CLAIMS

1. A fusion protein comprising at least one first polypeptide moiety and at least one second polypeptide moiety, wherein the first polypeptide moiety is a single-chain polypeptide capable of binding a target entity, and the second polypeptide moiety comprises a single-chain α-helix-containing domain, wherein the second polypeptide moiety does not have binding affinity for said target entity.

2. The fusion protein according to claim 1, wherein presence of the second polypeptide moiety improves at least one property of the fusion protein as compared to the property of the first polypeptide moiety alone, wherein said improved property is selected from the group consisting of: alkaline stability, recombinant protein expression and coupling to a support.

3. The fusion protein according to claim 2, wherein improved alkaline stability is represented by the fusion protein as a whole having an alkaline stability that is increased as compared to the alkaline stability of the first polypeptide moiety alone.

4. The fusion protein according to any one of claims 1-3, wherein the second polypeptide moiety is a polypeptide domain, such as an α-helix-containing domain.

5. The fusion protein according to any one of claims 1-4, wherein the second polypeptide moiety comprises at least 1 α-helix, such as at least 2 α-helices, such as 3, 4, 5 or 6 α-helices.

6. The fusion protein according to any one of claims 1-5, wherein the second polypeptide moiety is an α-helix bundle domain.

7. The fusion protein according to any one of claims 1-6, wherein the second polypeptide is or is derived from a protein domain of SpA.

8. The fusion protein according to any one of claims 1-7, wherein the second polypeptide moiety

(i) has lower binding affinity for an Fc region of trastuzumab compared to the binding of SEQ ID NO:8 for the same Fc region, and/or

(ii) has lower binding affinity for the VH3 region of trastuzumab compared to the binding of SEQ ID NO:6 for the same VH3 region.

9. The fusion protein according to claim 8, wherein the second polypeptide moiety that has lower affinity for an Fc region of trastuzumab comprises an amino acid selected from the group consisting of SEQ ID NO: 64-110, 31-40 and 59-63.

10. The fusion protein according to claim 8, wherein the second polypeptide moiety that has lower affinity for the VH3 region of trastuzumab comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 64-110 and 9-30.

11. The fusion protein according to claim 8, wherein the second polypeptide moiety that has lower binding affinity for an Fc region of trastuzumab comprises an amino acid sequence wherein the amino acid in the position corresponding to position X_{33} of SEQ ID NO:64 is selected from T, S, G, Q, A, E, H, R; the amino acid in the position corresponding to position X_{40} of SEQ ID NO:64 is selected from E, G, R, D, K, Q, H and S; and the amino acid in the position corresponding to X_{51} is selected from L, V, S, I, R and G; with the proviso that when X_{51} is L then $X_{33}X_{40}$ is selected from AD, HK, EG, ER, GR, AK, AR, PK, RR and KK and when X_{51} is G then $X_{33}X_{40}$ is TK.

12. The fusion protein according to any one of claims 7-11, wherein the second polypeptide moiety comprises an amino acid sequence derived from a protein domain of SpA and in which

the amino acid residue in the position corresponding to position 9 of SEQ ID NO: 64 is selected from L, E, R, A and Y, and preferably is A;

the amino acid residue in the position corresponding to position 10 of SEQ ID NO: 64 is selected from L, E, R, A and Y, and preferably is Y

the amino acid residue in the position corresponding to position 11 of SEQ ID NO: 64 is selected from L, E, R, A and Y, and preferably is R;

the amino acid residue in the position corresponding to position 13 of SEQ ID NO: 64 is selected from L, E, R, A and Q, and preferably is L, R, A or Q;

the amino acid residue in the position corresponding to position 14 of SEQ ID NO: 64 is selected from L, E, R, A, Q and K, and preferably is A or R;

the amino acid residue in the position corresponding to position 17 of SEQ ID NO: 64 is selected from L, E, R and A, and preferably is A;

the amino acid residue in the position corresponding to position 18 of SEQ ID NO: 64 is selected from L, E, R and A, and preferably is R;

the amino acid residue in the position corresponding to position 28 of SEQ ID NO: 64 is selected from L, E, R and A, and preferably is R or A;

the amino acid residue in the position corresponding to position 29 of SEQ ID NO: 64 is selected from L, E, R and A, and preferably is R or A;
the amino acid residue in the position corresponding to position 33 of SEQ ID NO: 64 is selected from T, S, G, Q, A, E, H and R, and preferably is S;
the amino acid residue in the position corresponding to position 40 of SEQ ID NO: 64 is selected from E, G, R, D, K, Q, H and S, and preferably is G;
the amino acid residue in the position corresponding to position 51 of SEQ ID NO: 64 is selected from L, V, S, I, R and G, and preferably is V.

