MULTISPECIFIC ANTIBODY CONSTRUCTS

The present disclosure relates to certain multi-specific antibody constructs, pharmaceutical formulations comprising the construct, DNA encoding the constructs and vectors comprising same. The disclosure also extends to a method of expressing the constructs, for example in a host cell and methods for formulating same as a pharmaceutical composition. The disclosure also relates to use of the multi-specific antibody constructs and formulations in treatment.

There are a number of approaches for generating bi-specific antibodies, many of which are based on a format originally described by Morrison *et al* (Coloma and Morrison 1997, Nat Biotechnol. 15, 159-163) involving the fusion of single chain variable fragments (scFv) to whole antibodies, e.g. IgG, or to antibody Fab fragments, Schoonjans *et al*., 2000, Journal of Immunology, 165, 7050-7057.

In the case of Fab-scFv, the V_H and V_L domains of the scFvs used in such bi-specific and tri specific molecules are usually held together by peptide linkers. However, for certain combinations of V_H and V_L variable domains, the peptide linkers are unable to confer sufficient stability to the scFv, resulting in variable domain 'breathing' and promiscuous intermolecular pairing with variable domains and thus a tendency to form multimers through the single chain Fv portion thereof. This is illustrated in Figure 1 in the context of a bispecific molecule.

The present inventors have re-engineered the multi-specific antibody molecules concerned to provide antibody molecules with equivalent functionality, whilst minimising multimerisation at the expression stage and/or post purification. This facilitates increasing the yield of "monomeric" material obtained and provides molecules of suitable stability for use in treatment after purification, concentration and formulation.

Thus, in one aspect, there is provided a multi-specific antibody molecule comprising or consisting of:

a) a polypeptide chain of formula (**I**):

$$\mathbf{V_H\text{-}CH_1\text{-}X\text{-}V_1;\ and}$$

b) a polypeptide chain of formula (**II**):

$$\mathbf{V_L\text{-}C_L\text{-}Y\text{-}V_2};$$

wherein:

V_H represents a heavy chain variable domain;

CH_1 represents a domain of a heavy chain constant region, for example domain 1 thereof;

X represents a bond or linker;

Y represents a bond or linker;

V_1 represents a dsFv, a sdAb, a scFv or a dsscFv;

V_L represents a light chain variable domain;

C_L represents a domain from a light chain constant region, such as Ckappa;

V_2 represents dsFv, a sdAb, a scFv or a dsscFv;

wherein at least one of V_1 or V_2 is a dsFv or dsscFv.

Advantageously, the multi-specific antibody molecules of the present disclosure minimise the amount of aggregation seen after purification and maximise the amount of monomer in the formulations of the construct at pharmaceutical concentrations, including maintaining high monomer levels over time upon storage, for example the monomer may be present as 50%, 60%, 70% or 75% or more, such as 80 or 90% or more such as 91, 92, 93, 94, 95, 96, 97, 98 or 99% or more of the total protein.

Detailed Description of the Invention

"Multi-specific antibody" as employed herein refers to an antibody molecule as described herein which has two or more binding domains, for example two or three binding domains.

In one embodiment the antibody construct is a tri-specific antibody.

"Tri-specific antibody" as employed herein refers to an antibody molecule with three antigen binding sites, which may independently bind the same or different antigens. In one example a trispecific antibody molecule binds two different antigens, i.e. two binding sites bind the same antigen and the third binding site binds a second, different antigen. Preferably the three binding sites of a trispecific antibody molecule of the invention independently bind three different antigens.

In one embodiment the construct is a bi-specific antibody.

"Bi-specific molecule" as employed herein refers to a molecule with two antigen binding sites, which may bind the same or different antigens.

In one embodiment the domains all bind the same antigen, including binding the same epitope on the antigen or binding different epitopes on the antigen.

In one embodiment there are three binding domains and each of the three binding domains bind different (distinct) antigens.

In one embodiment there are three binding domains and two binding domains bind the same antigen, including binding the same epitope or different epitopes on the same antigen, and the third binding domain binds a different (distinct) antigen.

"Antigen binding site" as employed herein refers to a portion of the molecule, which comprises a pair of variable regions, in particular a cognate pair that interact specifically with the target antigen.

Binding domains as employed herein includes a single domain antibody i.e. a variable region and antigen binding sites.

"Specifically" as employed herein is intended to refer to a binding site or binding domain that only recognises the antigen to which it is specific or a binding site or binding domain that has significantly higher binding affinity to the antigen to which is specific compared to affinity to antigens to which it is non-specific, for example 5, 6, 7, 8, 9, 10 times higher binding affinity.

Binding affinity may be measured by standard assay, for example surface plasmon resonance, such as BIAcore.

In one embodiment, the multi-specific antibody molecule according to the present disclosure is provided as a dimer of a heavy and light chain of:

Formula **(I)** and **(II)** respectively, wherein the V_H-CH_1 portion together with the V_L-C_L portion form a functional Fab or Fab' fragment.

V_H represents a variable domain, for example a heavy chain variable domain. In one embodiment V_H represents a heavy chain variable domain. In one embodiment V_H is a chimeric variable domain, that is to say it comprises components derived from at least two species, for example a human framework and non-human CDRs. In one embodiment V_H is humanised. In one embodiment the V_H is human.

V_L represents a variable domain, for example a light chain variable domain. In one embodiment V_L represents a light chain variable domain. In one embodiment V_L is a chimeric variable domain, that is to say it comprises components derived from at least two species, for example a human framework and non-human CDRs. In one embodiment V_L is humanised. In one embodiment V_H is humanised. In one embodiment the V_H is human

Generally V_H and V_L together form an antigen binding domain. In one embodiment V_H and V_L form a cognate pair.

"Cognate pair" as employed herein refers to a pair of variable domains from a single antibody, which was generated *in vivo*, i.e. the naturally occurring pairing of the variable domains isolated from a host. A cognate pair is therefore a V_H and V_L pair. In one example the cognate pair bind the antigen co-operatively.

"Variable region" as employed herein refers to the region in an antibody chain comprising the CDRs and a framework, in particular a suitable framework.

Variable regions for use in the present disclosure will generally be derived from an antibody, which may be generated by any method known in the art.

"Derived from" as employed herein refers to the fact that the sequence employed or a sequence highly similar to the sequence employed was obtained from the original genetic material, such as the light or heavy chain of an antibody.

"Highly similar" as employed herein is intended to refer to an amino acid sequence which over its full length is 95% similar or more, such as 96, 97, 98 or 99% similar.

Variable regions for use in the present invention, as described herein above for V_H and V_L may be from any suitable source and may be for example, fully human or humanised.

In one embodiment the binding domain formed by V_H and V_L are specific to a first antigen.

In one embodiment the binding domain formed by V_1 is specific to a second antigen.

In one embodiment the binding domain formed by V_2 is specific to a second or third antigen.

In one embodiment the CH_1 domain is a naturally occurring domain 1 from an antibody heavy chain or a derivative thereof.

In one embodiment the C_L fragment, in the light chain, is a constant kappa sequence or a constant lambda sequence or a derivative thereof.

A derivative of a naturally occurring domain as employed herein is intended to refer to where one, two, three, four or five amino acids in a naturally occurring sequence have been

replaced or deleted, for example to optimize the properties of the domain such as by eliminating undesirable properties but wherein the characterizing feature(s) of the domain is/are retained.

In one embodiment one or more natural or engineered inter chain (i.e. inter light and heavy chain) disulphide bonds are present in the functional Fab or Fab' fragment.

In one embodiment a "natural" disulfide bond is present between a CH_1 and C_L in the polypeptide chains of Formula **(I)** and **(II)**.

When the C_L domain is derived from either Kappa or Lambda the natural position for a bond forming cysteine is 214 in human cKappa and cLambda (Kabat numbering 4th edition 1987).

The exact location of the disulfide bond forming cysteine in CH_1 depends on the particular domain actually employed. Thus, for example in human gamma-1 the natural position of the disulfide bond is located at position 233 (Kabat numbering 4th edition 1987). The position of the bond forming cysteine for other human isotypes such as gamma 2, 3, 4, IgM and IgD are known, for example position 127 for human IgM, IgE, IgG2, IgG3, IgG4 and 128 of the heavy chain of human IgD and IgA2B.

Optionally there may be a disulfide bond between the V_H and V_L of the polypeptides of formula I and II.

In one embodiment the multi-specific antibody according to the disclosure has a disulfide bond in a position equivalent or corresponding to that naturally occurring between CH_1 and C_L.

In one embodiment a constant region comprising CH_1 and a constant region such as C_L has a disulfide bond which is in a non-naturally occurring position. This may be engineered into the molecule by introducing cysteine(s) into the amino acid chain at the position or positions required. This non-natural disulfide bond is in addition to or as an alternative to the natural disulfide bond present between CH_1 and C_L. The cysteine(s) in natural positions can be replaced by an amino acid such as serine which is incapable on forming a disulfide bridge.

Introduction of engineered cysteines can be performed using any method known in the art. These methods include, but are not limited to, PCR extension overlap mutagenesis, site-directed mutagenesis or cassette mutagenesis (see, generally, Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY, 1989; Ausbel et al., Current Protocols in Molecular Biology, Greene Publishing & Wiley-Interscience, NY, 1993). Site-directed mutagenesis kits are commercially available, e.g. QuikChange® Site-Directed Mutagenesis kit (Stratagene, La Jolla, CA). Cassette mutagenesis can be performed based on Wells *et al.*, 1985, Gene, 34:315-323. Alternatively, mutants can be made by total gene synthesis by annealing, ligation and PCR amplification and cloning of overlapping oligonucleotides.

In one embodiment a disulfide bond between CH_1 and C_L is completely absent, for example the interchain cysteines may be replaced by another amino acid, such as serine. Thus in one embodiment there are no interchain disulphide bonds in the functional Fab fragment of the molecule. Disclosures such as WO2005/003170, incorporated herein by reference, describe how to provide Fab fragments without an inter chain disulphide bond.

V_1 represents a dsFv, a sdAb, a scFv, or a dsscFv, for example a dsFv, scFv or a dsscFv.

V_2 represents a dsFv, a sdAb, a scFv, or a dsscFv, for example a dsFv, scFv or a dsscFv.

In one embodiment, V_1 and V_2 are both dsscFv.

In one embodiment, V_1 and V_2 are both dsFv. When both V_1 and V_2 are dsFv, either the V_H or the V_L variable domains are the same for V_1 and V_2. In one embodiment, V_1 and V_2 have the same V_H variable domain. In another embodiment, V_1 and V_2 have the same V_L variable domain. In one embodiment the V_H and V_L variable domains are the same for V_1 and V_2. The latter allows for cross-linking which may be desirable for some targets.

In one embodiment V_1 is a dsFv and V_2 is a scFv. In one embodiment V_1 is a scFv and V_2 is a dsFv. In one embodiment V_1 is a dsscFv and V_2 is a dsFv. In one embodiment V_1 is a dsFv and V_2 is a dsscFv. In one embodiment V_1 is a dsscFv and V_2 is a scFv. In one embodiment V_1 is a scFv and V_2 is a dsscFv. In one embodiment, V_1 is not a scFv. In one embodiment, V_2 is not a scFv. In one embodiment, both V_1 and V_2 are not scFv.

Thus, in one aspect, there is provided a multi-specific antibody molecule comprising or consisting of:

a) a polypeptide chain of formula (**I**):

$$\mathbf{V_H\text{-}CH_1\text{-}X\text{-}V_1;}\ \text{and}$$

b) a polypeptide chain of formula (**II**):

$$\mathbf{V_L\text{-}C_L\text{-}Y\text{-}V_2;}$$

wherein:

V_H represents a heavy chain variable domain;

CH_1 represents a domain of a heavy chain constant region, for example domain 1 thereof;

X represents a bond or linker;

Y represents a bond or linker;

V_1 represents a dsFv or a dsscFv;

V_L represents a light chain variable domain;

C_L represents a domain from a constant region, for example a light chain constant region domain, such as Ckappa;

V_2 represents dsFv or a dsscFv;

"Single chain variable fragment" or "scFv" as employed herein refers to a single chain variable fragment comprising or consisting of a heavy chain variable domain (V_H) and a light chain variable domain (V_L) which is stabilised by a peptide linker between the V_H and V_L variable domains. The V_H and V_L variable domains may be in any suitable orientation, for example the C-terminus of V_H may be linked to the N-terminus of V_L or the C-terminus of V_L may be linked to the N-terminus of V_H.

"Disulphide-stabilised single chain variable fragment" or "dsscFv" as employed herein refers to a single chain variable fragment which is stabilised by a peptide linker between the V_H and V_L variable domain and also includes an inter-domain disulphide bond between V_H and V_L.

"Disulphide-stabilised variable fragment" or "dsFv" as employed herein refers to a single chain variable fragment which does not include a peptide linker between the V_H and V_L variable domains and is instead stabilised by an interdomain disulphide bond between V_H and V_L.

"Single domain antibody" or "sdAb" as employed herein refers to an antibody fragment consisting of a single monomeric variable antibody domain, such as V_H or V_L or VHH.

In one embodiment, when V_1 and/or V_2 are a dsFv or a dsscFv, the disulfide bond between the variable domains V_H and V_L of V_1 and/or V_2 is between two of the residues listed below (unless the context indicates otherwise Kabat numbering is employed in the list below). Wherever reference is made to Kabat numbering the relevant reference is Kabat *et al.*, 1987, in Sequences of Proteins of Immunological Interest, US Department of Health and Human Services, NIH, USA.

In one embodiment the disulfide bond is in a position selected from the group comprising:

- V_H37 + V_L95C see for example Protein Science 6, 781-788 Zhu et al (1997);
- V_H44 + V_L100 see for example; Biochemistry 33 5451-5459 Reiter et al (1994); or Journal of Biological Chemistry Vol. 269 No. 28 pp.18327-18331 Reiter et al (1994); or Protein Engineering, vol.10 no.12 pp.1453-1459 Rajagopal et al (1997);
- V_H44 + V_L105 see for example J Biochem. 118, 825-831 Luo et al (1995);
- V_H45 + V_L87 see for example Protein Science 6, 781-788 Zhu et al (1997);
- V_H55 + V_L101 see for example FEBS Letters 377 135-139 Young et al (1995);
- V_H100 + V_L50 see for example Biochemistry 29 1362-1367 Glockshuber et al (1990);
- V_H100b + V_L49;
- V_H98 + V_L 46 see for example Protein Science 6, 781-788 Zhu et al (1997);
- V_H101 + V_L46;
- V_H105 + V_L43 see for example; Proc. Natl. Acad. Sci. USA Vol. 90 pp.7538-7542 Brinkmann *et al* (1993); or Proteins 19, 35-47 Jung et al (1994),
- V_H106 + V_L57 see for example FEBS Letters 377 135-139 Young *et al* (1995)

and a position corresponding thereto in variable region pair located in the molecule.

In one embodiment, the disulphide bond is formed between positions V_H44 and V_L100.

The amino acid pairs listed above are in the positions conducive to replacement by cysteines such that disulfide bonds can be formed. Cysteines can be engineered into these desired positions by known techniques. In one embodiment therefore an engineered cysteine according to the present disclosure refers to where the naturally occurring residue at a given amino acid position has been replaced with a cysteine residue.

