATLSC (SEQ ID NO: 214) or ENVLTQSPATLSLSPGERATLSC (SEQ ID NO: 215).

41. A V_L antibody binding domain as claimed in any one of claims 38 to 40 in which the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188).

42. A V_L antibody binding domain as claimed in any one of claims 38 to 41 in which the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189).

43. A V_L antibody binding domain as claimed in any one of claims 38 to 42 in which the sequence of the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190).

44. A V_L antibody binding domain as claimed in any one of claims 38 to 43 in which the sequence of the sequence of FR3 is

GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC (SEQ ID NO: 216) or GIPDRFSGSGSGNDFTLTISRLEPEDFAVYYC (SEQ ID NO: 217).

45. A V_L antibody binding domain as claimed in any one of claims 38 to 44 in which the sequence of the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192).

46. A V_L antibody binding domain as claimed in any one of claims 38 to 45 in which the sequence of the sequence of FR4 is FGGGTKVEIKR (SEQ ID NO: 193).

47. A V_L antibody binding domain as claimed in any one of claims 38 to 46 further comprising a constant domain.

48. A V_L antibody binding domain as claimed in claim 47 in which the constant domain has the sequence TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 93).

49. An antibody comprising a V_H binding domain as claimed in any one of claims 27 to 35 and a V_L binding domain as claimed in any one of claims 38 to 46.

50. An antibody as claimed in claim 49 in which the V_H binding domain and/or the V_L binding domain further comprise a constant domain.

51. An antibody as claimed in claim 50 in which the constant domain of the V_H binding domain has the sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGF

YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC DKTHTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

52. An antibody as claimed in claim 50 or claim 51 in which the constant domain of the V_L binding domain has the sequence TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS QESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN RGEC (SEQ ID NO: 93).

53. An antibody comprising two light chains and two heavy chains in which the sequence of the light chains is as shown in SEQ ID NO: 7 and the sequence of the heavy chains is as shown in SEQ ID NO: 50.

54. An antibody comprising two light chains and two heavy chains in which the sequence of the light chains is as shown in SEQ ID NO: 7 and the sequence of the heavy chains is as shown in SEQ ID NO: 94.

55. An antibody as claimed in any one of claims 23 to 26 or 49 to 54 in which the antibody has a reduced level of fucose.

56. A method of treating cancer in a subject wherein the cancer is selected from the group consisting of colorectal, ovarian, pancreatic, prostatic and lung, the method comprising administering to the subject a therapeutically effective quantity of a binding domain or antibody according to any one of claims 1 to 55.

57. A method of detecting the presence of cancer cells in a sample, the method comprising contacting the cell sample with a binding domain or antibody according to any one of claims 1 to 55 and detecting binding of the binding domain or antibody to the cells.

CLAIMS

1. A V_H antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

   (i) the sequence of FR1 is X_1VQLQESGPGLVKPSETLSLTCTVX_2GYSX_3X_4 (SEQ ID: 95) wherein;
   X_1 is Q or E
   X_2 is S or T
   X_3 is I, L or V
   X_4 is S or T
   or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

   (ii) the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

   (iii) the sequence of FR2 is WIRQX_5PGKGLX_6WX_7G (SEQ ID NO: 97) wherein
   X_5 is S or P
   X_6 is Q or E
   X_7 is M or I
   or a sequence at least 90% similar, preferably at least 90% identical, thereto;

   (iv) the sequence of CDR2 is HIHX_8SGRPTYX_9PSLX_{10}S (SEQ ID NO: 98) wherein
   X_8 is F, Y or W
   X_9 is N or D
   X_{10} is K, L, H, F, R or S
   or a sequence at least 90% similar, preferably at least 90% identical, thereto;

   (v) the sequence of FR3 is
   R$X_{11}X_{12}$IS$X_{13}X_{14}$TAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 99) wherein
   X_{11} is V or I
   X_{12} is T or S
   X_{13} is R or K
   X_{14} is E or D

or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto with the proviso that the residue at position 6 must be R or K;

(vi) the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(vii) the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

2. A V_H antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95%, identical to the sequence

QVQLQESGPGLVKPSETLSLTCTVSGYSX$_3$SWIRQPPGKGLQWIGRVTISX$_{13}$ ETAKNQFSLKLTSMTAADTAVYYCARWGQGTLVTVSS (SEQ ID NO: 102);
wherein X_3 is I, L or V and X_{13} is R or K;
and the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;
the sequence of CDR2 is HIHX$_8$SGRPTYX$_9$PSLX$_{10}$S (SEQ ID NO: 98) wherein
X_8 is F, Y or W
X_9 is N or D
X_{10} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto and;
the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

