			WGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVT LTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGG GGAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGGGGSGGGGSGGGGSGGGGSAPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
1458	IgG3 hinge		ELKTPLGDTTHTCPRCP
1459	IgG1 hinge		EPKSCDKTHTCPPCP
1460	VH-VL of F6A		EVQLVESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
1461	VH-VL-P of F6A		EVQLLESGGGLVQPGGSLKLSCAASGFTFNIYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYVSFFAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALW YSNRWVFGGGTKLTVL
1462	VH-VL of H2C		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
1463	VH-VL-P of H2C		EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALW YSNRWVFGGGTKLTVL
1464	VH-VL of H1E		EVQLVESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
1465	VH-VL-P of H1E		EVQLLESGGGLEQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYLSFWAYWGQGTLVTVSSGGGGSGGGGSGG GGSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL

1466	VH-VL of G4H		EVQLVESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
1467	VH-VL-P of G4H		EVQLLESGGGLVQPGGSLKLSCAASGFTFNRYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYLSYFAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALW YSNRWVFGGGTKLTVL
1468	VH-VL of A2J		EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPG QAPRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
1469	VH-VL-P of A2J		EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYLSWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQ APRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
1470	VH-VL of E1L		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
1471	VH-VL-P of E1L		EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKSRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYTSYYAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCALW YSNRWVFGGGTKLTVL
1472	VH-VL of E2M		EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGL EWVARIRSKYNNYATYYADSVKERFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPG QAPRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC ALWYSNRWVFGGGTKLTVL
1473	VH-VL-P of E2M		EVQLLESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKERFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHRNFGNSYLSWFAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCRSSTGAVTSGYYPNWVQQKPGQA PRGLIGATDMRPSGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCAL WYSNRWVFGGGTKLTVL
1474	VH-VL of F7O		EVQLVESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPG

			QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
1475	VH-VL-P of F7O		EVQLLESGGGLVQPGGSLKLSCAASGFTFNVYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKKRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGYYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCA LWYSNRWVFGGGTKLTVL
1476	VH-VL of F12Q		EVQLVESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
1477	VH-VL-P of F12Q		EVQLLESGGGLVQPGGSLKLSCAASGFTFNSYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGG GGSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
1478	VH-VL of I2C		EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL
1479	VH-VL-P of I2C		EVQLLESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSELVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVL WYSNRWVFGGGTKLTVL

Claims

1. A single-chain bispecific antibody construct comprising at least a first domain, a second domain, and a third domain in an amino to carboxyl order, wherein:
   - the first domain is a single chain variable fragment (scFv) that binds to a target cell surface antigen,
   - the second domain is an scFv that binds to an extracellular epitope comprised within amino acid residues 1-27 of the human CD3ε chain; and
   - the third domain comprises two polypeptide monomers, each comprising a hinge, a CH2 and a CH3 domain, wherein said two polypeptide monomers are fused to each other via a peptide linker, wherein said third domain comprises in an amino to carboxyl order:

     hinge-CH2-CH3-linker-hinge-CH2-CH3,

     wherein a glycosylation site at Kabat position 314 of the CH2 domains is removed by an N314X substitution, wherein X is any amino acid excluding Q, and wherein the CH2 domains comprise an intra-domain cysteine disulfide bridge.

2. The antibody construct of claim 1, wherein each of said polypeptide monomers has the amino acid sequence of SEQ ID NO: 17 or 18.

3. The antibody construct of claim 1 or 2, wherein the third domain comprises the amino acid sequence of SEQ ID NO: 25 or 26.

4. The antibody construct of any one of claims 1 to 3, wherein the intra-domain cysteine disulfide bridge is formed by V321C and R309C substitutions in the CH2 domain, wherein the positions are according to the Kabat numbering system.

5. The antibody construct of claim 1 or 2, wherein the first and second domain are fused to the third domain via a peptide linker.

6. The antibody construct of any one of claims 1 to 5, wherein the antibody construct comprises in an amino to carboxyl order:
   (a) the first domain;
   (b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-3;

(c) the second domain;

(d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 9, 10, 11 and 12;

(e) the first polypeptide monomer of the third domain;

(f) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 6, 7 and 8; and

(g) the second polypeptide monomer of the third domain.

7. The antibody construct of any one of claims 1 to 6, wherein the target cell surface antigen is a tumor antigen, an antigen specific for an immunological disorder or a viral antigen.

8. The antibody construct of claim 7, wherein the tumor antigen is selected from the group consisting of CDH19, MSLN, DLL3, FLT3, EGFRvIII, CD33, CD19, CD20, and CD70.