Introduction of engineered cysteines can be performed using any method known in the art. These methods include, but are not limited to, PCR extension overlap mutagenesis, site-directed mutagenesis or cassette mutagenesis (see, generally, Sambrook et al., Molecular Cloning, A Laboratory Manual, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY, 1989; Ausbel et al., Current Protocols in Molecular Biology, Greene Publishing & Wiley-Interscience, NY, 1993). Site-directed mutagenesis kits are commercially available, e.g. QuikChange® Site-Directed Mutagenesis kit (Stratagen, La Jolla, CA). Cassette mutagenesis can be performed based

on Wells *et al.*, 1985, Gene, 34:315-323. Alternatively, mutants can be made by total gene synthesis by annealing, ligation and PCR amplification and cloning of overlapping oligonucleotides.

Accordingly, in one embodiment when V_1 and/or V_2 are a dsFv or a dsscFv, the variable domains V_H and V_L of V_1 and/or the variable domains V_H and V_L of V_2 may be linked by a disulfide bond between two cysteine residues, wherein the position of the pair of cysteine residues is selected from the group consisting of: V_H37 and V_L95, V_H44 and V_L100, V_H44 and V_L105, V_H45 and V_L87, V_H100 and V_L50, V_H100b and V_L49, V_H98 and V_L46, V_H101 and V_L46, V_H105 and V_L43 and V_H106 and V_L57.

In one embodiment when V_1 and/or V_2 are a dsFv or a dsscFv, the variable domains V_H and V_L of V_1 and/or the variable domains V_H and V_L of V_2 may be linked by a disulfide bond between two cysteine residues, one in V_H and one in V_L, which are outside of the CDRs wherein the position of the pair of cysteine residues is selected from the group consisting of V_H37 and V_L95, V_H44 and V_L100, V_H44 and V_L105, V_H45 and V_L87, V_H100 and V_L50, V_H98 and V_L46, V_H105 and V_L43 and V_H106 and V_L57.

In one embodiment when V_1 is a dsFv or a dsscFv, the variable domains V_H and V_L of V_1 are linked by a disulphide bond between two engineered cysteine residues, one at position V_H44 and the other at V_L100.

In one embodiment when V_2 is a dsFv or a dsscFv, the variable domains V_H and V_L of V_2 are linked by a disulphide bond between two engineered cysteine residues, one at position V_H44 and the other at V_L100.

In one embodiment when V_1 is a dsFv, a dsscFv, or a scFv, the V_H domain of V_1 is attached to X.

In one embodiment when V_1 is a dsFv, a dsscFv, or a scFv, the V_L domain of V_1 is attached to X.

In one embodiment when V_2 is a dsFv, a dsscFv, or a scFv, the V_H domain of V_2 is attached to Y.

In one embodiment when V_2 is a dsFv, a dsscFv, or a scFv, the V_L domain of V_2 is attached to Y.

The skilled person will appreciate that when V_1 and/or V_2 represents a dsFv, the multi-specific antibody will comprise a third polypeptide encoding the corresponding free V_H or V_L domain which is not attached to X or Y. When V_1 and V_2 are both a dsFv then the "free variable domain" (i.e. the domain linked to via a disulphide bond to the remainder of the polypeptide) will be common to both chains. Thus whilst the actual variable domain fused or linked via X or Y to the polypeptide may be different in each polypeptide chain the free variable domains paired therewith will generally be identical to each other.

In one embodiment X is a bond.

In one embodiment Y is a bond.

In one embodiment both X and Y are bonds.

In one embodiment X is a linker, preferably a peptide linker, for example a suitable peptide for connecting the portions CH_1 and V_1.

In one embodiment Y is a linker, preferably a peptide linker, for example a suitable peptide for connecting the portions C_L and V_2.

In one embodiment both X and Y are linkers. In one embodiment both X and Y are peptide linkers.

The term "peptide linker" as used herein refers to a peptide comprised of amino acids. A range of suitable peptide linkers will be known to the person of skill in the art.

In one embodiment the peptide linker is 50 amino acids in length or less, for example 20 amino acids or less, such as about 15 amino acids or less, such as 9, 10, 11, 12, 13 or 14 amino acids in length.

In one embodiment the linker is selected from a sequence shown in sequence 1 to 67.

In one embodiment the linker is selected from a sequence shown in SEQ ID NO: 1 or SEQ ID NO: 2.

In one embodiment X has the sequence SGGGGTGGGGS (SEQ ID NO: 1).

In one embodiment Y has the sequence SGGGGTGGGGS (SEQ ID NO: 1).

In one embodiment X has the sequence SGGGGSGGGGS (SEQ ID NO: 2). In one embodiment Y has the sequence SGGGGSGGGGS (SEQ ID NO: 2).

In one embodiment X has the sequence given in SEQ ID NO:1 and Y has the sequence given in SEQ ID NO:2.

In one embodiment X has the sequence given in SEQ ID NO:69 or 70. In one embodiment Y has the sequence given in SEQ ID NO:69 or 70. In one embodiment X has the sequence given in SEQ ID NO:69 and Y has the sequence given in SEQ ID NO:70.

Table 1. Hinge linker sequences

SEQ ID NO:	SEQUENCE
3	DKTHTCAA
4	DKTHTCPPCPA
5	DKTHTCPPCPATCPPCPA
6	DKTHTCPPCPATCPPCPATCPPCPA
7	DKTHTCPPCPAGKPTLYNSLVMSDTAGTCY
8	DKTHTCPPCPAGKPTHVNVSVVMAEVDGTCY
9	DKTHTCCVECPPCPA
10	DKTHTCPRCPEPKSCDTPPPCPRCPA
11	DKTHTCPSCPA

Table 2. Flexible linker sequences

SEQ ID NO:	SEQUENCE
12	SGGGGSE
13	DKTHTS
14	(S)GGGGS
15	(S)GGGGSGGGGS
16	(S)GGGGSGGGGSGGGGS
17	(S)GGGGSGGGGSGGGGSGGGGS
18	(S)GGGGSGGGGSGGGGSGGGGSGGGGS
19	AAAGSG-GASAS
20	AAAGSG-XGGGS-GASAS
21	AAAGSG-XGGGSXGGGS –GASAS
22	AAAGSG- XGGGSXGGGSXGGGS –GASAS
23	AAAGSG- XGGGSXGGGSXGGGSXGGGS-GASAS
24	AAAGSG-XS-GASAS
25	PGGNRGTTTTRRPATTTGSSPGPTQSHY
26	ATTTGSSPGPT
27	ATTTGS
-	GS
28	EPSGPISTINSPPSKESHKSP
29	GTVAAPSVFIFPPSD
30	GGGGIAPSMVGGGGS
31	GGGGKVEGAGGGGGS
32	GGGGSMKSHDGGGGS
33	GGGGNLITIVGGGGS
34	GGGGVVPSLPGGGGS
35	GGEKSIPGGGGS
36	RPLSYRPPFPFGFPSVRP
37	YPRSIYIRRRHPSPSLTT
38	TPSHLSHILPSFGLPTFN
39	RPVSPFTFPRLSNSWLPA
40	SPAAHFPRSIPRPGPIRT
41	APGPSAPSHRSLPSRAFG
42	PRNSIHFLHPLLVAPLGA
43	MPSLSGVLQVRYLSPPDL
44	SPQYPSPLTLTLPPHPSL
45	NPSLNPPSYLHRAPSRIS
46	LPWRTSLLPSLPLRRRP

47	PPLFAKGPVGLLSRSFPP
48	VPPAPVVSLRSAHARPPY
49	LRPTPPRVRSYTCCPTP-
50	PNVAHVLPLLTVPWDNLR
51	CNPLLPLCARSPAVRTFP

(S) is optional in sequences 14 to 18.

Examples of rigid linkers include the peptide sequences GAPAPAAPAPA (SEQ ID NO: 52), PPPP (SEQ ID NO: 53) and PPP.

In one embodiment the peptide linker is an albumin binding peptide.

Examples of albumin binding peptides are provided in WO2007/106120 and include:

Table 3

SEQ ID NO:	**SEQUENCE**
54	DLCLRDWGCLW
55	DICLPRWGCLW
56	MEDICLPRWGCLWGD
57	QRLMEDICLPRWGCLWEDDE
58	QGLIGDICLPRWGCLWGRSV
59	QGLIGDICLPRWGCLWGRSVK
60	EDICLPRWGCLWEDD
61	RLMEDICLPRWGCLWEDD
62	MEDICLPRWGCLWEDD
63	MEDICLPRWGCLWED
64	RLMEDICLARWGCLWEDD
65	EVRSFCTRWPAEKSCKPLRG
66	RAPESFVCYWETICFERSEQ
67	EMCYFPGICWM

Advantageously use of albumin binding peptides as a linker may increase the half-life of the multi-specific antibody molecule.

In one embodiment when V_1 is a scFv or a dsscFv, there is a linker for example a suitable peptide for connecting the variable domains V_H and V_L of V_1.

In one embodiment when V_2 is a scFv or a dsscFv, there is a linker for example a suitable peptide for connecting the variable domains V_H and V_L of V_2.

In one embodiment the peptide linker in the scFv or dsscFv is in range about 12 to 25 amino acids in length, such as 15 to 20 amino acids.

In one embodiment when V_1 is a scFv or a dsscFv, the linker connecting the variable domains V_H and V_L of V_1 has the sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 68).

In one embodiment when V_2 is a scFv or a dsscFv, the linker connecting the variable domains V_H and V_L of V_2 has the sequence GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 68).

In one embodiment when V_1 is a scFv or a dsscFv, the linker connecting the variable domains V_H and V_L of V_1 has the sequence SGGGGSGGGGSGGGGS (SEQ ID NO: 69).

In one embodiment when V_2 is a scFv or a dsscFv, the linker connecting the variable domains V_H and V_L of V_2 has the sequence SGGGGSGGGGSGGGGS (SEQ ID NO: 69)

In one embodiment when V_1 is a scFv or a dsscFv, the linker connecting the variable domains V_H and V_L of V_1 has the sequence SGGGGSGGGGTGGGGS (SEQ ID NO: 70).

In one embodiment when V_2 is a scFv or a dsscFv, the linker connecting the variable domains V_H and V_L of V_2 has the sequence SGGGGSGGGGTGGGGS SEQ ID NO: 70).

Accordingly, in one aspect there is provided a multi-specific antibody molecule, comprising or consisting of:

a) a polypeptide chain of formula (**I**):

$$\mathbf{V_H\text{-}CH_1\text{-}X\text{-}V_1;}\ \text{and}$$

b) a polypeptide chain of formula (**II**):

$$\mathbf{V_L\text{-}C_L\text{-}Y\text{-}V_2;}$$

wherein:

V_H represents a heavy chain variable domain;

CH_1 represents a domain of a heavy chain constant region, for example domain 1 thereof;

X represents a bond or linker;

Y represents a bond or linker;

V_1 represents a dsFv, a sdAb, a scFv or a dsscFv;

V_L represents a light chain variable domain;

C_L represents a domain from a light chain constant region, such as Ckappa;

V_2 represents dsFv, a sdAb, a scFv or a dsscFv;

wherein at least one of V_1 or V_2 is a dsFv or dsscFv.

The present disclosure also provides sequences which are 80%, 90%, 91%, 92%, 93% 94%, 95% 96%, 97%, 98% or 99% similar to a sequence disclosed herein.

"Identity", as used herein, indicates that at any particular position in the aligned sequences, the amino acid residue is identical between the sequences.

"Similarity", as used herein, indicates that, at any particular position in the aligned sequences, the amino acid residue is of a similar type between the sequences. For example, leucine may be substituted for isoleucine or valine. Other amino acids which can often be substituted for one another include but are not limited to:

- phenylalanine, tyrosine and tryptophan (amino acids having aromatic side chains);
- lysine, arginine and histidine (amino acids having basic side chains);
- aspartate and glutamate (amino acids having acidic side chains);
- asparagine and glutamine (amino acids having amide side chains); and
- cysteine and methionine (amino acids having sulphur-containing side chains).

Degrees of identity and similarity can be readily calculated (Computational Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988; Biocomputing. Informatics and Genome Projects, Smith, D.W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part 1, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987, Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991, the BLAST™ software available from NCBI (Altschul, S.F. et al., 1990, J. Mol. Biol. 215:403-410; Gish, W. & States, D.J. 1993, Nature Genet. 3:266-272. Madden, T.L. et al., 1996, Meth. Enzymol. 266:131-141; Altschul, S.F. et al., 1997, Nucleic Acids Res. 25:3389-3402; Zhang, J. & Madden, T.L. 1997, Genome Res. 7:649-656,).

Antibodies for use in the multispecific constructs of the present invention may be gerenated by any suitable method known in the art.

Antibodies generated against an antigen polypeptide may be obtained, where immunisation of an animal is necessary, by administering the polypeptides to an animal, preferably a non-human animal, using well-known and routine protocols, see for example Handbook of Experimental Immunology, D. M. Weir (ed.), Vol 4, Blackwell Scientific Publishers, Oxford, England, 1986). Many warm-blooded animals, such as rabbits, mice, rats, sheep, cows, camels or pigs may be immunized. However, mice, rabbits, pigs and rats are generally most suitable.

Monoclonal antibodies may be prepared by any method known in the art such as the hybridoma technique (Kohler & Milstein, 1975, Nature, 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al* 1983, Immunology Today, 4:72) and the EBV-hybridoma technique (Cole et al., Monoclonal Antibodies and Cancer Therapy, pp77-96, Alan R Liss, Inc., 1985).

Antibodies may also be generated using single lymphocyte antibody methods by cloning and expressing immunoglobulin variable region cDNAs generated from single lymphocytes selected for the production of specific antibodies by, for example, the methods described by Babcook, J. *et al* 1996, Proc. Natl. Acad. Sci. USA 93(15):7843-7848l; WO92/02551; WO2004/051268 and WO2004/106377.

The antibodies for use in the present disclosure can also be generated using various phage display methods known in the art and include those disclosed by Brinkman *et al.* (in J. Immunol. Methods, 1995, 182: 41-50), Ames *et al.* (J. Immunol. Methods, 1995, 184:177-186), Kettleborough *et al.* (Eur. J. Immunol. 1994, 24:952-958), Persic *et al.* (Gene, 1997 187 9-18), Burton *et al.* (Advances in Immunology, 1994, 57:191-280) and WO90/02809; WO91/10737; WO92/01047; WO92/18619; WO93/11236; WO95/15982; WO95/20401; and US 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743; 5,969,108, and WO20011/30305.

In one embodiment the multi-specific molecules according to the disclosure are humanised.

Humanised (which include CDR-grafted antibodies) as employed herein refers to molecules having one or more complementarity determining regions (CDRs) from a non-human species and a

framework region from a human immunoglobulin molecule (see, e.g. US 5,585,089; WO91/09967). It will be appreciated that it may only be necessary to transfer the specificity determining residues of the CDRs rather than the entire CDR (see for example, Kashmiri et al., 2005, Methods, 36, 25-34). Humanised antibodies may optionally further comprise one or more framework residues derived from the non-human species from which the CDRs were derived.

As used herein, the term "humanised antibody molecule" refers to an antibody molecule wherein the heavy and/or light chain contains one or more CDRs (including, if desired, one or more modified CDRs) from a donor antibody (e.g. a murine monoclonal antibody) grafted into a heavy and/or light chain variable region framework of an acceptor antibody (e.g. a human antibody). For a review, see Vaughan *et al*, Nature Biotechnology, 16, 535-539, 1998. In one embodiment rather than the entire CDR being transferred, only one or more of the specificity determining residues from any one of the CDRs described herein above are transferred to the human antibody framework (see for example, Kashmiri et al., 2005, Methods, 36, 25-34). In one embodiment only the specificity determining residues from one or more of the CDRs described herein above are transferred to the human antibody framework. In another embodiment only the specificity determining residues from each of the CDRs described herein above are transferred to the human antibody framework.

