

**WHAT IS CLAIMED:**

1. A precursor polypeptide comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a heavy chain leader sequence, (ii) an antibody heavy chain variable region, (iii) an antibody heavy chain constant region, (iv) an optional hinge region, (v) a transmembrane region, (vi) an intracellular region, (vii) a self-cleaving sequence, (viii) a light chain leader sequence, (ix) an antibody light chain variable region, and (x) an antibody light chain constant region, wherein the self-cleaving sequence permits cleaving the of the precursor polypeptide into a first and second polypeptide chain.
2. A precursor polypeptide comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a light chain leader sequence (ii) an antibody light chain variable region, (iii) an antibody light chain constant region, (iv) an optional hinge region, (v) a transmembrane region, (vi) an intracellular region, (vii) a self-cleaving sequence, (viii) a heavy chain leader sequence, (ix) an antibody heavy chain variable region, and (x) an antibody heavy chain constant region, wherein the self-cleaving sequence permits cleaving the of the precursor polypeptide into a first and second polypeptide chain.
3. The precursor polypeptide of claim 1 or 2, wherein the antibody heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 6, 12, 14, 16, 18, 20, 22, 24, 26, or 28.
4. The precursor polypeptide of any one of claims 1-3, wherein the antibody heavy chain constant region comprises:
  - a) a human IgG, IgA, IgD, IgE, or IgM CH1 domain;
  - b) a human IgG1, IgG2, IgG3, or IgG4 CH1 domain;
  - c) a human IgG1 domain;
  - d) an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:7 or 29; or
  - e) the amino acid sequence of SEQ ID NO:7 or 29.

5. The precursor polypeptide of any one of claims 1-4, wherein the antibody light chain variable region comprises the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30.
6. The precursor polypeptide of any one of claims 1-5, wherein the antibody light chain constant region comprises:
  - a) a human Ig kappa constant domain;
  - b) a human Ig lambda constant domain;
  - c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:11 or 31; or
  - d) the amino acid sequence of SEQ ID NO:11 or 31.
7. The precursor polypeptide of any one of claims 1-6, wherein the hinge region comprises a hinge sequence from an antibody selected from a group consisting of IgG, IgA, IgM, IgE and IgD.
8. The precursor polypeptide of any one of claims 1-6, wherein the hinge comprises a CD8 $\alpha$  and/or CD28 hinge region.
9. The precursor polypeptide of any one of claims 1-6, wherein the hinge region comprises a CPPC or SPPC amino acid sequence.
10. The precursor polypeptide of any one of claims 1-6, wherein the hinge region comprises the amino acid sequence of SEQ ID NO:34, 35 or 36.
11. The precursor polypeptide of any one of claims 1-10, wherein the transmembrane region comprises a transmembrane sequence from CD8 $\alpha$ , CD8 $\beta$ , 4-1BB/CD137, CD28, CD34, CD4, Fc $\epsilon$ RI $\gamma$ , CD16, OX40/CD134, CD3 $\zeta$ , CD3 $\epsilon$ , CD3 $\gamma$ , CD3 $\delta$ , TCR $\alpha$ , TCR $\beta$ , TCR $\zeta$ , CD32, CD64, CD64, CD45, CD5, CD9, CD22, CD33, CD37, CD64, CD80, CD86, CD137, CD154, LFA-1 T cell co-receptor, CD2 T cell co-receptor/adhesion molecule, CD40, CD40L/CD154, VEGFR2, FAS, and FGFR2B.
12. The precursor polypeptide of any one of claims 1-11, wherein the transmembrane region comprises the amino acid sequence of SEQ ID NO: 37, 38, 39 or 40.

13. The precursor polypeptide of any one of claims 1-12, wherein the intracellular region comprises one intracellular sequence or comprises 2-5 intracellular sequences in any order and any combination of intracellular sequences selected from a group consisting of 4-1BB, CD3zeta having ITAM 1, 2 and 3, CD3zeta having ITAM 1, CD3zeta having ITAM 3, CD28, CD27, OX40, CD30, CD40, PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, GITR (TNFRSF18), DR3 (TNFRSF25), TNFR2 and/or CD226.
14. The precursor polypeptide of any one of claims 1-12, wherein the intracellular region comprises:
- i) a CD3zeta having ITAM 1, 2 and 3 which comprises the amino acid sequence of SEQ ID NO:44,
  - ii) a CD3zeta ITAM 1 which comprises the amino acid sequence of SEQ ID NO:45,
  - iii) a CD3zeta ITAM 2 which comprises the amino acid sequence of SEQ ID NO:46, or
  - iv) a CD3zeta having ITAM 3 which comprises the amino acid sequence of SEQ ID NO:47.
15. The precursor polypeptide of any one of claims 1-12, wherein the intracellular region comprises:
- i) intracellular sequences from CD28 and from CD3zeta having ITAM 1, 2 and 3, comprising the amino acid sequence of SEQ ID NO:48 or 50, or
  - ii) intracellular sequences from 4-1BB and from CD3zeta having ITAM 1, 2 and 3, comprising the amino acid sequence of SEQ ID NO:49, or
  - iii) intracellular sequences from CD28, from 4-1BB and from CD3zeta having ITAM 1, 2 and 3, comprising the amino acid sequence of SEQ ID NO:51 or 88, or
  - iv) intracellular sequences from 4-1BB and from CD3zeta having ITAM 3, comprising the amino acid sequence of SEQ ID NO:52, or
  - v) intracellular sequences from CD28 (SEQ ID NO:42) and from CD3zeta having ITAM 3 (SEQ ID NO:47), or
  - vi) intracellular sequences from CD28, from 4-1BB and from CD3zeta having ITAM 3, comprising the amino acid sequence of SEQ ID NO:53 or 89.