13. The fusion protein according to claim 11 or 12, wherein the second polypeptide moiety comprises, or consists of an amino acid sequence selected from the group consisting of SEQ ID NOs: 64-110 and 7-63; preferably SEQ ID NOs: 64-110, and amino acid sequences having at least 80 % identity thereto, preferably at least 85 % or at least 90 % identity thereto.

14. The fusion protein according to any one of the preceding claims, wherein the second polypeptide moiety comprises an amino acid sequence having at least 85 %, 90 % or 95 % identity to SEQ ID NO: 64, 8, 103 or 110.

15. The fusion protein according to any one of the preceding claims, wherein the at least one second polypeptide, including any additional amino acids, is located at the C-terminus of the fusion protein.

16. The fusion protein according to any one of the preceding claims, wherein the first polypeptide moiety is a natural or synthetic antibody domain or antibody fragment or a modified variant thereof, such as a single-chain polypeptide, a single-chain variable fragment or a single-domain antibody or a variant thereof.

17. The fusion protein according to any one of the preceding claims, wherein the first polypeptide moiety has a binding affinity for a biological entity, wherein the biological entity is a virus particle or a viral vector, such as an adenovirus, a retrovirus (γ-retroviruses and lentiviruses), a poxvirus, an adeno-associated virus (AAV), a baculovirus, or a herpes simplex virus.

18. The fusion protein according to any one of the preceding claims, which is a multimeric fusion protein comprising at least two of said first polypeptide moiety.

19. The fusion protein according to any one of claims 2-18, wherein the alkaline stability is measured as the ability of the first polypeptide moiety to maintain target binding capacity after exposure to alkaline conditions.

20. The fusion protein according to claim 19, wherein exposure to alkaline conditions is repeated exposure to a solution of at least 0.1 M NaOH, such as 0.5 M NaOH, for a time period of 10 min.

21. Use of the fusion protein according to any one of claims 1-20 for *in vitro* capture of said target entity, such as for the detection of said target entity within a sample or for separation of said target entity from other components of a sample.

22. An adsorbent material comprising the fusion protein according to any one of claims 1-20 coupled to a support.

23. The adsorbent material according to claim 22, wherein the support is selected from a chip, a plate, a well, a sheet, a fiber, a particle, a bead, a fibrous matrix, a membrane, a filter and a porous monolith.

24. The adsorbent material according to claim 22, wherein the support is a chromatography matrix.

25. Use of an alkaline stable α-helix-containing polypeptide domain to improve the *in vitro* alkaline stability of an antigen-binding polypeptide by fusing the α-helix-containing polypeptide to the C-terminus of said antigen-binding polypeptide, wherein the α-helix-containing polypeptide domain is a second polypeptide moiety as defined in any one of claims 1-20 and wherein the antigen-binding polypeptide is a first polypeptide moiety as defined in any one of claims 1-20.

26. A method of separation, comprising the steps of

(a) Providing an adsorbent material according to claim 22-24, wherein the fusion protein has a binding capacity for a target entity,
(b) Contacting the adsorbent material with a liquid sample comprising said target entity under conditions allowing the target entity to bind to the first polypeptide of the fusion protein,
(c) Optionally washing the adsorbent material,
(d) Eluting the target entity from the adsorbent material, and
(e) Cleaning the adsorbent material with a cleaning liquid, such as an alkaline cleaning liquid.

27. The method of claim 26, wherein steps (a)-(e) are repeated at least 10 times, such as at least 20 times.

28. The method of claim 27, wherein after 10 cycles of contact with alkaline cleaning liquid, the fusion protein retains at least 50 % such as at least 60 %, such as at least 80 %, such as at least 90 %, of the initial target entity binding capacity.

29. The method of claim 27-28, wherein, after 10 cycles of contact with alkaline cleaning liquid, the fusion protein retains at least 50 % such as at least 60 %, such as at least 80 %, such as at least 90 %, such as at least 95 %, such as at least 98 %, of the target entity binding capacity of the 2nd cycle.