When the CDRs or specificity determining residues are grafted, any appropriate acceptor variable region framework sequence may be used having regard to the class/type of the donor antibody from which the CDRs are derived, including mouse, primate and human framework regions. Suitably, the humanised antibody according to the present invention has a variable domain comprising human acceptor framework regions as well as one or more of the CDRs provided herein.

Examples of human frameworks which can be used in the present disclosure are KOL, NEWM, REI, EU, TUR, TEI, LAY and POM (Kabat *et al supra*). For example, KOL and NEWM can be used for the heavy chain, REI can be used for the light chain and EU, LAY and POM can be used for both the heavy chain and the light chain. Alternatively, human germline sequences may be used; these are available at: http://www2.mrc-lmb.cam.ac.uk/vbase/list2.php.

In a humanised antibody molecule of the present disclosure, the acceptor heavy and light chains do not necessarily need to be derived from the same antibody and may, if desired, comprise composite chains having framework regions derived from different chains.

The framework regions need not have exactly the same sequence as those of the acceptor antibody. For instance, unusual residues may be changed to more frequently-occurring residues for that acceptor chain class or type. Alternatively, selected residues in the acceptor framework regions may be changed so that they correspond to the residue found at the same position in the donor antibody (see Reichmann *et al* 1998, Nature, 332, 323-324). Such changes should be kept to the minimum necessary to recover the affinity of the donor antibody. A protocol for selecting residues in the acceptor framework regions which may need to be changed is set forth in WO91/09967.

Derivatives of frameworks may have 1, 2, 3 or 4 amino acids replaced with an alternative amino acid, for example with a donor residue.

Donor residues are residues from the donor antibody, i.e. the antibody from which the CDRs were originally derived. Donor residues may be replaced by a suitable residue derived from a human receptor framework (acceptor residues).

In one embodiment the multi-specific antibodies of the present disclosure are fully human, in particular one or more of the variable domains are fully human.

Fully human molecules are those in which the variable regions and the constant regions (where present) of both the heavy and the light chains are all of human origin, or substantially identical to sequences of human origin, not necessarily from the same antibody. Examples of fully human antibodies may include antibodies produced, for example by the phage display methods described above and antibodies produced by mice in which the murine immunoglobulin variable and optionally the constant region genes have been replaced by their human counterparts e.g. as described in general terms in EP0546073, US5,545,806, US5,569,825, US5,625,126, US5,633,425, US5,661,016, US5,770,429, EP 0438474 and EP0463151.

In one embodiment the multi-specific antibody molecules of the disclosure are capable of selectively binding two, three or more different antigens of interest.

In one embodiment, antigens of interest bound by the antigen binding domain formed by V_H/V_L, or V_1 or V_2 are independently selected from a cell-associated protein, for example a cell surface protein on cells such as bacterial cells, yeast cells, T-cells, B-cells, endothelial cells or tumour cells, and a soluble protein.

Antigens of interest may also be any medically relevant protein such as those proteins upregulated during disease or infection, for example receptors and/or their corresponding ligands. Particular examples of antigens include cell surface receptors such as T cell or B cell signalling receptors, co-stimulatory molecules, checkpoint inhibitors, natural killer cell receptors, Immunoglobulin receptors, TNFR family receptors, B7 family receptors, adhesion molecules, integrins, cytokine/chemokine receptors, GPCRs, growth factor receptors, kinase receptors, tissue-specific antigens, cancer antigens, pathogen recognition receptors, complement receptors, hormone receptors or soluble molecules such as cytokines, chemokines, leukotrienes, growth factors, hormones or enzymes or ion channels, epitopes, fragments and post translationally modified forms thereof.

In one embodiment the multispecific antibody molecule of the disclosure may be used to functionally alter the activity of the antigen(s) of interest. For example, the antibody fusion protein may neutralize, antagonize or agonise the activity of said antigen, directly or indirectly.

In one embodiment V_1 and V_2 are specific for the same antigen, for example binding the same or a different epitope therein. In one embodiment V_1 is specific for human serum albumin. In one embodiment V_2 is specific for human serum albumin. In one embodiment V_1 and V_2 are specific for two different antigens.

In one embodiment V_1 and V_2 are specific for the same antigens, for example the same or different epitopes on the same antigen.

In one embodiment, an antigen of interest bound by V_H/V_L or V_1 or V_2 provides the ability to recruit effector functions, such as complement pathway activation and/or effector cell recruitment.

The recruitment of effector function may be direct in that effector function is associated with a cell, said cell bearing a recruitment molecule on its surface. Indirect recruitment may occur when binding of an antigen to an antigen binding domain (such as V_1 or V_2) in the molecule according to present disclosure to a recruitment polypeptide causes release of, for example, a factor which in turn may directly or indirectly recruit effector function, or may be via activation of a signalling pathway. Examples include IL2, IL6, IL8, IFNγ, histamine, C1q, opsonin and other members of the classical and alternative complement activation cascades, such as C2, C4, C3-convertase, and C5 to C9.

As used herein, "a recruitment polypeptide" includes a FcγR such as FcγRI, FcγRII and FcγRIII, a complement pathway protein such as, but without limitation, C1q and C3, a CD marker protein (Cluster of Differentiation marker) or a fragment thereof which retains the ability to recruit cell-mediated effector function either directly or indirectly. A recruitment polypeptide also includes immunoglobulin molecules such as IgG1, IgG2, IgG3, IgG4, IgE and IgA which possess effector function.

In one embodiment an antigen binding domain (such as V_1 or V_2 or V_H/V_L) in the multi-specific antibody molecule according to the present disclosure has specificity for a complement pathway protein, with C1q being particularly preferred.

Further, multi-specific antibody molecules of the present disclosure may be used to chelate radionuclides by virtue of a single domain antibody which binds to a nuclide chelator protein. Such fusion proteins are of use in imaging or radionuclide targeting approaches to therapy.

In one embodiment an antigen binding domain within a molecule according to the disclosure (such as V_1 or V_2 or V_H/V_L) has specificity for a serum carrier protein, a circulating immunoglobulin molecule, or CD35/CR1, for example for providing an extended half-life to the antibody fragment with specificity for said antigen of interest by binding to said serum carrier protein, circulating immunoglobulin molecule or CD35/CR1.

As used herein, "serum carrier proteins" include thyroxine-binding protein, transthyretin, α1-acid glycoprotein, transferrin, fibrinogen and albumin, or a fragment of any thereof.

As used herein, a "circulating immunoglobulin molecule" includes IgG1, IgG2, IgG3, IgG4, sIgA, IgM and IgD, or a fragment of any thereof.

CD35/CR1 is a protein present on red blood cells which have a half-life of 36 days (normal range of 28 to 47 days; Lanaro *et al.,* 1971, Cancer, 28(3):658-661).

In one embodiment, the antigen of interest for which V_H/V_L has specificity is a serum carrier protein, such as a human serum carrier, such as human serum albumin.

In one embodiment, the antigen of interest for which V_1 has specificity is a serum carrier protein, such as a human serum carrier, such as human serum albumin.

In one embodiment, the antigen of interest for which V_2 has specificity is a serum carrier protein, such as a human serum carrier, such as human serum albumin.

In one embodiment only one of V_H/V_L, V_1 or V_2 has specificity for a serum carrier protein, such as a human serum carrier, such as human serum albumin.

In one embodiment a binding site in the construct of the present disclosure comprises 6 CDRs, for example SEQ ID NO: 71 for CDRH1, SEQ ID NO: 72 for CDRH2, SEQ ID NO: 73 for CDRH3, SEQ ID NO: 74 for CDRL1, SEQ ID NO: 75 for CDRL2 and SEQ ID NO: 76 for CDRL3.

In one embodiment the said 6 CDRs SEQ ID NO: 71 to 76 are in the position V_H/V_L in the constructs of the present disclosure. In one embodiment the said 6 CDRs SEQ ID NO: 71 to 76 are in the position V_1 in the constructs of the present disclosure. In one embodiment the said 6 CDRs SEQ ID NO: 71 to 76 are in the position V_2 in the constructs of the present disclosure. In one embodiment the said 6 CDRs SEQ ID NO: 71 to 76 are in the position V_1 and V_2 in the constructs of the present disclosure. In one embodiment the said 6 CDRs SEQ ID NO: 71 to 76 are in the position V_H/V_L and V_1 in the constructs of the present disclosure. In one embodiment the said 6 CDRs SEQ ID NO: 71 to 76 are in the position V_H/V_L and V_2 in the constructs of the present disclosure.

In one embodiment the albumin binding site in a construct of the present disclosure comprises a heavy variable domain selected from SEQ ID NO: 77 and SEQ ID NO: 78 and a light chain variable domain selected from SEQ ID NO: 79 and SEQ ID NO: 80, in particular SEQ ID NO: 77 and 79 or SEQ ID NO: 78 and 80 for the heavy and light chain respectively. In one embodiment these domains are in the position V_H/V_L in the constructs of the present disclosure. In one embodiment these variable domains are in the position V_1. In one embodiment these variable domains are in the position V_2. In one embodiment these variable domains are in the position V_1 and V_2. In one embodiment these variable domains are in the position V_H/V_L and V_1 in the constructs of the present disclosure. In one embodiment these variable domains are in the position V_H/V_L and V_2 in the constructs of the present disclosure. When the variable domains are in two locations in the constructs of the present disclosure the same pair of variable domains may be in each location or two different pairs of variable domains may be employed.

In one embodiment the multi-specific antibody molecules of the present disclosure are processed to provide improved affinity for a target antigen or antigens. Such variants can be obtained by a number of affinity maturation protocols including mutating the CDRs (Yang *et al* J. Mol. Biol., 254, 392-403, 1995), chain shuffling (Marks et al., Bio/Technology, 10, 779-783, 1992), use of mutator strains of E. coli (Low et al., J. Mol. Biol., 250, 359-368, 1996), DNA shuffling (Patten et al., Curr. Opin. Biotechnol., 8, 724-733, 1997), phage display (Thompson et al., J. Mol. Biol., 256, 77-88, 1996) and sexual PCR (Crameri *et al* Nature, 391, 288-291, 1998). Vaughan *et al* (*supra*) discusses these methods of affinity maturation.

Improved affinity as employed herein in this context refers to an improvement over the starting molecule.

If desired a multispecific antibody construct for use in the present disclosure may be conjugated to one or more effector molecule(s). It will be appreciated that the effector molecule may comprise a single effector molecule or two or more such molecules so linked as to form a single moiety that can be attached to the antibodies of the present invention. Where it is desired to obtain an antibody fragment linked to an effector molecule, this may be prepared by standard chemical or recombinant DNA procedures in which the antibody fragment is linked either directly or via a coupling agent to the effector molecule. Techniques for conjugating such effector molecules to antibodies are well known in the art (see, Hellstrom *et al* Controlled Drug Delivery, 2nd Ed., Robinson *et al* eds., 1987, pp. 623-53; Thorpe *et al* 1982, Immunol. Rev., 62:119-58 and Dubowchik *et al* 1999, Pharmacology and Therapeutics, 83, 67-123). Particular chemical procedures include, for example, those described in WO93/06231, WO92/22583, WO89/00195, WO89/01476 and WO03031581. Alternatively, where the effector molecule is a protein or polypeptide the linkage may be achieved using recombinant DNA procedures, for example as described in WO86/01533 and EP0392745.

The term "effector molecule" as used herein includes, for example, biologically active proteins, for example enzymes, other antibody or antibody fragments, synthetic or naturally occurring polymers, nucleic acids and fragments thereof e.g. DNA, RNA and fragments thereof, radionuclides, particularly radioiodide, radioisotopes, chelated metals, nanoparticles and reporter groups such as fluorescent compounds or compounds which may be detected by NMR or ESR spectroscopy.

Other effector molecules may include chelated radionuclides such as 111In and 90Y, Lu177, Bismuth213, Californium252, Iridium192 and Tungsten188/Rhenium188; or drugs such as but not limited to, alkylphosphocholines, topoisomerase I inhibitors, taxoids and suramin.

Other effector molecules include proteins, peptides and enzymes. Enzymes of interest include, but are not limited to, proteolytic enzymes, hydrolases, lyases, isomerases, transferases. Proteins, polypeptides and peptides of interest include, but are not limited to, immunoglobulins, toxins such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin, a protein such as insulin, α-interferon, β-interferon, nerve growth factor, platelet derived growth factor or tissue plasminogen activator, a thrombotic agent or an anti-angiogenic agent, e.g. angiostatin or endostatin, or, a biological response modifier such as a lymphokine, interleukin-1 (IL-1), interleukin-2 (IL-2), granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), nerve growth factor (NGF) or other growth factor and immunoglobulins.

Other effector molecules may include detectable substances useful for example in diagnosis. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive nuclides, positron emitting metals (for use in positron emission tomography), and nonradioactive paramagnetic metal ions. See generally US4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics.

Suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; suitable prosthetic groups include streptavidin, avidin and biotin; suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride and phycoerythrin; suitable luminescent materials include luminol; suitable bioluminescent materials include luciferase, luciferin, and aequorin; and suitable radioactive nuclides include 125I, 131I, 111In and 99Tc.

In another embodiment the effector molecule may increase the half-life of the antibody *in vivo*, and/or reduce immunogenicity of the antibody and/or enhance the delivery of an antibody across an epithelial barrier to the immune system. Examples of suitable effector molecules of this type include polymers, albumin, albumin binding proteins or albumin binding compounds such as those described in WO05/117984.

Where the effector molecule is a polymer it may, in general, be a synthetic or a naturally occurring polymer, for example an optionally substituted straight or branched chain polyalkylene, polyalkenylene or polyoxyalkylene polymer or a branched or unbranched polysaccharide, e.g. a homo- or hetero- polysaccharide.

Specific optional substituents which may be present on the above-mentioned synthetic polymers include one or more hydroxy, methyl or methoxy groups.

Specific examples of synthetic polymers include optionally substituted straight or branched chain poly(ethyleneglycol), poly(propyleneglycol) poly(vinylalcohol) or derivatives thereof, especially optionally substituted poly(ethyleneglycol) such as methoxypoly(ethyleneglycol) or derivatives thereof.

Specific naturally occurring polymers include lactose, amylose, dextran, glycogen or derivatives thereof.

"Derivatives" as used herein is intended to include reactive derivatives, for example thiol-selective reactive groups such as maleimides and the like. The reactive group may be linked directly or through a linker segment to the polymer. It will be appreciated that the residue of such a group will in some instances form part of the product as the linking group between the antibody fragment and the polymer.

The size of the polymer may be varied as desired, but will generally be in an average molecular weight range from 500Da to 50000Da, for example from 5000 to 40000Da such as from 20000 to 40000Da. The polymer size may in particular be selected on the basis of the intended use of the product for example ability to localize to certain tissues such as tumors or extend circulating half-life (for review see Chapman, 2002, Advanced Drug Delivery Reviews, 54, 531-545). Thus, for example, where the product is intended to leave the circulation and penetrate tissue, for example for use in the treatment of a tumour, it may be advantageous to use a small molecular weight polymer, for example with a molecular weight of around 5000Da. For applications where the product remains in the circulation, it may be advantageous to use a higher molecular weight polymer, for example having a molecular weight in the range from 20000Da to 40000Da.

Suitable polymers include a polyalkylene polymer, such as a poly(ethyleneglycol) or, especially, a methoxypoly(ethyleneglycol) or a derivative thereof, and especially with a molecular weight in the range from about 15000Da to about 40000Da.