3. A V_H antibody binding domain as claimed in claim 1 or claim 2 in which the sequence of FR1 is selected from the group consisting of
QVQLQESGPGLVKPSETLSLTCTVSGYSIS, (SEQ ID NO: 103)
QVQLQESGPGLVKPSETLSLTCTVSGYSIT, (SEQ ID NO: 104)
QVQLQESGPGLVKPSETLSLTCTVSGYSLS, (SEQ ID NO: 105)
QVQLQESGPGLVKPSETLSLTCTVSGYSLT, (SEQ ID NO: 106)
QVQLQESGPGLVKPSETLSLTCTVSGYSVS, (SEQ ID NO: 107)
QVQLQESGPGLVKPSETLSLTCTVSGYSVT, (SEQ ID NO: 108)
QVQLQESGPGLVKPSETLSLTCTVTGYSIS, (SEQ ID NO: 109)
QVQLQESGPGLVKPSETLSLTCTVTGYSIT, (SEQ ID NO: 110)

QVQLQESGPGLVKPSETLSLTCTVTGYSLS, (SEQ ID NO: 111)
QVQLQESGPGLVKPSETLSLTCTVTGYSLT, (SEQ ID NO: 112)
QVQLQESGPGLVKPSETLSLTCTVTGYSVS, (SEQ ID NO: 113)
QVQLQESGPGLVKPSETLSLTCTVTGYSVT, (SEQ ID NO: 114)
EVQLQESGPGLVKPSETLSLTCTVSGYSIS, (SEQ ID NO: 115)
EVQLQESGPGLVKPSETLSLTCTVSGYSIT, (SEQ ID NO: 116)
EVQLQESGPGLVKPSETLSLTCTVSGYSLS, (SEQ ID NO: 117)
EVQLQESGPGLVKPSETLSLTCTVSGYSLT, (SEQ ID NO: 118)
EVQLQESGPGLVKPSETLSLTCTVSGYSVS, (SEQ ID NO: 119)
EVQLQESGPGLVKPSETLSLTCTVSGYSVT, (SEQ ID NO: 120)
EVQLQESGPGLVKPSETLSLTCTVTGYSIS, (SEQ ID NO: 121)
EVQLQESGPGLVKPSETLSLTCTVTGYSIT, (SEQ ID NO: 122)
EVQLQESGPGLVKPSETLSLTCTVTGYSLS, (SEQ ID NO: 123)
EVQLQESGPGLVKPSETLSLTCTVTGYSLT, (SEQ ID NO: 124)
EVQLQESGPGLVKPSETLSLTCTVSTGYSVS, (SEQ ID NO: 125) and
EVQLQESGPGLVKPSETLSLTCTVTGYSVT (SEQ ID NO: 126).

4. A V_H antibody binding domain as claimed in any one of claims 1 to 3 in which the sequence of CDR1 is SGYSWH (SEQ ID NO: 96).

5. A V_H antibody binding domain as claimed in any one of claims 1 to 4 in which the sequence of FR2 is selected from the group consisting of WIRQSPGKGLQWIG (SEQ ID NO: 127), WIRQSPGKGLQWMG (SEQ ID NO: 128), WIRQSPGKGLEWIG (SEQ ID NO: 129), WIRQSPGKGLEWMG (SEQ ID NO: 130), WIRQPPGKGLQWIG (SEQ ID NO: 131), WIRQPPGKGLQWMG (SEQ ID NO: 132), WIRQPPGKGLEWIG (SEQ ID NO: 133), and WIRQPPGKGLEWMG (SEQ ID NO: 134).

