**Claims:**

1. A method of increasing the percentage of monomer in a composition of recombinantly expressed antibody molecules, wherein the antibody molecule comprises at least one Fv with specificity for an antigen of interest comprising one VH and one VL wherein said VH and VL are connected directly or indirectly via one or more linkers and are stabilised by a disulfide bond therebetween, said method comprises:

    a) a conversion step of treating the composition with a denaturant selected from urea and/or Guanidine hydrochloride;

    b) wherein step a) is performed in the presence of a reducing agent or after treatment with a reducing agent, wherein the reducing agent is 2-mercaptoethylamine at a concentration of 10 to 150 millimolar.

2. A method according to claim 1, wherein the 2-mercaptoethylamine is 50 to 150 millimolar.

3. A method according to claim 2, wherein the 2-mercaptoethylamine is 95 to 135 millimolar, for example 110 to 120 millimolar.

4. A method according to any one of claims 1 to 3, wherein the denaturant is urea and is at a concentration of 1 to 5 molar.

5. A method according to claim 4, wherein the urea is at a concentration of 3 to 5 molar.

6. A method according to claim 5, wherein the urea is at a concentration of 4.5 to 4.9 molar, for example 4.7 molar.

7. A method according to any one of claims 1 to 3, wherein the denaturant is Guanidine hydrochloride and is at a concentration of 1 to 2 molar.

8. A method according to any one of claims 1 to 7, wherein step a) is carried out for a period in the range 2 to 70 hours, for example 3 to 50 hours, such as 4 to 25 hours, in particular 4 to 6 hours, for example 6 hours.

9. A method according to any one of claims 1 to 8, wherein the method is performed at room temperature.

10. A method according to any one of claims 1 to 9, wherein the antibody is at a concentration in the range 0.5g/L to 5g/L.

11. A method according to any one of claims 1 to 10, wherein the conversion step is performed in the presence of concomitant stirring.

12. A method according to claim 11, wherein the stirring rate is in the range 100 to 1200 rpm.

13. A method according to any one of claims 1 to 12, comprising a further step of downstream purification.

14. A method according to claim 13, wherein downstream processing comprises the step chromatography.

15. A method according to any of claims 1 to 14, wherein the VH and VL which are connected directly or indirectly via one or more linkers and are stabilised by a disulfide bond therebetween, are a complementary VH/VL pair which form an antigen binding site.

16. A method according to any preceding claim, wherein the VH and VL are connected directly via a linker.

17. A method according to claim 16, wherein the antibody is selected from a dsscFv, a Fab-2xdsscFv, a Fab-dsscFv-dsFv, a Fab-dsscFv-sdAb, a Fab-dsscFv-scFv and a Fab-dsscFv.

18. A method according to any of claims 1 to 15, wherein each VH and VL comprise a linker which indirectly connect the VH and VL via a second antibody.

19, A method according to claim 18, wherein the antibody is a Fab-dsFv.

20. A method according to claim 19, wherein the antibody is a bispecific antibody fusion protein which binds human OX40 and human serum albumin comprising:

a heavy chain comprising, in sequence from the N-terminal, a first heavy chain variable domain ($V_H1$), a $C_H1$ domain and a second heavy chain variable domain ($V_H2$),

a light chain comprising, in sequence from the N-terminal, a first light chain variable domain ($V_L1$), a $C_L$ domain and a second light chain variable domain ($V_L2$),

wherein said heavy and light chains are aligned such that $V_H1$ and $V_L1$ form a first antigen binding site and $V_H2$ and $V_L2$ form a second antigen binding site,

wherein the antigen bound by the first antigen binding site is human OX40 and the antigen bound by the second antigen binding site is human serum albumin.

21. A method according to claim 20, wherein the first variable domain of the heavy chain ($V_H1$) comprises the sequence given in SEQ ID NO:1 for CDR-H1, the sequence given in SEQ ID NO:2 for CDR-H2 and the sequence given in SEQ ID NO:3 for CDR-H3 and the first variable domain of the light chain ($V_L1$) comprises the sequence given in SEQ ID NO:4 for CDR-L1, the sequence given in SEQ ID NO:5 for CDR-L2 and the sequence given in SEQ ID NO:6 for CDR-L3,

wherein the second heavy chain variable domain ($V_H2$) has the sequence given in SEQ ID NO:11 and the second light chain variable domain ($V_L2$) has the sequence given in SEQ ID NO: 12 and

the second heavy chain variable domain ($V_H2$) and second light chain variable domain ($V_L2$) are linked by a disulfide bond.

22. A composition comprising 2-mercaptoethylamine and a denaturant selected from urea and Guanidine hydrochloride for converting multimeric species of an antibody molecule to monomers wherein the antibody molecule comprises at least one Fv with specificity for an antigen of interest comprising one VH and one VL wherein said VH and VL are connected directly or indirectly via one or more linkers and are stabilised by a disulfide bond therebetween, wherein the 2-mercaptoethylamine is at a concentration of 10 to 150 millimolar.

23. A composition according to claim 22, wherein urea is 3 to 5 molar and 2-mercaptoethylamine is 80 to 150 millimolars.

24. Use of a composition comprising 2-mercaptoethylamine and a denaturant selected from urea and Guanidine hydrochloride for converting multimeric species of an antibody molecule to monomers, wherein the antibody molecule comprises at least one Fv with specificity for an antigen of interest comprising one VH and one VL wherein said VH and VL are connected directly or indirectly via one or more linkers and are stabilised by a disulfide bond therebetween, wherein the 2-mercaptoethylamine is at a concentration of 10 to 150 millimolar.