In one embodiment antibodies for use in the present disclosure are attached to poly(ethyleneglycol) (PEG) moieties. In one particular example the antibody is an antibody fragment and the PEG molecules may be attached through any available amino acid side-chain or terminal amino acid functional group located in the antibody fragment, for example any free amino, imino, thiol, hydroxyl or carboxyl group. Such amino acids may occur naturally in the antibody fragment or may be engineered into the fragment using recombinant DNA methods (see for example US5,219,996; US 5,667,425; WO98/25971, WO2008/038024). In one embodiment the antibody molecule of the present invention is a modified Fab fragment wherein the modification is the addition to the C-terminal end of its heavy chain one or more amino acids to allow the attachment of an effector molecule. Suitably, the additional amino acids form a modified hinge region containing one or more cysteine residues to which the effector molecule may be attached. Multiple sites can be used to attach two or more PEG molecules.

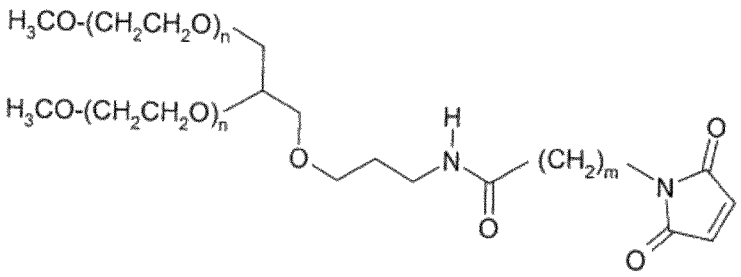
Suitably PEG molecules are covalently linked through a thiol group of at least one cysteine residue located in the antibody fragment. Each polymer molecule attached to the modified antibody fragment may be covalently linked to the sulphur atom of a cysteine residue located in the fragment. The covalent linkage will generally be a disulphide bond or, in particular, a sulphur-carbon bond. Where a thiol group is used as the point of attachment appropriately activated effector molecules, for example thiol selective derivatives such as maleimides and cysteine derivatives may be used. An activated polymer may be used as the starting material in the preparation of polymer-modified antibody fragments as described above. The activated polymer may be any polymer containing a thiol reactive group such as an α-halocarboxylic acid or ester, e.g. iodoacetamide, an imide, e.g. maleimide, a vinyl sulphone or a disulphide. Such starting materials may be obtained commercially (for example from Nektar, formerly Shearwater Polymers Inc., Huntsville, AL, USA) or may be prepared from commercially available starting materials using conventional chemical procedures. Particular PEG molecules include 20K methoxy-PEG-amine (obtainable from Nektar, formerly Shearwater; Rapp Polymere; and SunBio) and M-PEG-SPA (obtainable from Nektar, formerly Shearwater).

In one embodiment, a $F(ab')_2$, Fab or Fab' in the molecule is PEGylated, i.e. has PEG (poly(ethyleneglycol)) covalently attached thereto, e.g. according to the method disclosed in EP 0948544 or EP1090037 [see also "Poly(ethyleneglycol) Chemistry, Biotechnical and Biomedical Applications", 1992, J. Milton Harris (ed), Plenum Press, New York, "Poly(ethyleneglycol) Chemistry and Biological Applications", 1997, J. Milton Harris and S. Zalipsky (eds), American Chemical Society, Washington DC and "Bioconjugation Protein Coupling Techniques for the Biomedical Sciences", 1998, M. Aslam and A. Dent, Grove Publishers, New York; Chapman, A. 2002, Advanced Drug Delivery Reviews 2002, 54:531-545]. In one embodiment PEG is attached to a cysteine in the hinge region. In one example, a PEG modified Fab fragment has a maleimide

group covalently linked to a single thiol group in a modified hinge region. A lysine residue may be covalently linked to the maleimide group and to each of the amine groups on the lysine residue may be attached a methoxypoly(ethyleneglycol) polymer having a molecular weight of approximately 20,000Da. The total molecular weight of the PEG attached to the Fab fragment may therefore be approximately 40,000Da.

Particular PEG molecules include 2-[3-(N-maleimido)propionamido]ethyl amide of N,N'-bis(methoxypoly(ethylene glycol) MW 20,000) modified lysine, also known as PEG2MAL40K (obtainable from Nektar, formerly Shearwater).

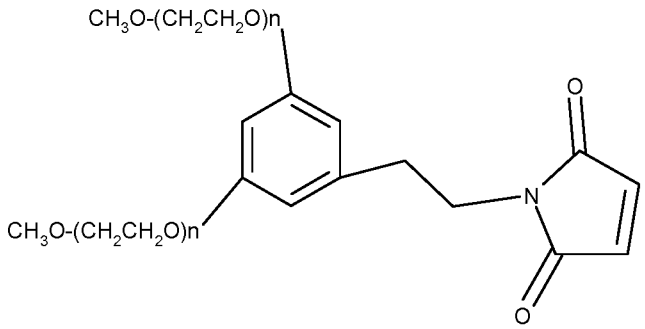
Alternative sources of PEG linkers include NOF who supply GL2-400MA2 (wherein m in the structure below is 5) and GL2-400MA (where m is 2) and n is approximately 450:



m is 2 or 5

That is to say each PEG is about 20,000Da.

Further alternative PEG effector molecules of the following type:



are available from Dr Reddy, NOF and Jenkem.

In one embodiment there is provided an antibody molecule which is PEGylated (for example with a PEG described herein), attached through a cysteine amino acid residue at or about amino acid 226 in the chain, for example amino acid 226 of the heavy chain (by sequential numbering).

In one embodiment there is provided a polynucleotide sequence encoding a molecule of the present disclosure, such as a DNA sequence.

In one embodiment there is provided a polynucleotide sequence encoding one or more, such as two or more, or three or more polypeptide components of a molecule of the present disclosure, for example:

a) a polypeptide chain of formula (**I**):

$$\mathbf{V_H\text{-}CH_1\text{-}X\text{-}V_1;}\ \text{and}$$

b) a polypeptide chain of formula (**II**):

$$\mathbf{V_L\text{-}C_L\text{-}Y\text{-}V_2;}$$

wherein:

V_H represents a heavy chain variable domain;

CH_1 represents a domain of a heavy chain constant region, for example domain 1 thereof;

X represents a bond or linker;

Y represents a bond or linker;

V_1 represents a dsFv, a sdAb, a scFv or a dsscFv;

V_L represents a light chain variable domain;

C_L represents a domain from a light chain constant region, such as Ckappa;

V_2 represents dsFv, a sdAb, a scFV or a dsscFv;

wherein at least one of V_1 or V_2 is a dsFv or dsscFv.

In one embodiment the polynucleotide, such as the DNA is comprised in a vector.

The skilled person will appreciate that when V_1 and/or V_2 represents a dsFv, the multi-specific antibody will comprise a third polypeptide encoding the corresponding free V_H or V_L domain which is not attached to X or Y. Accordingly the multispecific protein of the present invention may be encoded by one or more, two or more or three or more polynucleotides and these may be incorporated into one or more vectors.

General methods by which the vectors may be constructed, transfection methods and culture methods are well known to those skilled in the art. In this respect, reference is made to "Current Protocols in Molecular Biology", 1999, F. M. Ausubel (ed), Wiley Interscience, New York and the Maniatis Manual produced by Cold Spring Harbor Publishing.

Also provided is a host cell comprising one or more cloning or expression vectors comprising one or more DNA sequences encoding a multispecific protein of the present invention. Any suitable host cell/vector system may be used for expression of the DNA sequences encoding the antibody molecule of the present invention. Bacterial, for example *E. coli*, and other microbial systems may be used or eukaryotic, for example mammalian, host cell expression systems may also be used. Suitable mammalian host cells include CHO, myeloma, NSO myeloma cells and SP2 cells, COS cells or hybridoma cells.

The present disclosure also provides a process for the production of a multispecific protein according to the present disclosure comprising culturing a host cell containing a vector of the present invention under conditions suitable for leading to expression of protein from DNA encoding the multispecific protein of the present invention, and isolating the multispecific protein.

For production of products comprising both heavy and light chains, the cell line may be transfected with two vectors, a first vector encoding a light chain polypeptide and a second vector encoding a heavy chain polypeptide. Alternatively, a single vector may be used, the vector including sequences encoding light chain and heavy chain polypeptides. In one example the cell line may be transfected with two vectors, each encoding a polypeptide chain of an antibody molecule of the present invention. Where V_1 and/or V_2 are a dsFv the cell line may be transfected with three vectors, each encoding a polypeptide chain of a multispecific protein of the invention.

In one embodiment the cell line is transfected with two vectors each one encoding a different polypeptide selected from:

a) a polypeptide chain of formula (**I**):

$$\mathbf{V_H\text{-}CH_1\text{-}X\text{-}V_1;}$$

b) a polypeptide chain of formula (**II**):

$$\mathbf{V_L\text{-}C_L\text{-}Y\text{-}V_2;}$$

wherein:

V_H represents a heavy chain variable domain;

CH_1 represents a domain of a heavy chain constant region, for example domain 1 thereof;

X represents a bond or linker;

Y represents a bond or linker;

V_1 represents a dsFv, a sdAb, a scFv or a dsscFv;

V_L represents a light chain variable domain;

C_L represents domain from a light chain constant region, such as Ckappa;

V_2 represents dsFv, a sdAb, a scFV or a dsscFv;

wherein at least one of V_1 or V_2 is a dsFv or dsscFv.

In one embodiment when V_1 is a dsFv and the V_H domain of V_1 is attached to X, the cell line may be transfected with a third vector which encodes the V_L domain of V_1.

In one embodiment when V_1 is a dsFv and the V_L domain of V_1 is attached to X, the cell line may be transfected with a third vector which encodes the V_H domain of V_1.

In one embodiment when V_2 is a dsFv and the V_H domain of V_2 is attached to Y, the cell line may be transfected with a third vector which encodes the V_L domain of V_2.

In one embodiment when V_2 is a dsFv and the V_L domain of V_2 is attached to Y, the cell line may be transfected with a third vector which encodes the V_H domain of V_2.

In one embodiment when both V_1 and V_2 are a dsFv and the V_L domain of V_2 is attached to Y and the V_L domain of V_1 is attached to X, the cell line may be transfected with a third vector which encodes the common V_H domain of both V_1 and V_2.

In one embodiment when both V_1 and V_2 are a dsFv and the V_H domain of V_2 is attached to Y and the V_H domain of V_1 is attached to X, the cell line may be transfected with a third vector which encodes the common V_L domain of both V_1 and V_2.

It will be appreciated that the ratio of each vector transfected into the host cell may be varied in order to optimise expression of the multi-specific antibody product. In one embodiment where two vectors are used the ratio of vectors may be 1:1. In one embodiment where three vectors are used the ratio of vectors may be 1:1:1. It will be appreciated that the skilled person is able to find an optimal ratio by routine testing of protein expression levels following transfection. Alternatively or in addition, the levels of expression of each polypeptide chain of the multi-specific construct from each vector may be controlled by using the same or different promoters.

It will be appreciated that two or more or where present, three of the polypeptide components may be encoded by a polynucleotide in a single vector. It will also be appreciated that where two or more, in particular three or more, of the polypeptide components are encoded by a polynucleotide in a single vector the relative expression of each polypeptide component can be varied by utilising different promoters for each polynucleotide encoding a polypeptide component of the present disclosure.

In one embodiment the vector comprises a single polynucleotide sequence encoding two or where present, three, polypeptide chains of the multispecific antibody molecule of the present invention under the control of a single promoter.

In one embodiment the vector comprises a single polynucleotide sequence encoding two, or where present, three, polypeptide chains of the multispecific antibody molecule of the present disclosure wherein each polynucleotide sequence encoding each polypeptide chain is under the control of a different promoter.

The multispecific proteins according to the present disclosure are expressed at good levels from host cells. Thus the properties of the antibodies and/or fragments appear to be optimised and conducive to commercial processing.

Advantageously, the multi-specific antibody molecules of the present disclosure minimise the amount of aggregation seen after purification and maximise the amount of monomer in the formulations of the construct at pharmaceutical concentrations, for example the monomer may be present as 50%, 60%, 70% or 75% or more, such as 80 or 90% or more such as 91, 92, 93, 94, 95, 96, 97, 98 or 99% or more of the total protein. In one example, a purified sample of a multi-specific antibody molecule of the present disclosure remains greater than 98% or 99% monomeric after 28 days storage at 4^0C. In one example, a purified sample of a multi-specific antibody molecule of the present disclosure at 5mg/ml in phosphate buffered saline (PBS) remains greater than 98% monomeric after 28 days storage at 4^0C.

The antibody molecules of the present disclosure and compositions comprising the same are useful in the treatment, for example in the treatment and/or prophylaxis of a pathological condition.

The present disclosure also provides a pharmaceutical or diagnostic composition comprising an antibody molecule of the present disclosure in combination with one or more of a pharmaceutically acceptable excipient, diluent or carrier. Accordingly, provided is the use of an antibody of the present disclosure for use in treatment and for the manufacture of a medicament, in particular for an indication disclosed herein.

The composition will usually be supplied as part of a sterile, pharmaceutical composition that will normally include a pharmaceutically acceptable carrier. A pharmaceutical composition of the present disclosure may additionally comprise a pharmaceutically-acceptable adjuvant.

The present disclosure also provides a process for preparation of a pharmaceutical or diagnostic composition comprising adding and mixing the antibody molecule of the present disclosure together with one or more of a pharmaceutically acceptable excipient, diluent or carrier.

The antibody molecule may be the sole active ingredient in the pharmaceutical or diagnostic composition or may be accompanied by other active ingredients including other antibody ingredients, for example anti- IL-1β, anti-T cell, anti-IFNγ or anti-LPS antibodies, or non-antibody ingredients such as xanthines. Other suitable active ingredients include antibodies capable of inducing tolerance, for example, anti-CD3 or anti-CD4 antibodies.

In a further embodiment the antibody, fragment or composition according to the disclosure is employed in combination with a further pharmaceutically active agent.

The pharmaceutical compositions suitably comprise a therapeutically effective amount of the antibody molecule of the invention. The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent needed to treat, ameliorate or prevent a targeted disease or condition, or to exhibit a detectable therapeutic or preventative effect. For any antibody, the therapeutically effective amount can be estimated initially either in cell culture assays or in animal models, usually in rodents, rabbits, dogs, pigs or primates. The animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

The precise therapeutically effective amount for a human subject will depend upon the severity of the disease state, the general health of the subject, the age, weight and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities and tolerance/response to therapy. This amount can be determined by routine experimentation and is within the judgement of the clinician. Generally, a therapeutically effective amount will be from 0.01 mg/kg to 50 mg/kg, for example 0.1 mg/kg to 20 mg/kg. Alternatively, the dose may be 1 to 500mg per day such as 10 to 100, 200, 300 or 400mg per day. Pharmaceutical compositions may be conveniently presented in unit dose forms containing a predetermined amount of an active agent of the invention.

Compositions may be administered individually to a patient or may be administered in combination (*e.g.* simultaneously, sequentially or separately) with other agents, drugs or hormones.

The dose at which the antibody molecule of the present disclosure is administered depends on the nature of the condition to be treated, the extent of the inflammation present and on whether the antibody molecule is being used prophylactically or to treat an existing condition.

The frequency of dose will depend on the half-life of the antibody molecule and the duration of its effect. If the antibody molecule has a short half-life (e.g. 2 to 10 hours) it may be necessary to give one or more doses per day. Alternatively, if the antibody molecule has a long half-life (e.g. 2

to 15 days) it may only be necessary to give a dosage once per day, once per week or even once every 1 or 2 months.