6. A V_H antibody binding domain as claimed in any one of claims 1 to 5 in which the sequence of CDR2 is selected from the group consisting of HIHFSGRPTYNPSLSS (SEQ ID NO: 135), HIHFSGRPTYNPSLKS (SEQ ID NO: 136), HIHFSGRPTYNPSLLS (SEQ ID NO: 137), HIHFSGRPTYNPSLHS (SEQ ID NO: 138), HIHFSGRPTYNPSLFS (SEQ ID NO: 139), HIHFSGRPTYNPSLRS (SEQ ID NO: 140), HIHWSGRPTYNPSLSS (SEQ ID NO: 141), HIHWSGRPTYNPSLKS (SEQ ID NO: 142), HIHWSGRPTYNPSLLS (SEQ ID NO: 143), HIHWSGRPTYNPSLHS (SEQ ID NO: 144), HIHWSGRPTYNPSLFS (SEQ ID NO: 145), HIHWSGRPTYNPSLRS (SEQ ID NO: 146), HIHYSGRPTYNPSLSS (SEQ ID NO: 147), HIHYSGRPTYNPSLKS (SEQ ID NO: 148), HIHYSGRPTYNPSLLS (SEQ ID NO: 149), HIHYSGRPTYNPSLHS (SEQ ID NO: 150),

HIHYSGRPTYNPSLFS (SEQ ID NO: 151), HIHYSGRPTYNPSLRS (SEQ ID NO: 152), HIHFSGRPTYDPSLSS (SEQ ID NO: 153), HIHFSGRPTYDPSLKS (SEQ ID NO: 154), HIHFSGRPTYDPSLLS (SEQ ID NO: 155), HIHFSGRPTYDPSLHS (SEQ ID NO: 156), HIHFSGRPTYDPSLFS (SEQ ID NO: 157), HIHFSGRPTYDPSLRS (SEQ ID NO: 158), HIHWSGRPTYDPSLSS (SEQ ID NO: 159), HIHWSGRPTYDPSLKS (SEQ ID NO: 160), HIHWSGRPTYDPSLLS (SEQ ID NO: 161), HIHWSGRPTYDPSLHS (SEQ ID NO: 162), HIHWSGRPTYDPSLFS (SEQ ID NO: 163), HIHWSGRPTYDPSLRS (SEQ ID NO: 164), HIHYSGRPTYDPSLSS (SEQ ID NO: 165), HIHYSGRPTYDPSLKS (SEQ ID NO: 166), HIHYSGRPTYDPSLLS (SEQ ID NO: 167), HIHYSGRPTYDPSLHS (SEQ ID NO: 168), HIHYSGRPTYDPSLFS (SEQ ID NO: 169), and HIHYSGRPTYDPSLRS (SEQ ID NO: 170).

7. A V_H antibody binding domain as claimed in any one of claims 1 to 6 in which the sequence of FR3 is selected from the group consisting of RVTISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 171), RVTISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 172), RVTISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 173), RVTISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 174), RVSISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 175), RVSISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 176), RVSISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 177), RVSISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 178), RITISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 179), RITISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 180), RITISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 181), RITISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 182), RISISRETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 183), RISISRDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 184), RISISKETAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 185), and RISISKDTAKNQFSLKLTSMTAADTAVYYCAR (SEQ ID NO: 186).

8. A V_H antibody binding domain as claimed in any one of claims 1 to 7 in which the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100).

9. A V_H antibody binding domain as claimed in any one of claims 1 to 8 in which the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101).

10. A V_H antibody binding domain as claimed in any one of claims 1 to 9 further comprising a constant domain.

11. A V_H antibody binding domain as claimed in claim 10 in which the constant domain has the sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD
KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD
KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCD
KTHTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYKCKV
SNKALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

12. A V_L antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is EX_{13}VLTQSPGTLSLSX_{14}GERATLSC (SEQ ID NO: 187) wherein,
X_{13} is I or N,
X_{14} is A or P,

or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iii) the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iv) the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(v) the sequence of FR3 is GIPDRFSGSGSGX_{15}DFTLTISRVEPEDFAVYYC (SEQ ID NO: 191) wherein,
X_{15} is T or N
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(vi) the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(vii) the sequence of FR4 is FGQGTKLEIKR (SEQ ID NO: 193) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

13. A V_L antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95%, identical to the sequence

EIVLTQSPGTLSLSPGERATLSCWYQQKPGQAPRLLIYGIPDRFSGSGSGTDFT LTISRVEPEDFAVYYCFGQGTKLEIKR (SEQ ID NO: 194);
and the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence at least 90% similar, preferably at least 90% identical, thereto;
the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190) or a sequence at least 80% similar, preferably at least 80% identical, thereto and;
the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto.

14. A V_L antibody binding domain as claimed in claim 12 or claim 13 in which the sequence of FR1 is selected from the group EIVLTQSPGTLSLSPGERATLSC (SEQ ID NO: 195), EIVLTQSPGTLSLSAGERATLSC (SEQ ID NO: 196),

ENVLTQSPGTLSLSPGERATLSC (SEQ ID NO: 197), and
ENVLTQSPGTLSLSAGERATLSC (SEQ ID NO: 198).