9. The antibody construct of any one of claims 1 to 8, wherein the antibody construct comprises in an amino to carboxyl order:

(a) the first domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 52, 70, 58, 76, 88, 106, 124, 94, 112, 130, 142,160, 178, 148, 166, 184, 196, 214, 232, 202, 220, 238, 250, 266, 282, 298, 255, 271, 287, 303, 322, 338, 354, 370, 386, 402, 418, 434, 450, 466, 482, 498, 514, 530, 546, 327, 343, 359, 375, 391, 407, 423, 439, 455, 471, 487, 503, 519, 353, 551, 592, 608, 624, 640, 656, 672, 688, 704, 720, 736, 752, 768, 784, 800, 816, 832, 848, 864, 880, 896, 912, 928, 944, 960, 976, 992, 1008, 1024, 1040, 1056, 1072, 1088, 1104, 1120, 1136, 1152, 1168, 1184, 597, 613, 629, 645, 661, 677, 693, 709, 725, 741, 757, 773, 789, 805, 821, 837, 853, 869, 885, 901, 917, 933, 949, 965, 981, 997, 1013, 1029, 1045, 1061, 1077, 1093, 1109, 1125, 1141, 1157, 1173, 1189,1277, 1289, 1301, 1313, 1325, 1337, 1349, 1361, 1373, 1385, 1397, 1409, 1421, 1433, and 1445;

(b) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-3;

(c) the second domain having an amino acid sequence selected from the group consisting of SEQ ID NOs: 15 and 1460-1479;

(d) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 1, 2, 3, 9, 10, 11 and 12;

(e) the first polypeptide monomer of the third domain having an amino acid sequence of SEQ ID NO:17 or 18;

(f) a peptide linker having an amino acid sequence selected from the group consisting of SEQ ID NOs: 5, 6, 7 and 8; and

(g) the second polypeptide monomer of the third domain having an amino acid sequence of SEQ ID NO:17 or 18.

10. An antibody construct having an amino acid sequence selected from the group consisting of:

(a) SEQ ID NOs: 54, 55, 60, and 61;

(b) SEQ ID NOs: 72, 73, 78, and 79;

(c) SEQ ID NOs: 90, 91, 96, 97, 108, 109, 114, and 115;

(d) SEQ ID NOs: 144, 145, 150, 151, 162, 163, 168, 169, 180, 181, 186, and 187;

(e) SEQ ID NOs: 198, 199, 204, 205, 216, 217, 222, 223, 234, 235, 240, and 241;

(f) SEQ ID NOs: 252, 306, 257, 307, 268, 308, 273, 309, 284, 310, 289, 311, 300, 312, 305, and 313;

(g) SEQ ID NOs: 324, 554, 329, 555, 340, 556, 345, 557, 356, 558, 361, 559, 372, 560, 377, 561, 388, 562, 393, 563, 404, 564, 409, 565, 420, 566, 425, 567, 436, 568, 441, 569, 452, 570, 457, 571, 468, 572, 473, 573, 484, 574, 489, 575, 500, 576, 505, 577, 516, 578, 521, 579, 532, 580, 537, 581, 548, 582, 553, and 583;

(h) SEQ ID NOs: 594, 610, 626, 642, 658, 674, 690, 706, 722, 738, 754, 770, 786, 802, 818, 834, 850, 866, 882, 898, 914, 930, 946, 962, 978, 994, 1010, 1026, 1042, 1058, 1074, 1090, 1106, 1122, 1138, 1154, 1170, 1186, 599, 615, 631, 647, 663, 679, 695, 711, 727, 743, 759, 775, 791, 807, 823, 839, 855, 871, 887, 903, 919, 935, 951, 967, 983, 999, 1015, 1031, 1047, 1063, 1079, 1095, 1111, 1127, 1143, 1159, 1175, 1191, and 1192-1267;

(i) SEQ ID NO: 43; and

(j) SEQ ID NOs: 1279, 1280, 1291, 1292, 1303, 1304, 1315, 1316, 1327, 1328, 1339, 1340, 1351, 1352, 1363, 1364, 1375, 1376, 1387, 1388, 1399, 1400, 1411, 1412, 1423, 1424, 1435, 1436, 1447, 1448.

11. A polynucleotide encoding an antibody construct of any one of claims 1 to 10.

12. A vector comprising a polynucleotide of claim 11.

13. A host cell transformed or transfected with the polynucleotide of claim 11 or with the vector of claim 12.

14. A process for the production of an antibody construct according to any one of claims 1 to 10, said process comprising culturing a host cell of claim 13 under conditions allowing the expression of the antibody construct and recovering the produced antibody construct from the culture.

15. A pharmaceutical composition comprising an antibody construct of any one of claims 1 to 10, or an antibody construct produced according to the process of claim 14.

16. The pharmaceutical composition of claim 15, which is stable for at least four weeks at about -20°C.

17. The antibody construct of any one of claims 1 to 10, for use in the treatment or amelioration of a condition selected from a proliferative disease, a tumorous disease, a viral disease or an immunological disorder, wherein the target cell surface antigen bound by the first domain of the antibody construct is an antigen specific for said condition.

18. Use of the antibody construct of any one of claims 1 to 10 in the manufacture of a medicament for the treatment or amelioration of a condition that is a proliferative disease, a tumorous disease, a viral disease or an immunological disorder, wherein the target cell surface antigen bound by the first domain of the antibody construct is an antigen specific for said condition.

19. A kit comprising an antibody construct of any one of claims 1 to 10, a polynucleotide of claim 11, a vector of claim 12, and/or a host cell of claim 13.