The pharmaceutically acceptable carrier should not itself induce the production of antibodies harmful to the individual receiving the composition and should not be toxic. Suitable carriers may be large, slowly metabolised macromolecules such as proteins, polypeptides, liposomes, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers and inactive virus particles.

Pharmaceutically acceptable salts can be used, for example mineral acid salts, such as hydrochlorides, hydrobromides, phosphates and sulphates, or salts of organic acids, such as acetates, propionates, malonates and benzoates.

Pharmaceutically acceptable carriers in therapeutic compositions may additionally contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents or pH buffering substances, may be present in such compositions. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries and suspensions, for ingestion by the patient.

Suitable forms for administration include forms suitable for parenteral administration, e.g. by injection or infusion, for example by bolus injection or continuous infusion. Where the product is for injection or infusion, it may take the form of a suspension, solution or emulsion in an oily or aqueous vehicle and it may contain formulatory agents, such as suspending, preservative, stabilising and/or dispersing agents. Alternatively, the antibody molecule may be in dry form, for reconstitution before use with an appropriate sterile liquid.

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals. However, in one or more embodiments the compositions are adapted for administration to human subjects.

In one embodiment, in formulations according to the present disclosure, the pH of the final formulation is not similar to the value of the isoelectric point of the antibody or fragment, for if the pH of the formulation is 7 then a pI of from 8-9 or above may be appropriate. Whilst not wishing to be bound by theory it is thought that this may ultimately provide a final formulation with improved stability, for example the antibody or fragment remains in solution.

The pharmaceutical compositions of this disclosure may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, transcutaneous (for example, see WO98/20734), subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, intravaginal or rectal routes. Hyposprays may also be used to administer the pharmaceutical compositions of the invention. Typically, the therapeutic compositions may be prepared as injectables, either as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Preferably the antibody molecules of the present invention are administered subcutaneously, by inhalation or topically.

Direct delivery of the compositions will generally be accomplished by injection, subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a specific tissue of interest. Dosage treatment may be a single dose schedule or a multiple dose schedule.

It will be appreciated that the active ingredient in the composition will be an antibody molecule. As such, it will be susceptible to degradation in the gastrointestinal tract. Thus, if the composition is to be administered by a route using the gastrointestinal tract, the composition will need to contain agents which protect the antibody from degradation but which release the antibody once it has been absorbed from the gastrointestinal tract.

A thorough discussion of pharmaceutically acceptable carriers is available in Remington's Pharmaceutical Sciences (Mack Publishing Company, N.J. 1991).

In one embodiment the formulation is provided as a formulation for topical administrations including inhalation.

Suitable inhalable preparations include inhalable powders, metering aerosols containing propellant gases or inhalable solutions free from propellant gases (such as nebulisable solutions or suspensions). Inhalable powders according to the disclosure containing the active substance may consist solely of the abovementioned active substances or of a mixture of the above mentioned active substances with physiologically acceptable excipient.

These inhalable powders may include monosaccharides (e.g. glucose or arabinose), disaccharides (e.g. lactose, saccharose, maltose), oligo- and polysaccharides (e.g. dextranes), polyalcohols (e.g. sorbitol, mannitol, xylitol), salts (e.g. sodium chloride, calcium carbonate) or mixtures of these with one another. Mono- or disaccharides are suitably used, the use of lactose or glucose, particularly but not exclusively in the form of their hydrates.

Particles for deposition in the lung require a particle size less than 10 microns, such as 1-9 microns for example from 0.1 to 5 μm, in particular from 1 to 5 μm. The particle size of the active agent (such as the antibody or antibody fragment) is of primary importance.

The propellent gases which can be used to prepare the inhalable aerosols are known in the art. Suitable propellent gases are selected from among hydrocarbons such as n-propane, n-butane or isobutane and halohydrocarbons such as chlorinated and/or fluorinated derivatives of methane, ethane, propane, butane, cyclopropane or cyclobutane. The abovementioned propellent gases may be used on their own or in mixtures thereof.

Particularly suitable propellent gases are halogenated alkane derivatives selected from among TG 11, TG 12, TG 134a and TG227. Of the abovementioned halogenated hydrocarbons, TG134a (1,1,1,2-tetrafluoroethane) and TG227 (1,1,1,2,3,3,3-heptafluoropropane) and mixtures thereof are particularly suitable.

The propellent-gas-containing inhalable aerosols may also contain other ingredients such as cosolvents, stabilisers, surface-active agents (surfactants), antioxidants, lubricants and means for adjusting the pH. All these ingredients are known in the art.

The propellant-gas-containing inhalable aerosols according to the invention may contain up to 5 % by weight of active substance. Aerosols according to the invention contain, for example, 0.002 to 5 % by weight, 0.01 to 3 % by weight, 0.015 to 2 % by weight, 0.1 to 2 % by weight, 0.5 to 2 % by weight or 0.5 to 1 % by weight of active.

Alternatively topical administrations to the lung may also be by administration of a liquid solution or suspension formulation, for example employing a device such as a nebulizer, for example, a nebulizer connected to a compressor (e.g., the Pari LC-Jet Plus(R) nebulizer connected to a Pari Master(R) compressor manufactured by Pari Respiratory Equipment, Inc., Richmond, Va.).

In one embodiment the formulation is provided as discrete ampoules containing a unit dose for delivery by nebulisation.

In one embodiment the antibody is supplied in lyophilised form, for reconstitutions or alternatively as a suspension formulation.

The antibody of the present disclosure can be delivered dispersed in a solvent, e.g., in the form of a solution or a suspension. It can be suspended in an appropriate physiological solution, e.g., physiological saline, a pharmacologically acceptable solvent or a buffered solution. Buffered solutions known in the art may contain 0.05 mg to 0.15 mg disodium edetate, 8.0 mg to 9.0 mg NaCl, 0.15 mg to 0.25 mg polysorbate, 0.25 mg to 0.30 mg anhydrous citric acid, and 0.45 mg to 0.55 mg sodium citrate per 1 ml of water so as to achieve a pH of about 4.0 to 5.0. As mentioned *supra* a suspension can made, for example, from lyophilised antibody.

The therapeutic suspensions or solution formulations can also contain one or more excipients. Excipients are well known in the art and include buffers (e.g., citrate buffer, phosphate buffer, acetate buffer and bicarbonate buffer), amino acids, urea, alcohols, ascorbic acid, phospholipids, proteins (e.g., serum albumin), EDTA, sodium chloride, liposomes, mannitol, sorbitol, and glycerol. Solutions or suspensions can be encapsulated in liposomes or biodegradable microspheres. The formulation will generally be provided in a substantially sterile form employing sterile manufacture processes.

This may include production and sterilization by filtration of the buffered solvent solution used for the formulation, aseptic suspension of the antibody in the sterile buffered solvent solution, and dispensing of the formulation into sterile receptacles by methods familiar to those of ordinary skill in the art.

Nebulisable formulation according to the present disclosure may be provided, for example, as single dose units (e.g., sealed plastic containers or vials) packed in foil envelopes. Each vial contains a unit dose in a volume, e.g., 2 ml, of solvent/solution buffer.

The antibodies of the present disclosure are thought to be suitable for delivery via nebulisation.

It is also envisaged that the antibody of the present invention may be administered by use of gene therapy. In order to achieve this, DNA sequences encoding the heavy and light chains of the

antibody molecule under the control of appropriate DNA components are introduced into a patient such that the antibody chains are expressed from the DNA sequences and assembled *in situ*.

The pathological condition or disorder, may, for example be selected from the group consisting of infections (viral, bacterial, fungal and parasitic), endotoxic shock associated with infection, arthritis such as rheumatoid arthritis, asthma such as severe asthma, chronic obstructive pulmonary disease (COPD), pelvic inflammatory disease, Alzheimer's Disease, inflammatory bowel disease, Crohn's disease, ulcerative colitis, Peyronie's Disease, coeliac disease, gallbladder disease, Pilonidal disease, peritonitis, psoriasis, vasculitis, surgical adhesions, stroke, Type I Diabetes, lyme disease, meningoencephalitis, autoimmune uveitis, immune mediated inflammatory disorders of the central and peripheral nervous system such as multiple sclerosis, lupus (such as systemic lupus erythematosus) and Guillain-Barr syndrome, Atopic dermatitis, autoimmune hepatitis, fibrosing alveolitis, Grave's disease, IgA nephropathy, idiopathic thrombocytopenic purpura, Meniere's disease, pemphigus, primary biliary cirrhosis, sarcoidosis, scleroderma, Wegener's granulomatosis, other autoimmune disorders, pancreatitis, trauma (surgery), graft-versus-host disease, transplant rejection, heart disease including ischaemic diseases such as myocardial infarction as well as atherosclerosis, intravascular coagulation, bone resorption, osteoporosis, osteoarthritis, periodontitis and hypochlorhydia.

The present disclosure also provides a multi-specific antibody molecule according to the present invention for use in the treatment or prophylaxis of pain, particularly pain associated with inflammation.

Thus there is provided a multi-specific antibody according to the present disclosure for use in treatment and methods of treatment employing same.

In one embodiment there is provided a process for purifiying a multi-specific antibody (in particular an antibody or fragment according to the invention).

In one embodiment there is provided a process for purifiying a multi-specific antibody (in particular an antibody or fragment according to the invention) comprising the steps: performing anion exchange chromatography in non-binding mode such that the impurities are retained on the column and the antibody is maintained in the unbound fraction. The step may, for example be performed at a pH about 6-8.

The process may further comprise an initial capture step employing cation exchange chromatography, performed for example at a pH of about 4 to 5.

The process may further comprise of additional chromatography step(s) to ensure product and process related impurities are appropriately resolved from the product stream.

The purification process may also comprise of one or more ultra-filtration steps, such as a concentration and diafiltration step.

Purified form as used *supra* is intended to refer to at least 90% purity, such as 91, 92, 93, 94, 95, 96, 97, 98, 99% w/w or more pure.

Substantially free of endotoxin is generally intended to refer to an endotoxin content of 1 EU per mg antibody product or less such as 0.5 or 0.1 EU per mg product.

Substantially free of host cell protein or DNA is generally intended to refer to host cell protein and/or DNA content 400µg per mg of antibody product or less such as 100µg per mg or less, in particular 20µg per mg, as appropriate.

The antibody molecule of the present invention may also be used in diagnosis, for example in the *in vivo* diagnosis and imaging of disease states.

In one embodiment there is provided a method of selecting a multi-specific protein construct according to the present invention comprising:

a) determining the yield of monomeric multi-specific protein when either V_1 or V_2 is a dsscFv for a given variable region pair
b) determining the yield of monomeric multi-specific protein when whichever of V_1 or V_2 was tested in (a) is a dsFv for the same variable region pair and
c) comparing the yield of monomer obtained in (a) and (b) and selecting the multi-specific protein with the highest monomeric yield.

Typically the "variable region pair" in step (a) and (b) of the method are a V_H and V_L pair. Generally V_H and V_L together form an antigen binding domain, V_1 or V_2. The method therefore allows the V_H and V_L pair to be tested as both a dsscFv and a dsFv in the constructs of the present invention and the most monomeric construct is selected in step (c).

Typically in step (a) and (b) of the method the yield is determined following purification, such as following affinity chromatography. Monomer yield may be determined using any suitable method, such as size exclusion chromatography.

"Comprising" in the context of the present specification is intended to meaning including. Where technically appropriate, embodiments of the invention may be combined. Embodiments are described herein as comprising certain features/elements. The disclosure also extends to separate embodiments consisting or consisting essentially of said features/elements.

Technical references such as patents and applications are incorporated herein by reference. Any embodiments specifically and explicitly recited herein may form the basis of a disclaimer either alone or in combination with one or more further embodiments.

The present disclosure is further described by way of illustration only in the following examples, which refer to the accompanying Figures, in which:

Brief Description of the Figures

Figure 1 shows the Fab-2xdsscFv and Fab-dsscFv-dsFv constructs of the present disclosure.

Figure 2 shows SDS-PAGE analysis of protein G-purified, HEK293-expressed Fab-1xdsscFv,1xscFv and Fab-2xdsscFv proteins.

Figure 3 shows G3000 SE HPLC analysis of protein G-purified, HEK293-expressed Fab-1xdsscFv,1xscFv and Fab-2xdsscFv proteins

Figure 4 SDS-PAGE analysis of purified, HEK293-expressed Fab-2xdsscFv#3 proteins

Figure 5 S200 SE HPLC analysis of purified, HEK293-expressed Fab-2xdsscFv#3 proteins

Figure 6 shows SDS-PAGE analysis of various protein G purified Fab-dsscFv-dsFv constructs of the present disclosure.
(A) Fab-dsscFv-dsscFv samples. **(B)** Fab-dsscFv-dsFv samples

Figure 7 shows G3000 SE HPLC analysis of protein G-purified Fab-dssFv-dsFv constructs of the present disclosure.

Figure 8 shows SDS-PAGE analysis of various constructs according to the present disclosure under reducing conditions.

Figure 9 shows G3000 SE-HPLC time-course analysis of monomeric Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

Figure 10 shows SDS-Page analysis of protein-G purified EXPiHEK expressed Fab-2xscFv and Fab-2xdsscFv formats

EXAMPLES

Antibody fragments to ANTIGEN 1 are labelled #1
Antibody fragments to ANTIGEN 2 are labelled #2
Antibody fragments to ANTIGEN 3 are labelled #3
Antibody fragments to ANTIGEN 4 are labelled #4

EXAMPLE 1: Fab-2xdsscFv

Construction of plasmids for expression in mammalian cells

Plasmids for the expression of Fab#2-(HC)dsscFv#3,(LC)dsscFv#4 and Fab#2-(LC)dsscFv#3,(HC)dsscFv#4 (see Figure 1), were constructed by fusing scFv#3 and scFv#4 to the C-terminus of the Km3 allotype human kappa constant region of the #2 light chain using the flexible linker SGGGGSGGGGS [also referred herein as S, 2xG4S] (SEQ ID NO: 2), or by fusing scFv#3 and scFv#4 to the C-terminus of the, γ1 isotype human gamma-1 CH_1 constant region of the #2 heavy chain using the flexible linker SGGGGTGGGGS [also referred to herein as S, G4T, G4S] (SEQ ID NO: 1). In addition, point mutations were introduced into the DNA sequences at selected residues in the framework region of both vL#3/vL#4 and vH#3/vH#4. The mutations (heavy chain G44C and light chain G100C) were introduced to create an interchain disulphide bond between the heavy and light chains of the Fv#3. The mutations (heavy chain G44C and light chain Q100C) were introduced to create an interchain disulphide bond between the heavy and light chains of the Fv#4.