15. A V_L antibody binding domain as claimed in any one of claims 12 to 14 in which the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188).

16. A V_L antibody binding domain as claimed in any one of claims 12 to 15 in which the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189).

17. A V_L antibody binding domain as claimed in any one of claims 12 to 16 in which the sequence of the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190).

18. A V_L antibody binding domain as claimed in any one of claims 12 to 17 in which the sequence of the sequence of FR3 is

GIPDRFSGSGSGTDFTLTISRVEPEDFAVYYC (SEQ ID NO: 199) or
GIPDRFSGSGSGNDFTLTISRVEPEDFAVYYC (SEQ ID NO: 200).

19. A V_L antibody binding domain as claimed in any one of claims 12 to 18 in which the sequence of the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192).

20. A V_L antibody binding domain as claimed in any one of claims 12 to 19 in which the sequence of the sequence of FR4 is FGQGTKLEIKR (SEQ ID NO: 193).

21. A V_L antibody binding domain as claimed in any one of claims 12 to 20 further comprising a constant domain.

22. A V_L antibody binding domain as claimed in claim 21 in which the constant domain has the sequence
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
C (SEQ ID NO: 93).

23. An antibody comprising a V_H binding domain as claimed in any one of claims 1 to 9 and a V_L binding domain as claimed in any one of claims 12 to 20.

24. An antibody as claimed in claim 23 in which the V_H binding domain and/or the V_L binding domain further comprise a constant domain.

25. An antibody as claimed in claim 24 in which the constant domain of the V_H binding domain has the following sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

26. An antibody as claimed in claim 24 or claim 25 in which the constant domain of the V_L binding domain has the sequence
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
C (SEQ ID NO: 93).

27. A V_H antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is EVQLQQWGAGLLKPSETLSLTCAVYGYS$X_{18}X_{19}$ (SEQ ID NO: 201) wherein;
X_{18} is I, L or V
X_{19} is S or T

or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(iii) the sequence of FR2 is WIRQPPGKGLEWX_{20}G (SEQ ID NO: 202) wherein
X_{20} is M or I
or a sequence at least 90% similar, preferably identical, thereto;

(iv) the sequence of CDR2 is HIHX_{21}SGRPTYX_{22}PSLX_{23}S (SEQ ID NO: 98) wherein
X_{21} is F, Y or W
X_{22} is N or D
X_{23} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(v) the sequence of FR3 is
R$X_{24}X_{25}$ISX_{26}DTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 203) wherein
X_{24} is V or I
X_{25} is S or T
X_{26} is R or K
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto with the proviso that the residue at position 6 must be R or K;

(vi) the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(vii) the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

28. A V_H antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95%, identical to the sequence

EVQLQQWGAGLLKPSETLSLTCAVYGYSX$_{18}$SWIRQPPGKGLEWIGRVTISX$_{26}$ DTSKNQFSLKLSSVTAADTAVYYCARWGQGTLVTVSS (SEQ ID NO: 204); wherein X_{18} is I, L or V and X_{26} is R or K
and the sequence of CDR1 is SGYSWH (SEQ ID NO: 96) or a sequence at least 80% similar, preferably at least 80% identical, thereto;
the sequence of CDR2 is HIHX$_{21}$SGRPTYX$_{22}$PSLX$_{23}$S (SEQ ID NO: 98) wherein
X_{21} is F, Y or W
X_{22} is N or D
X_{23} is K, L, H, F, R or S
or a sequence at least 90% similar, preferably at least 90% identical, thereto and;
the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

29. A V_H antibody binding domain as claimed in claim 27 or claim 28 in which the sequence of FR1 is selected from the group consisting of EVQLQQWGAGLLKPSETLSLTCAVYGYSIS (SEQ ID NO: 205), EVQLQQWGAGLLKPSETLSLTCAVYGYSIT (SEQ ID NO: 206), EVQLQQWGAGLLKPSETLSLTCAVYGYSLS (SEQ ID NO: 207), EVQLQQWGAGLLKPSETLSLTCAVYGYSLT (SEQ ID NO: 208), EVQLQQWGAGLLKPSETLSLTCAVYGYSVS (SEQ ID NO: 209), and EVQLQQWGAGLLKPSETLSLTCAVYGYSVT (SEQ ID NO: 210).