Gene fragments encoding scFv#4 and dsscFv#4 (vHvL and vLvH orientation) were manufactured chemically and fused to Fab#2 as detailed above to generate:

Plasmid e1: Light#2-(SGGGGSGGGGS [SEQ ID NO: 2])-vL#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO 68])-vH#4;

Plasmid f1: Light#2-(SGGGGSGGGGS [SEQ ID NO: 2])-dsvL#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-dsvH#4;

Plasmid e2: Light#2-(SGGGGSGGGGS [SEQ ID NO: 2])-vH#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-vL#4;

Plasmid f2: Light#2-(SGGGGSGGGGS [SEQ ID NO: 2])-dsvH#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])- dsvL#4;

Plasmid g1 Heavy#2-(SGGGGTGGGGS [SEQ ID NO: 1])-vL#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-vH#4;

Plasmid h1: Heavy#2-(SGGGGTGGGGS [SEQ ID NO: 1])-dsvL#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-dsvH#4;

Plasmid g2: Heavy#2-(SGGGGTGGGGS [SEQ ID NO: 1])-vH#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-vL#4; and

Plasmid h2: Heavy#2-(SGGGGTGGGGS [SEQ ID NO: 1])-dsvH#4-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-dsvL#4.

pND1 plasmid (Fab#2 Heavy-(SGGGGTGGGGS SEQ ID NO: 1)-dsvH#3-(GGGGSGGGGSGGGGSGGGGS SEQ ID NO: 68)-dsvL#3) **[Plasmid i]** was already available. The gene fragment encoding dsHLscFv#3 was excised from pND1 and fused to light chain#2 as detailed above to generate: Light#2-(SGGGGSGGGGS SEQ ID NO: 2)-dsvH#3-(GGGGSGGGGSGGGGSGGGGS SEQ ID NO: 68)-dsvL#3 **[Plasmid j].**

All Fab fusion formats were cloned into mammalian expression vectors under the control of the HCMV-MIE promoter and SV40E polyA sequence.

HEK293 expression of Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

HEK293 cells were transfected with the relevant plasmids using Invitrogen's 293fectin transfection reagent according to the manufacturer's instructions. Plasmids were mixed as shown in Table 4 to express the different constructs:

Table 4

Antibody Construct	**Plasmids used**
Fab#2-(HC)dsHLscFv#3,(LC)HLscFv#4	1. **Plasmid e2** 2. **Plasmid i**
Fab#2-(HC)dsHLscFv#3,(LC)dsHLscFv#4	1. **Plasmid f2** 2. **Plasmid i**
Fab#2-(HC)dsHLscFv#3,(LC)LHscFv#4	1. **Plasmid e1** 2. **Plasmid i**
Fab#2-(HC)dsHLscFv#3,(LC)dsLHscFv#4	1. **Plasmid f1** 2. **Plasmid i**
Fab#2-(LC)dsHLscFv#3,(HC)HLscFv#4	**1. Plasmid g2** **2. Plasmid j**

Fab#2-(LC)dsHLscFv#3,(HC)dsHLscFv#4	**1. Plasmid h2** **2. Plasmid j**
Fab#2-(LC)dsHLscFv#3,(HC)LHscFv#4	**1. Plasmid g1** **2. Plasmid j**
Fab#2-(LC)dsHLscFv#3,(HC)dsLHscFv#4	**1. Plasmid h1** **2. Plasmid j**

The ratio of the plasmids used for the transfections was 1:1. A total of 50µg plasmid DNA was incubated with 125µl 293fectin + 4.25ml Optimem media for 20mins at RT. The mixture was then added to 50ml HEK293 cells in suspension at 1 x 10^6 cells/ml and incubated with shaking at 37°C. Supernatants were harvested on day 10 by centrifugation at 1500g to remove cells and the supernatant was passed through a 0.22µm filter. Expression level was determined by Protein-G HPLC.

Table 5 shows the results of the Protein-G HPLC assay. As can be seen, the levels of expression of all the constructs were comparable to each other, covering a range of 11-23µg/ml. Those denoted with an asterisk (*) were expressed in a separate transfection, therefore the absolute expression levels of LC-scFv#3,HC-scFv#4 cannot be compared with HC-scFv#3,LC-scFv#4.

Table 5

Antibody Construct	**Expression level (µg/ml)**
Fab#2(HC)dsHLscFv#3,(LC)HLscFv#4	23
Fab#2(HC)dsHLscFv#3,(LC)dsHLscFv#4	18
Fab#2(HC)dsHLscFv#3,(LC)LHscFv#4	21
Fab#2(HC)dsHLscFv#3,(LC)dsLHscFv#4	20
Fab#2(LC)dsHLscFv#3,(HC)HLscFv#4	13*
Fab#2(LC)dsHLscFv#3,(HC)dsHLscFv#4	12*
Fab#2(LC)dsHLscFv#3,(HC)LHscFv#4	12*
Fab#2(LC)dsHLscFv#3,(HC)dsLHscFv#4	11*

Protein-G purification of HEK293 expressed Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

The ~50ml HEK293 supernatants were concentrated ~25 fold to ~2ml using 10kDa molecular weight cut off centrifugation concentrators. The concentrated supernatants were applied to a 1ml HiTrap Protein-G FF column (GE Healthcare) equilibrated in 20mM phosphate, 40mM NaCl pH7.4. The column was washed with 20mM phosphate, 40mM NaCl pH7.4 and the bound material was eluted with 0.1M glycine/HCl pH2.7. The elution peak was collected and pH adjusted to ~pH7.0 with 2M Tris/HCl pH8.5. The pH adjusted elutions were concentrated and buffer exchanged into PBS pH7.4 using 10kDa molecular weight cut off centrifugation concentrators.

SDS-PAGE analysis of Protein-G purified, HEK293 expressed Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

Samples (2µg) were diluted with PBS to a volume of 9.75µl to which 3.75µl 4xLDS sample buffer and 1.5µl 100 mM N-ethylmaleimide (non-reduced samples) or 1.5µl 10x NuPAGE reducing agent (reduced samples) was added. The samples were vortexed, incubated at 70ºC for 10 minutes,

cooled and centrifuged at 12500 rpm for 30 seconds. The prepared samples were loaded onto a 4-20% acrylamide Tris/Glycine SDS gel and run for ~100 minutes at 125V, constant voltage. SeeBluePlus2 (Life Technologies) molecular weight ladder was used. The gels were stained with Instant Blue protein stain (Expedeon) and destained with distilled water.

The expected band sizes after reducing and non-reducing SDS-PAGE are indicated in Table 6.

Table 6:

Expected band sizes after SDS-PAGE (kDa) (H=heavy chain, L=light chain, +/- reducing agent)					
	- Red	+ Red		- Red	+ Red
Fab-1xdsscFv, 1x scFv	~100	H~50 L~50	**Fab-2xdsscFv**	~100	H~50 L~50

For all proteins, the non-reducing gel was expected to show a band at ~100kDa, whilst the reducing gels were expected to show a doublet at ~50kDa with equal staining in the both bands.

For all Fab-1xdsscFv-1xscFv and Fab-2xdsscFv proteins, the reducing SDS-PAGE gels showed banding patterns which indicated that the constructs were being expressed correctly in terms of both migration position and staining intensity with a doublet at ~50kDa (Figure 2B,D). The additional uppermost minor band is consistent with non-reduced full-length protein. As expected, disulphide linked multimers are seen on the non-reducing gel (Figure 2A,C), which disappear under reducing conditions (Figure 2B,D). The minor bands at ~50kDa on the non-reducing gel (Figure 2A,C) may be consistent with incomplete ds bond formation between the heavy and light chain in the Fab region.

G3000 SE-HPLC analysis of Protein-G purified, HEK293 expressed Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

10µg purified protein samples (100 µl of 0.1 mg/ml stock diluted in PBS) were injected onto a TSK Gel G3000SWXL, 7.8x300mm, column (Tosoh) 3 days post-purification and developed with an isocratic gradient of 200mM phosphate pH7.0 at 1ml/min. Signal detection was by absorbance at 280nm.

The results are shown in Figure 3. As can be seen from Figure 3, after Protein-G purification, the Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats were 83-89% monomer.

Although all the samples have similar monomer levels in the assay, those samples that contain a scFv lacking the Fv disulphide are in a dynamic equilibrium. This means the % monomer measured in the assay for these samples is dependent on the concentration of the sample, more concentrated samples give higher % monomer and less concentrated samples give lower % monomer. In contrast the samples where both scFv contain a disulphide are stable and are not in dynamic equilibrium. Therefore the % monomer measured in the assay does not change with changes in the sample concentration.

As the monomers and multimers in the Fab-2xdsscFv formats are stable and not in a dymamic equilibrium the samples can be easily further purified to increase the % monomer. The purified monomeric samples will also remain monomeric even when the concentration of the construct in a given formulation is increased, thereby making the constructs very suitable for use in pharmaceutical preparations. In contrast, Fab-2xscFv can after purification as monomer be subject to intermolecular dynamic domain exchange between the vL and vH of the scFv domains. In addition therefore to increased risk of formation of dimer, trimer, higher order structures and aggregate such molecules are difficult to observe since non-aggregated forms can resolve to monomer after dilution steps which are used during analytical methods. Hence, Fab-2xdsscFv provide additional clarity during analysis of pharmaceutical compositions.

CHOS expression of Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

CHOS cells were transfected with the relevant plasmids by electroporation methods at 1L scale. Plasmids were mixed as shown in Table 7 to express the protein. Cultures were grown in CD-CHO medium supplemented with 2 mM GlutaMAX and incubated at 37°C with 8% CO_2 at 140 rpm for 24 h and subsequently incubated for a further 13 days at 32°C. At day 4 post-transfection, sodium butyrate at a final concentration of 3 mM was added to the culture. On day 14 post-transfection, culture supernatants were harvested by centrifugation and 0.22 µm filter sterilized. Expression titres were measured by Protein G HPLC (Table 8).

Table 7:

Antibody Construct	**Plasmids used**
Fab#2-(LC)dsHLscFv#3,(HC)HLscFv#4	**3. Plasmid g2 1. Plasmid j**
Fab#2-(LC)dsHLscFv#3,(HC)dsHLscFv#4	**3. Plasmid h2 1. Plasmid j**
Fab#2-(LC)dsHLscFv#3,(HC)LHscFv#4	**3. Plasmid g1 1. Plasmid j**
Fab#2-(LC)dsHLscFv#3,(HC)dsLHscFv#4	**3. Plasmid h1 1. Plasmid j**

Table 8:

Antibody Construct	**Expression level (µg/ml)**
Fab#2-(LC)dsHLscFv#3,(HC)HLscFv#4	15
Fab#2-(LC)dsHLscFv#3,(HC)dsHLscFv#4	17
Fab#2-(LC)dsHLscFv#3,(HC)LHscFv#4	18
Fab#2-(LC)dsHLscFv#3,(HC)dsLHscFv#4	16

Protein-G purification of CHO expressed Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

The 1L CHO supernatants were concentrated ~25 fold to ~40 ml using a 10kDa molecular weight cut off Amicon stirred cell. The concentrated supernatants were loaded onto an AKTA Express Purification system with a Protein G column and PBS as the running buffer. The bound material was eluted with 0.1 M glycine/HCl pH2.7 and pH adjusted to ~pH7.0 with 2M Tris/HCl pH8.5. The eluted material was then concentrated using 10kDa molecular weight concentrators and the resulting concentrate was loaded onto a Superdex column (GE Healthcare) for gel filtration with PBS as the running buffer. Individual elution peaks were collected and analysed by size exclusion HPLC to determine the monomeric fraction. The final monomeric protein was concentrated to 5 mg/ml in PBS and stored at 4°C.

SDS-PAGE analysis of Protein-G purified, CHOS expressed monomeric fraction of Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

Samples (2 µg) were diluted with PBS to a volume of 9.75µl to which 3.75µl 4xLDS sample buffer and 1.5µl 100 mM N-ethylmaleimide (non-reduced samples) or 1.5µl 10x NuPAGE reducing agent (reduced samples) was added. The samples were vortexed, incubated at 70°C for 10 minutes, cooled and centrifuged at 12500 rpm for 30 seconds. The prepared samples were loaded onto a 4-20% acrylamide Tris/Glycine SDS gel and run for ~100 minutes at 125V, constant voltage. Mark12 (Life Technologies) molecular weight ladder was used. The gels were stained with Instant Blue protein stain (Expedeon) and destained with distilled water.

The expected band sizes after reducing and non-reducing SDS-PAGE are indicated in Table 9.

Table 9:

Expected band sizes after SDS-PAGE (kDa) (H=heavy chain, L=light chain, +/- reducing agent)					
	- Red	+ Red		- Red	+ Red
Fab-1xdsscFv, 1x scFv	~100	H~50 L~50	**Fab-2xdsscFv**	~100	H~50 L~50

For all proteins, the non-reducing gel was expected to show a band at ~100kDa, whilst the reducing gels were expected to show a doublet at ~50kDa with equal staining in the both bands.

For all Fab-1xdsscFv-1xscFv and Fab-2xdsscFv proteins, the reducing SDS-PAGE gels showed banding patterns which indicated that the constructs were monomeric and expressed correctly in terms of both migration position and staining intensity with a doublet at ~50kDa (Figure 8B, D). The additional uppermost minor band is consistent with non-reduced full-length protein (Figure 8B, D). For all proteins, the non-reducing gel showed a band at ~100kDa, indicative of the full-length protein (Figure 8A, a). The minor bands at ~50kDa on the non-reducing gel (Figure 8A, b) may be consistent with incomplete disulphide bond formation between the heavy and light chain in the Fab region.

G3000 SE-HPLC time-course analysis of monomeric Fab-1xdsscFv-1xscFv and Fab-2xdsscFv formats

A 5 mg/ml of purified monomer of the antibody formats was stored at 4°C in PBS and analysed on day 4, day 14 and day 28 after purification. Samples were diluted in PBS to 10 μg and injected onto a TSK Gel G3000SWXL, 7.8x300mm, column (Tosoh) and developed with an isocratic gradient of 200mM phosphate pH7.0 at 1ml/min. Signal detection was by absorbance at 280nm. The results are shown in Figure 9. On day 4 post-purification, analysis of Fab-2xdsscFv indicated that the majority of the protein was monomeric at the start of the experiment (solid lines), and remained monomeric and stable over the time course, with < 1 % defined as multimers (dimers, trimers, higher orders and large aggregates). On the other hand, a higher occurrence of multimerisation was detected for Fab-1xdsscFv-1xscFv which was observed to increase linearly over time (dashed lines). Indeed, the prevalence of multimerisation appeared to be more pronounced with formats containing non-disulphide stabilised scFvs in the V_L/V_H orientation. However, it is clear that formats that contain a scFv lacking the Fv disulphide are in dynamic equilibrium and more prone to multimerisation during storage than scFvs which are disulphide stabilized. Indeed, formats that contain scFvs that are both disulphide stabilized have been shown to remain monomeric even when the concentration of the protein in a given formulation is increased. This makes constructs where both scFvs contain an Fv disulphide ideally suitable for use in pharmaceutical preparations where the risk of forming higher orders of multimers or large aggregates during periods of storage critically needs to be insignificant.

EXAMPLE 2: Fab-2xdsscFv (Bivalent with two of the same dsscFv)

Construction of plasmids for expression in mammalian cells

Plasmids for the expression of Fab#2-(HC)dsscFv#3,(LC)dsscFv#3 (see Figure 4), were constructed by fusing dsscFv#3 to the C-terminus of the Km3 allotype human kappa constant region of the light chain#2 using the flexible linker SGGGGSGGGGS [also referred herein as S, 2xG4S] (SEQ ID NO: 2), or by fusing dsscFv#3 to the C-terminus of the, γ1 isotype human gamma-1 CH_1 constant region of the heavy chain#2 using the flexible linker SGGGGTGGGGS [also referred to herein as S, G4T, G4S] (SEQ ID NO: 1). Point mutations were introduced into the DNA sequences at selected residues in the framework region of both vL#3/vL#1 and vH#3/vH#1. The mutations (heavy chain G44C and light chain G100C) were introduced to create an interchain disulphide bond between the heavy and light chains of the Fv#3.

pND1 plasmid (Fab#2 Heavy-(SGGGGTGGGGS [SEQ ID NO: 1)-dsvH#3-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-dsvL#3) **[Plasmid i]** was already available. The gene fragment encoding dsHLscFv#3 was excised from pND1 and fused to light chain#2 as detailed above to generate: Light#2-(SGGGGSGGGGS [SEQ ID NO: 2])- dsvH#3-(GGGGSGGGGSGGGGSGGGGS [SEQ ID NO: 68])-dsvL#3 **[Plasmid j].**

The Fab fusion formats were cloned into mammalian expression vectors under the control of the HCMV-MIE promoter and SV40E polyA sequence.