30. A V_H antibody binding domain as claimed in any one of claims 27 to 29 in which the sequence of CDR1 is SGYSWH (SEQ ID NO: 96).

31. A V_H antibody binding domain as claimed in any one of claims 27 to 30 in which the sequence of FR2 is WIRQPPGKGLEWIG (SEQ ID NO: 133) or WIRQPPGKGLEWMG (SEQ ID NO: 134).

32. A V_H antibody binding domain as claimed in any one of claims 27 to 31 in which the sequence of CDR2 is selected from the group consisting of HIHFSGRPTYNPSLSS (SEQ ID NO: 135), HIHFSGRPTYNPSLKS (SEQ ID NO: 136), HIHFSGRPTYNPSLLS (SEQ ID NO: 137), HIHFSGRPTYNPSLHS (SEQ ID NO: 138), HIHFSGRPTYNPSLFS (SEQ ID NO: 139), HIHFSGRPTYNPSLRS (SEQ ID NO: 140), HIHWSGRPTYNPSLSS (SEQ ID NO: 141), HIHWSGRPTYNPSLKS (SEQ ID NO: 142), HIHWSGRPTYNPSLLS (SEQ ID NO: 143), HIHWSGRPTYNPSLHS (SEQ ID NO: 144), HIHWSGRPTYNPSLFS (SEQ ID NO: 145), HIHWSGRPTYNPSLRS (SEQ ID NO: 146), HIHYSGRPTYNPSLSS (SEQ ID NO: 147), HIHYSGRPTYNPSLKS (SEQ ID NO: 148), HIHYSGRPTYNPSLLS

(SEQ ID NO: 149), HIHYSGRPTYNPSLHS (SEQ ID NO: 150), HIHYSGRPTYNPSLFS (SEQ ID NO: 151), HIHYSGRPTYNPSLRS (SEQ ID NO: 152), HIHFSGRPTYDPSLSS (SEQ ID NO: 153), HIHFSGRPTYDPSLKS (SEQ ID NO: 154), HIHFSGRPTYDPSLLS (SEQ ID NO: 155), HIHFSGRPTYDPSLHS (SEQ ID NO: 156), HIHFSGRPTYDPSLFS (SEQ ID NO: 157), HIHFSGRPTYDPSLRS (SEQ ID NO: 158), HIHWSGRPTYDPSLSS (SEQ ID NO: 159), HIHWSGRPTYDPSLKS (SEQ ID NO: 160), HIHWSGRPTYDPSLLS (SEQ ID NO: 161), HIHWSGRPTYDPSLHS (SEQ ID NO: 162), HIHWSGRPTYDPSLFS (SEQ ID NO: 163), HIHWSGRPTYDPSLRS (SEQ ID NO: 164), HIHYSGRPTYDPSLSS (SEQ ID NO: 165), HIHYSGRPTYDPSLKS (SEQ ID NO: 166), HIHYSGRPTYDPSLLS (SEQ ID NO: 167), HIHYSGRPTYDPSLHS (SEQ ID NO: 168), HIHYSGRPTYDPSLFS (SEQ ID NO: 169), and HIHYSGRPTYDPSLRS (SEQ ID NO: 170).

33. A V_H antibody binding domain as claimed in any one of claims 27 to 32 in which the sequence of FR3 is selected from the group consisting of RVTISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 218), RVTISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 219), RVSISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 220), RVSISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 221), RITISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 222), RITISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 223), RISISRDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 224), RISISKDTSKNQFSLKLSSVTAADTAVYYCAR (SEQ ID NO: 225).

34. A V_H antibody binding domain as claimed in any one of claims 27 to 33 in which the sequence of CDR3 is KGKGSDDGLNY (SEQ ID NO: 100).

35. A V_H antibody binding domain as claimed in any one of claims 27 to 34 in which the sequence of FR4 is WGQGTLVTVSS (SEQ ID NO: 101).

36. A V_H antibody binding domain as claimed in any one of claims 27 to 35 further comprising a constant domain.

37. A V_H antibody binding domain as claimed in claim 36 in which the constant domain has the sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN

WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

38. A V_L antibody binding domain, the binding domain comprising, in sequence, a first framework region (FR1), a first CDR (CDR1), a second framework region (FR2), a second CDR (CDR2), a third framework region (FR3), a third CDR (CDR3) and a fourth framework region (FR4), wherein:

(i) the sequence of FR1 is EX23VLTQSPATLSLSPGERATLSC (SEQ ID NO: 211) wherein,
X23 is I or N,
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(ii) the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iii) the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189) or a sequence at least 90% similar, preferably at least 90% identical, thereto;

(iv) the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(v) the sequence of FR3 is GIPDRFSGSGSGX24DFTLTISRLEPEDFAVYYC (SEQ ID NO: 212) wherein,
X24 is T or N
or a sequence at least 90% or at least 95% similar, preferably at least 90% or at least 95% identical, thereto;

(vi) the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto;

(vii) the sequence of FR4 is FGGGTKVEIKR (SEQ ID NO: 193) or a sequence at least 90% similar, preferably at least 90% identical, thereto.

39. A V_L antibody binding domain, the binding domain comprising a framework sequence and a first, second and third CDR positioned within the framework sequence in which the sequence of the framework regions is at least 90%, preferably at least 95% identical to the sequence

EIVLTQSPATLSLSPGERATLSCWYQQKPGQAPRLLIYGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCFGGGTKVEIKR (SEQ ID NO: 213);
and the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188) or a sequence at least 90% similar, preferably at least 90% identical, thereto;
the sequence of CDR2 is DTSNLAS (SEQ ID NO: 140) or a sequence at least 80% similar, preferably at least 80% identical, thereto and;
the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192) or a sequence at least 80% similar, preferably at least 80% identical, thereto.

40. A V_L antibody binding domain as claimed in claim 38 or claim 39 in which the sequence of FR1 is selected from the group EIVLTQSPATLSLSPGERATLSC (SEQ ID NO: 214) or ENVLTQSPATLSLSPGERATLSC (SEQ ID NO: 215).

41. A V_L antibody binding domain as claimed in any one of claims 38 to 40 in which the sequence of CDR1 is SASSSLSYIH (SEQ ID NO: 188).

42. A V_L antibody binding domain as claimed in any one of claims 38 to 41 in which the sequence of FR2 is WYQQKPGQAPRLLIY (SEQ ID NO: 189).

43. A V_L antibody binding domain as claimed in any one of claims 38 to 42 in which the sequence of the sequence of CDR2 is DTSNLAS (SEQ ID NO: 190).

44. A V_L antibody binding domain as claimed in any one of claims 38 to 43 in which the sequence of the sequence of FR3 is

GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC (SEQ ID NO: 216) or GIPDRFSGSGSGNDFTLTISRLEPEDFAVYYC (SEQ ID NO: 217).

45. A V_L antibody binding domain as claimed in any one of claims 38 to 44 in which the sequence of the sequence of CDR3 is FQGSEYPLT (SEQ ID NO: 192).

46. A V_L antibody binding domain as claimed in any one of claims 38 to 45 in which the sequence of the sequence of FR4 is FGGGTKVEIKR (SEQ ID NO: 193).

47. A V_L antibody binding domain as claimed in any one of claims 38 to 46 further comprising a constant domain.

48. A V_L antibody binding domain as claimed in claim 47 in which the constant domain has the sequence TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE C (SEQ ID NO: 93).

49. An antibody comprising a V_H binding domain as claimed in any one of claims 27 to 35 and a V_L binding domain as claimed in any one of claims 38 to 46.

50. An antibody as claimed in claim 49 in which the V_H binding domain and/or the V_L binding domain further comprise a constant domain.

51. An antibody as claimed in claim 50 in which the constant domain of the V_H binding domain has the sequence:-

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK (SEQ ID NO: 52); or

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE

WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK (SEQ ID NO: 92); or

ASTKNPDVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT
HTCPPCPAPELLGGPDVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPEEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
ALHNHYTQKSLSLSPGK (SEQ ID NO: 53).

52. An antibody as claimed in claim 50 or claim 51 in which the constant domain of the V_L binding domain has the sequence
TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGE
C (SEQ ID NO: 93).

53. An antibody comprising two light chains and two heavy chains in which the sequence of the light chains is as shown in SEQ ID NO: 7 and the sequence of the heavy chains is as shown in SEQ ID NO: 50.

54. An antibody comprising two light chains and two heavy chains in which the sequence of the light chains is as shown in SEQ ID NO: 7 and the sequence of the heavy chains is as shown in SEQ ID NO: 94.

55. An antibody as claimed in any one of claims 23 to 26 or 49 to 54 in which the antibody has a reduced level of fucose.