HEK293 expression of Fab-2xdsscFv#3

HEK293 cells were transfected with the relevant plasmids using Invitrogen's 293fectin transfection reagent according to the manufacturer's instructions. Plasmids were mixed as shown in Table 10 to express the protein:

Table 10

Antibody Construct	Plasmids used
Fab#2-(HC)dsHLscFv#3,(LC)dsHLscFv#3	1. **Plasmid j** 2. **Plasmid i**

The ratio of the plasmids used for the transfections was 1:1. A total of 50µg plasmid DNA was incubated with 125µl 293fectin + 4.25ml Optimem media for 20mins at RT. The mixture was then added to 50ml HEK293 cells in suspension at 1 x 10^6 cells/ml and incubated with shaking at 37°C. Supernatants were harvested on day 10 by centrifugation at 1500g to remove cells and the supernatant was passed through a 0.22µm filter. Expression level was determined by Protein-G HPLC. Table 11 shows the results of the Protein-G HPLC assay. The level of expression was 20µg/ml.

Table 11

Antibody Construct	Expression level (µg/ml)
Fab#2(HC)dsHLscFv#3,(LC)dsHLscFv#3	20

Purification of HEK293 expressed Fab-2xdsscFv#3

The ~50ml HEK293 supernatants were concentrated ~25 fold to ~2ml using 30kDa molecular weight cut off centrifugation concentrators. The concentrated supernatants were purified and further concentrated and buffer exchanged into PBS pH7.4 using 30kDa molecular weight cut off centrifugation concentrators.

SDS-PAGE analysis of Protein-G purified, HEK293 expressed Fab-2xdsscFv#3

Samples (2µg) were diluted with PBS to a volume of 9.75µl to which 3.75µl 4xLDS sample buffer and 1.5µl 100 mM N-ethylmaleimide (non-reduced samples) or 1.5µl 10x NuPAGE reducing agent (reduced samples) was added. The samples were vortexed, incubated at 70°C for 10 minutes, cooled and centrifuged at 12500 rpm for 30 seconds. The prepared samples were loaded onto a 4-20% acrylamide Tris/Glycine SDS gel and run for ~100 minutes at 125V, constant voltage. SeeBluePlus2 (Life Technologies) molecular weight ladder was used. The gels were stained with Instant Blue protein stain (Expedeon) and destained with distilled water. The expected band sizes after reducing and non-reducing SDS-PAGE are indicated in Table 12.

Table 12:

Expected band sizes after SDS-PAGE (kDa) (H=heavy chain, L=light chain, +/- reducing agent)		
	- Red	+ Red
Fab-2xdsscFv#3	~100	H~50 L~50

The non-reducing gel was expected to show a band at ~100kDa, whilst the reducing gel was expected to show a doublet at ~50kDa with equal staining in both bands.

The reducing SDS-PAGE gels showed banding patterns which indicated that the constructs were being expressed correctly in terms of both migration position and staining intensity with a doublet at ~50kDa (Figure 4B), however some additional minor species were also observed possibly owing to sub-optimal purification scheme as opposed to the standard Protein G-mediated purification method, which is typically used for purification of Fabs. Disulphide linked multimers are seen on the non-reducing gel (Figure 4A), which disappear under reducing conditions (Figure 4B).

S200 SE-HPLC analysis of purified, HEK293 expressed Fab-2xdsscFv#3

10µg purified protein samples (100 µl of 0.1 mg/ml stock diluted in PBS) were injected onto a Superdex 200 10/300 GL Tricorn column (GE Healthcare) 3 days post-purification and developed with an isocratic gradient of PBS pH7.4 at 1ml/min, with continuous detection by absorbance at 280nm. The results are shown in Figure 5. As can be seen from Figure 5, after purification, the Fab-2xdsscFv#3 format was 81% monomer.

EXAMPLE 3: Fab-(HC)dsscFv-(LC)dsFv

Construction of Fab#2-(HC)dsscFv#3-(LC)dsscFv#1 and Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked) plasmids for expression in mammalian cells

The Fab#2 fusion proteins for the expression of Fab#2-(HC)dsscFv#3-(LC)dsscFv#1 and Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked) (see Figure 6), were constructed by fusing either dsscFv#1 (dsvH-4xG4S-dsvL) or dsvL#1 to the C-terminus of the Km3 allotype human kappa constant region of the light chain#2 using the flexible linker SGGGGSGGGGSGGGGS (SEQ ID NO: 69) to generate:

Light#2-(SGGGGSGGGGSGGGGS [SEQ ID NO: 69])-dsscFv#1 **[Plasmid b]** and

Light#2-(SGGGGSGGGGSGGGGS [SEQ ID NO: 69])-dsvL#1 **[Plasmid c]**; and

by fusing HLdsscFv#3 (dsvH-4xG4S-dsvL) to the C-terminus of the, γ1 isotype human gamma-1 CH1 constant region of the heavy chain#2 using the flexible linker SGGGGSGGGGTGGGGS (SEQ ID NO: 70) to generate:

Heavy#2-(SGGGGSGGGGTGGGGS [SEQ ID NO: 70])-dsscFv#3 **[Plasmid a]**.

Point mutations (heavy chain G44C and light chain G100C) were introduced into the DNA sequences at selected residues in the framework region of vL#3, vH#3, vL#1 and vH#1 to create an interchain disulphide bond between the heavy and light chains of the Fv#3 and Fv#1. Heavy and light chain Fab-fusion genes were cloned into mammalian expression vectors under the control of the HCMV-MIE promoter and SV40E polyA sequence. Genes encoding:

Heavy#2-(SGGGGSGGGGTGGGGS [SEQ ID NO: 70])-dsscFv#3 **[Plasmid a]** and

dsvH#1 free domain **[Plasmid d]**

were manufactured chemically and individually cloned into mammalian expression vectors under the control of the HCMV-MIE promoter and SV40E polyA sequence.

The genes encoding dsscFv#1 and dsvL#1 were manufactured chemically and fused to the C-terminal of light chain#2 to create:

Light#2-(SGGGGSGGGGSGGGGS [SEQ ID NO: 69])-dsscFv#1 **[Plasmid b]** and
Light#2-(SGGGGSGGGGSGGGGS [SEQ ID NO: 69])-dsvL#1 **[Plasmid c]**
and the entire constructs were cloned into a mammalian expression vector under the control of the HCMV-MIE promoter and SV40E polyA sequence.

HEK293 expression of:
Fab#2-(HC)dsscFv#3-(LC)dsscFv#1 and
Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked)
HEK293 cells were transfected with the relevant plasmids using Invitrogen's 293fectin transfection reagent according to the manufacturer's instructions. Plasmids were mixed as follows to express the different constructs as shown in Table 13 below:

Table 13

Antibody Construct	**Plasmids used**
Fab#2-(HC)dsscFv#3-(LC)dsscFv#1	1. **Plasmid a** 2. **Plasmid b**
Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked)	1. **Plasmid a** 2. **Plasmid c** 3. **Plasmid d**

For the 2 plasmid combination, the ratio of the plasmids used for the transfections was 1:1, whereas for the 3 plasmid combinations the ratio was 1:1:1. A total of 50µg plasmid DNA was incubated with 125µl 293fectin + 4.25ml Optimem media for 20mins at RT. The mixture was then added to 50ml HEK293 cells in suspension at 1 x 10^6 cells/ml and incubated with shaking at 37°C. Supernatants were harvested on day 10 by centrifugation at 1500g to remove cells and the supernatant was passed through a 0.22µm filter. Expression level was determined by Protein-G HPLC.

The results are shown in Table 14. As can be seen, the levels of expression of both constructs were comparable to each other (16-18µg/ml). There have been reports in the literature that the expression of Fv regions that lack either a linker between the vL and vH or a dimerisation motif to bring the vL and vH together have substantially lower expression levels than linked Fvs. Surprisingly, this is not observed in this data where there was no significant difference observed between the expression level of each type of construct.

Table 14:

Construct	**Expression level (µg/ml)**
Fab#2-(HC)dsscFv#3-(LC)dsscFv#1	18
Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked)	16

Protein-G purification of HEK293 expressed Fab#2-(HC)dsscFv#3-(LC)dsscFv#1 and Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked)

The ~50ml HEK293 supernatants were concentrated ~25 fold to ~2ml using 10kDa molecular weight cut off centrifugation concentrators. The concentrated supernatants were applied to a 1ml HiTrap Protein-G FF column (GE Healthcare) equilibrated in 20mM phosphate, 40mM NaCl

pH7.4. The column was washed with 20mM phosphate, 40mM NaCl pH7.4 and the bound material was eluted with 0.1M glycine/HCl pH2.7. The elution peak was collected and pH adjusted to ~pH7.0 with 2M Tris/HCl pH8.5. The pH adjusted elutions were concentrated and buffer exchanged into PBS pH7.4 using 10kDa molecular weight cut off centrifugation concentrators.

SDS-PAGE analysis of Protein-G purified, HEK293 expressed Fab#2-(HC)dsscFv#3-(LC) dsscFv#1 and Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked)

Samples (2µg) were diluted with PBS to a volume of 9.75µl to which 3.75µl 4xLDS sample buffer and 1.5µl 100 mM N- ethylmaleimide (non-reduced samples) or 1.5µl 10x NuPAGE reducing agent (reduced samples) was added. The samples were vortexed, incubated at 70^{0}C for 10 minutes, cooled and centrifuged at 12500 rpm for 30 seconds. The prepared samples were loaded onto a 4-20% acrylamide Tris/Glycine SDS gel and run for ~100 minutes at 125V, constant voltage. SeeBluePlus2 (Life Technologies) molecular weight ladder was used. The gels were stained with Instant Blue protein stain (Expedeon) and destained with distilled water.

The results are shown in Figure 6. For Fab#2-(HC)dsscFv#3-(LC)dsscFv#1, the non-reducing gel was expected to show a band at ~100kDa, whilst the reducing gel was expected to show a doublet at ~50kDa with roughly equal staining in both bands. For Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked), the non-reducing gel was expected to show a band at ~100kDa, whilst the reducing gel was expected to show 3 bands at ~50, ~36 and ~13kDa with staining roughly in the ratio 3:2:1 upper to lower band.

The reducing SDS-PAGE gels showed banding patterns which indicated that the constructs were being expressed correctly in terms of both migration position and staining intensity. Non-reducing SDS-PAGE gels showed significant banding patterns >200kDa for Fab-2xdsscFv that were consistent with multimerisation (Figure 6A, lane 2) but fewer high molecular weight species were observed in the Fab-dsscFv-dsFv sample (Figure 6B, lane 2).

G3000 SE-HPLC analysis of Protein-G purified, HEK293 expressed, Fab#2-(HC)dsscFv#3-(LC)dsscFv#1 and Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked)

10µg purified protein samples (100 µl of 0.1 mg/ml stock diluted in PBS) were injected onto a TSK Gel G3000SWXL, 7.8x300mm, column (Tosoh) 3 days post-purification and developed with an isocratic gradient of 200mM phosphate pH7.0 at 1ml/min. Signal detection was by absorbance at 280nm.

The results are shown in Figure 7. After Protein-G purification, the Fab#2-(HC)dsscFv#3-(LC)dsFv#1 (LC-vL linked) was 91% monomer, whereas the Fab#2-(HC)dsscFv#3-(LC)dsscFv#1 was 30% monomer.

dsscFv#1 is known to be particularly prone to multimerisation. Given that multimers are physically joined by the dsscFv linker (the vL#1 or vH#1 is paired with vH#1 or vL#1 from a different polypeptide chain), by replacing dsscFv#1 with dsFv#1 (which does not comprise a scFv linker), there was a significant increase in the percentage monomer obtained.

The skilled person will thus appreciate that, depending on the propensity of the dsscFv to multimerise, in some instances it would be advantageous to use a dsFv instead of a dsscFv.

EXAMPLE 4 Biacore Affinity and demonstration of simultaneous binding of antigen targets

The binding affinities and kinetic parameters for the interactions of Fab#2-(HC)dsHLscFv#3 (LC)dsHLscFv#4 were determined by surface plasmon resonance (SPR) conducted on a BIAcore T100 or a BIAcore 3000 using CM5 sensor chips (GE Healthcare Bio-Sciences AB) and HBS-EP (10mM HEPES (pH7.4), 150mM NaCl, 3mM EDTA, 0.05% v/v surfactant P20) running buffer. All experiments were performed at 25°C. The antibody samples were captured to the sensor chip surface using either a human F(ab')$_2$-specific goat Fab (Jackson ImmunoResearch) or an in-house generated anti human CH_1 monoclonal antibody. Covalent immobilisation of the capture antibody was achieved by standard amine coupling chemistry to a level of 6000-7000 response units (RU). Antigen #2, #3 or #4 was titrated separately over the captured antibody. Each assay cycle consisted of firstly capturing the antibody sample using a 1 min injection, before an association phase consisting of a 3 min injection of antigen, after which dissociation was monitored for 10 min. After each cycle, the capture surface was regenerated with 2 x 1 min injections of 40 mM HCl followed by 30s of 5 mM NaOH. The flow rates used were 10 µl min^{-1} for capture, 30 µl min^{-1} for association and dissociation phases, and 10µl min^{-1} for regeneration. Kinetic parameters were determined by simultaneous global-fitting of the resulting sensorgrams to a standard 1:1 binding model using BIAcore T100 Evaluation software v2.0.1 or BIAcore 3000 BIAEvaluation v3.2. The results are shown in Table 15. The antibody showed expected affinities within the pM – nM range for the antigens tested.

Table 15:

Analyte	ka(1/Ms)	kd(1/s)	KD(M)	KD(pM)
Antigen #2	5.06E+06	3.80E-05	7.51E-12	7.51
Antigen #3	5.54E+06	6.43E-05	1.16E-11	11.6
Antigen #4	7.75E+04	1.35E-04	1.74E-09	1740

The potential for of Fab#2-(HC)dsHLscFv#3 (LC)dsHLscFv#4 to bind simultaneously to all 3 antigens was assessed by capturing the tri-specific antibody to the sensor chip via immobilised anti-human IgG- F(ab')$_2$. Each antigen or a mixed solution of antigen #2, #3 and #4 was titrated over the captured antibody in 3 min injections. The binding responses observed for the independent injections and combined responses are shown in Table 16. The binding response for the combined antigen#2/#3/#4 solution was equivalent to the sum of the responses of the independent injections. This confirms that of Fab#2-(HC)dsHLscFv#3 (LC)dsHLscFv#4 is capable of simultaneous binding to all 3 antigens tested.

Table 16:

Analyte	Binding (RU)
Antigen #2	58

Antigen #3	38
Antigen #4	47
Antigens #2 + #3 + #4	**130 (143)**

Example 5 Comparison of monomeric yield between Fab-2xscFv and Fab-2xdsscFv formats

EXpiHEK cells were transfected with the relevant plasmids by electroporation methods at 50 ml scale. Plasmids were mixed as shown in Table 17 to express the protein. Cultures were grown in ExpiHEK expression medium and incubated at 37°C with 8% CO_2 at 120 rpm for 16-18h, prior to addition of enhancer 1 and 2. The cultures were subsequently incubated for a further 4 days at 37°C. Culture supernatants were harvested by centrifugation and 0.22 μm filter sterilized. Expression titres were measured by Protein G HPLC (Table 18).

Table 17:

Antibody Construct	**Plasmids used**
Fab#4-(LC)HLscFv#5,(HC)HLscFv#6	**1. Plasmid k1** **2. Plasmid l1**
Fab#4-(LC)dsHLscFv#5,(HC)dsHLscFv#6	**1. Plasmid k2** **2. Plasmid l2**
Fab#4-(LC)HLscFv#7,(HC)HLscFv#8	**1. Plasmid m1** **2. Plasmid n1**
Fab#4-(LC)dsHLscFv#7,(HC)dsHLscFv#8	**1. Plasmid m2** **2. Plasmid n2**
Fab#4-(LC) HLscFv#9,(HC)LHscFv#10	**1. Plasmid o1** **2. Plasmid p1**
Fab#4-(LC)dsHLscFv#9,(HC)dsLHscFv#10	**1. Plasmid o2** **2. Plasmid p2**
Fab#4-(LC)HLscFv#7,(HC)LHscFv#10	**4. Plasmid q1** **5. Plasmid r1**
Fab#4-(LC)dsHLscFv#7,(HC)dsLHscFv#10	**1. Plasmid q2** **2. Plasmid r2**

Table 18:

Antibody Construct	**Expression (μg/ml)**
Fab#4-(LC)HLscFv#5,(HC)HLscFv#6	62
Fab#4-(LC)dsHLscFv#5,(HC)dsHLscFv#6	31
Fab#4-(LC)HLscFv#7,(HC)HLscFv#8	195
Fab#4-(LC)dsHLscFv#7,(HC)dsHLscFv#8	34
Fab#4-(LC) HLscFv#9,(HC)LHscFv#10	298

Fab#4-(LC)dsHLscFv#9,(HC)dsLHscFv#10	55
Fab#4-(LC)HLscFv#7,(HC)LHscFv#10	226
Fab#4-(LC)dsHLscFv#7,(HC)dsLHscFv#10	58

Protein-G purification of EXPiHEK expressed Fab-2xscFvFv and Fab-2xdsscFv formats

Supernatants were concentrated ~25 fold to ~2 ml using a 10kDa molecular weight cut off concentrators. The concentrated supernatants were purified by protein G HPLC using phosphate buffer pH7.4. The bound material was eluted with 0.1 M glycine/HCl pH2.7 and pH adjusted to ~pH7.0 with 2M Tris/HCl pH8.5. The eluted material was concentrated using 10kDa molecular weight concentrators and buffer exchanged into PBS. The purified protein was concentrated to ~4-5 mg/ml in PBS and stored at 4°C.

SDS-PAGE analysis of Protein-G purified, EXPiHEK expressed Fab-2xscFv and Fab-2xdsscFv formats

Samples (2 µg) were diluted with PBS to a volume of 9.75µl to which 3.75µl 4xLDS sample buffer and 1.5µl 100 mM N-ethylmaleimide (non-reduced samples) or 1.5µl 10x NuPAGE reducing agent (reduced samples) was added. The samples were vortexed, incubated at 70°C for 10 minutes, cooled and centrifuged at 12500 rpm for 30 seconds. The prepared samples were loaded onto a 4-20% acrylamide Tris/Glycine SDS gel and run for ~100 minutes at 125V, constant voltage. Seeblue2 (Life Technologies) molecular weight ladder was used. The gels were stained with Instant Blue protein stain (Expedeon) and destained with distilled water.

The expected band sizes after reducing and non-reducing SDS-PAGE are indicated in Table 19.

Table 19:

Expected band sizes after SDS-PAGE (kDa) (H=heavy chain, L=light chain, +/- reducing agent)					
	- Red	+ Red		- Red	+ Red
Fab-2xscFv	~100	H~50 L~50	**Fab-2xdsscFv**	~100	H~50 L~50

For all proteins, the non-reducing gel was expected to show a band at ~100kDa, whilst the reducing gels were expected to show a doublet at ~50kDa with equal staining in the both bands.

For all Fab-2xscFv and Fab-2xdsscFv proteins, the reducing SDS-PAGE gels showed banding patterns which indicated that the constructs expressed correctly in terms of both migration position and staining intensity with a doublet at ~50kDa (Figure 10B,a). The additional uppermost minor band is consistent with non-reduced full-length protein (Figure 10B,b). For all proteins, the non-

reducing gel showed a band at ~130 kDa, indicative of the full-length protein (Figure 10A,a). The bands at ~50kDa on the non-reducing gel (Figure 10A, b) may be consistent with incomplete disulphide bond formation between the heavy and light chain in the Fab region.

G3000 SE-HPLC analysis of Fab-2xscFv and Fab-2xdsscFv formats

Purified antibody proteins at ~ 5 mg/ml were stored at 4°C in PBS for 24 h prior to analysis. Samples equivalent to a concentration of 25 µg were injected onto a TSK Gel G3000SWXL, 7.8x300mm, column (Tosoh) and developed with an isocratic gradient of 200mM phosphate pH7.0 at 1ml/min. Signal detection was by absorbance at 280nm. The results are shown in Table 20. Analysis indicated that all Fab-2xdsscFv proteins were > 90 % monomeric. On the other hand, a higher occurrence of multimerisation was detected for all Fab-2xscFv. It is clear that formats that contain scFvs with an Fv disulphide are more monomeric compared to scFvs lacking the Fv disulphide. This indicates a preference for using formats with scFvs that contain Fv disulphides in terms of selecting therapeutic molecules with stable qualities and also attributes that would be advantageous in a manufacturing process.

Table 20:

Format	% monomer
Fab#4-(LC)HLscFv#5,(HC)HLscFv#6	51.3
Fab#4-(LC)dsHLscFv#5,(HC)dsHLscFv#6	96.8
Fab#4-(LC)HLscFv#7,(HC)HLscFv#8	80.8
Fab#4-(LC)dsHLscFv#7,(HC)dsHLscFv#8	98.8
Fab#4-(LC) HLscFv#9,(HC)LHscFv#10	84.9
Fab#4-(LC)dsHLscFv#9,(HC)dsLHscFv#10	94.3
Fab#4-(LC)HLscFv#7,(HC)LHscFv#10	53.2
Fab#4-(LC)dsHLscFv#7,(HC)dsLHscFv#10	90.8

eolf-seql

SEQUENCE LISTING

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<120> Multispecific antibody constructs

<130> G0228_WO

<160> 80

<170> PatentIn version 3.5

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Pro Ala

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Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr
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1   5   10   15

Thr Pro Pro Pro Cys Pro Arg Cys Pro Ala
            20   25

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1 5 10

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<400> 18

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1   5   10   15

eolf-seql
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

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Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser
20 25

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Xaa Gly Gly Gly Ser Xaa Gly Gly Gly Ser Gly Ala Ser Ala Ser
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<400> 25

Pro Gly Gly Asn Arg Gly Thr Thr Thr Thr Arg Arg Pro Ala Thr Thr
1   5   10   15

Thr Gly Ser Ser Pro Gly Pro Thr Gln Ser His Tyr
            20   25

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1   5   10

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<400> 27

Ala Thr Thr Thr Gly Ser
1 5

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1 5 10 15

Ser His Lys Ser Pro
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Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
1 5 10 15

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1 5 10 15

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Gly Gly Gly Gly Lys Val Glu Gly Ala Gly Gly Gly Gly Gly Ser
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Gly Gly Glu Lys Ser Ile Pro Gly Gly Gly Gly Ser
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Arg Pro Leu Ser Tyr Arg Pro Pro Phe Pro Phe Gly Phe Pro Ser Val
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Arg Pro

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Thr Thr

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Thr Pro Ser His Leu Ser His Ile Leu Pro Ser Phe Gly Leu Pro Thr
1 5 10 15

Phe Asn

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Gly Ala

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Met Pro Ser Leu Ser Gly Val Leu Gln Val Arg Tyr Leu Ser Pro Pro
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Asp Leu

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<400> 44

Ser Pro Gln Tyr Pro Ser Pro Leu Thr Leu Thr Leu Pro Pro His Pro
1 5 10 15

Ser Leu

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Asn Pro Ser Leu Asn Pro Pro Ser Tyr Leu His Arg Ala Pro Ser Arg
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Ile Ser

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

Pro Pro

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Val Pro Pro Ala Pro Val Val Ser Leu Arg Ser Ala His Ala Arg Pro
1 5 10 15

Pro Tyr

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Leu Arg Pro Thr Pro Pro Arg Val Arg Ser Tyr Thr Cys Cys Pro Thr
1 5 10 15

Pro

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1 5 10 15

Leu Arg

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Cys Asn Pro Leu Leu Pro Leu Cys Ala Arg Ser Pro Ala Val Arg Thr
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Phe Pro

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<400> 52

Gly Ala Pro Ala Pro Ala Ala Pro Ala Pro Ala
1 5 10

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Pro Pro Pro Pro
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1 5 10

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<400> 55

Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10

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<400> 56

Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Gly Asp
1 5 10 15

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<400> 57

Gln Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10 15

Glu Asp Asp Glu
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Gln Gly Leu Ile Gly Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10 15

Gly Arg Ser Val
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<400> 59

Gln Gly Leu Ile Gly Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1   5   10   15

Gly Arg Ser Val Lys
            20

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<400> 60

Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu Asp Asp
1   5   10   15

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Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu
1   5   10   15

Asp Asp

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Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu Asp Asp
1 5 10 15

<210> 63
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<400> 63

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1 5 10 15

<210> 64
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<400> 64

Arg Leu Met Glu Asp Ile Cys Leu Ala Arg Trp Gly Cys Leu Trp Glu
1 5 10 15

Asp Asp

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<400> 65

Glu Val Arg Ser Phe Cys Thr Arg Trp Pro Ala Glu Lys Ser Cys Lys
1   5   10   15

Pro Leu Arg Gly
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<400> 66

Arg Ala Pro Glu Ser Phe Val Cys Tyr Trp Glu Thr Ile Cys Phe Glu
1   5   10   15

Arg Ser Glu Gln
            20

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<400> 67

Glu Met Cys Tyr Phe Pro Gly Ile Cys Trp Met
1   5   10

<210> 68
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1 5 10 15

Gly Gly Gly Ser
20

<210> 69
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<220>
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<400> 69

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

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<400> 70

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Thr Gly Gly Gly Gly Ser
1 5 10 15

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<220>
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1   5   10

<210> 72
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<220>
<223> CDRH2 dAbH1

<400> 72

Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys Gly
1   5   10   15

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<400> 73

Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu
1   5   10

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Gln Ser Ser Pro Ser Val Trp Ser Asn Phe Leu Ser
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Glu Ala Ser Lys Leu Thr Ser
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Gly Gly Gly Tyr Ser Ser Ile Ser Asp Thr Thr
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<400> 77

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr
20 25 30

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

Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
50 55 60

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

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

Arg Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
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<400> 78

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 Val Ser Gly Ile Asp Leu Ser Asn Tyr
20 25 30

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

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Gly Ile Ile Trp Ala Ser Gly Thr Thr Phe Tyr Ala Thr Trp Ala Lys
    50                  55                  60

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

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

Arg Thr Val Pro Gly Tyr Ser Thr Ala Pro Tyr Phe Asp Leu Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 79
<211> 112
<212> PRT
<213> Artificial

<220>
<223> Light chain variable domain of anti-albumin antibody (no ds)

<400> 79

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1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
            20                  25                  30

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

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

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
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Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gly Gly Tyr Ser Ser Ile
                85                  90                  95


Ser Asp Thr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110


<210>  80
<211>  112
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<220>
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1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ser Ser Pro Ser Val Trp Ser Asn
            20                  25                  30


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


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


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


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


Ser Asp Thr Thr Phe Gly Cys Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
```

Claims

1. A multi-specific antibody molecule comprising or consisting of:

   a) a polypeptide chain of formula **(I):**
   V_H-CH_1-X-V_1; and

   b) a polypeptide chain of formula **(II):**
   V_L-C_L-Y-V_2;
   wherein:

   V_H represents a heavy chain variable domain;

   CH_1 represents a domain of a heavy chain constant region, for example domain 1 thereof;

   X represents a bond or linker;

   Y represents a bond or linker;

   V_1 represents a dsscFv;

   V_L represents a light chain variable domain;

   C_L represents a domain from a light chain constant region, such as Ckappa;

   V_2 represents a dsscFv;

   wherein each of V_H/V_L, V_1, and V_2 forms an antigen binding site, and
   wherein only one of V_H/V_L, V_1 or V_2 has specificity for a serum carrier protein.

2. A multi-specific antibody molecule according to claim 1, wherein the serum carrier protein is selected from the list consisting of albumin, thyroxine-binding protein, transthyretin, α1-acid glycoprotein, transferrin, and fibrinogen.

3. A multi-specific antibody molecule according to claim 1 or 2, wherein the serum carrier protein is human serum albumin and wherein said V_H/V_L or V_1 or V_2 having specificity for a serum carrier protein forms an albumin binding site.

4. A multi-specific antibody molecule according to claim 3, wherein the albumin binding site comprises SEQ ID NO: 71 for CDRH1, SEQ ID NO: 72 for CDRH2, SEQ ID NO: 73 for CDRH3, SEQ ID NO: 74 for CDRL1, SEQ ID NO: 75 for CDRL2 and SEQ ID NO: 76 for CDRL3; or a heavy chain variable domain selected from SEQ ID NO: 77 and SEQ ID NO: 78 and a light chain variable domain selected from SEQ ID NO: 79 and SEQ ID NO: 80.

5. A multi-specific antibody molecule according to claim 4, wherein the 6 CDRs of SEQ ID NO: 71 to SEQ ID NO: 76, or the variable domains of SEQ ID NO: 77 to SEQ ID NO: 80 are in the position V_H/V_L or V_1 or V_2.

6. A multi-specific antibody molecule according to claim 4 or 5, wherein the heavy chain variable domain of SEQ ID NO: 78 and the light chain variable domain of SEQ ID NO: 80 are in the position V_2 and wherein the light chain variable domain or the heavy chain variable domain of V_2 is attached to Y, for example through a peptide bond.

7. A multi-specific antibody molecule according to any one of claims 1 to 6, wherein the antibody molecule is capable of selectively binding two or more different antigens of interest.

8. A multi-specific antibody molecule according to any one of claims 1 to 7, wherein the light chain and heavy chain variable domains of V_1 and/or the light chain and heavy chain variable domains of V_2 are linked by a disulfide bond between two engineered cysteine residues, wherein the position of the pair of cysteine residues is V_H44 and V_L100 (numbering according to Kabat).

9. A multi-specific antibody molecule according to any one of claims 1 to 8, wherein X and/or Y is a peptide linker, for example SEQ ID NO: 1, 2, 69 and 70.

10. A polynucleotide encoding a multi-specific antibody molecule according to any one of claims 1 to 9.

11. A vector comprising a polynucleotide defined in claim 10.

12. A host cell comprising a polynucleotide or vector of claim 10 or 11 respectively.

13. A host cell comprising two vectors, the first vector comprising a polynucleotide encoding a polypeptide chain of formula (I) of a multi-specific antibody molecule according to any one of claims 1 to 9, and the second vector comprising a polynucleotide encoding a polypeptide chain of formula (II) of said multi-specific antibody molecule.

14. A process comprising expressing a multi-specific antibody molecule from a host cell defined in claim 12 or claim 13.

15. A pharmaceutical composition comprising a multi-specific antibody molecule according to any one of claims 1 to 9 and at least one excipient.

16. A multi-specific antibody molecule according to any one of claims 1 to 9 or a pharmaceutical composition according to claim 15 for use in treatment.