16. The precursor molecule of claim 1, comprising the amino acid sequence of SEQ ID NO:63, 66, 69, 72, 75, 78, 81 or 84.
17. The precursor molecule of claim 2, comprising the orientation and amino acid sequences shown in Figures 4A and B.
18. The precursor molecule of any one of the preceding claims, wherein the self-cleaving sequence is other than a T2A sequence, e.g., the self-cleaving sequence is a P2A, E2A, or F2A sequence.
19. A dimeric antigen receptor (DAR) construct, comprising:
  - a) a first polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) an antibody heavy chain variable region, (ii) an antibody heavy chain constant region, (iii) an optional hinge region, (iv) a transmembrane region, and (v) an intracellular region;
  - b) a second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) an antibody light chain variable region, and (ii) an antibody light chain constant region, wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain for formation of the dimeric antigen receptor (DAR), and wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain.
20. A dimeric antigen receptor (DAR) construct, comprising:
  - a) a first polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) an antibody light chain variable region, (ii) an antibody light chain constant region, (iii) an optional hinge region, (iv) a transmembrane region, and (v) an intracellular region;

- b) a second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) an antibody heavy chain variable region, and (ii) an antibody heavy chain constant region, wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain for formation of the dimeric antigen receptor (DAR), and wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain.
21. The dimeric antigen receptor (DAR) construct of claim 18 or 19, wherein the antibody heavy chain constant region and the antibody light chain constant region dimerize via one or two disulfide bonds.
  22. The dimeric antigen receptor construct of any one of claims 18-20, wherein the hinge region comprises a hinge sequence from an antibody selected from a group consisting of IgG, IgA, IgM, IgE and IgD.
  23. The dimeric antigen receptor construct of any one of claims 18-20, wherein the hinge comprises a CD8 $\alpha$  and/or a CD28 hinge region.
  24. The dimeric antigen receptor construct of any one of claims 18-20, wherein the hinge region comprises a CPPC or SPPC amino acid sequence.
  25. The dimeric antigen receptor construct of any one of claims 18-23, wherein the transmembrane region comprises a transmembrane sequence from CD8 $\alpha$ , CD8 $\beta$ , 4-1BB/CD137, CD28, CD34, CD4, Fc $\epsilon$ RI $\gamma$ , CD16, OX40/CD134, CD3 $\zeta$ , CD3 $\epsilon$ , CD3 $\gamma$ , CD3 $\delta$ , TCR $\alpha$ , TCR $\beta$ , TCR $\zeta$ , CD32, CD64, CD45, CD5, CD9, CD22, CD33, CD37, CD64, CD80, CD86, CD137, CD154, LFA-1 T cell co-receptor, CD2 T cell co-receptor/adhesion molecule, CD40, CD40L/CD154, VEGFR2, FAS, and FGFR2B.
  26. The dimeric antigen receptor construct of any one of claims 18-24, wherein the intracellular region comprises one intracellular sequence or comprises 2-5 intracellular sequences in any order and any combination of intracellular sequences selected from a group consisting of 4-1BB, CD3zeta, CD28, CD27, OX40, CD30, CD40, PD-1, ICOS,

lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3, GITR (TNFRSF18), DR3 (TNFRSF25), TNFR2 and/or CD226.

27. The dimeric antigen receptor (DAR) construct of any one of claims 18-25, wherein the antigen binding domain binds a BMCA (B-cell maturation antigen) protein.
28. The dimeric antigen receptor (DAR) construct of claim 27, wherein the BMCA (B-cell maturation antigen) protein comprises the amino acid sequence of SEQ ID NO:1, 2 or 3.
29. The dimeric antigen receptor (DAR) construct of claim 27, wherein the antibody heavy chain variable region comprises the amino acid sequence of SEQ ID NO: 6, 12, 14, 16, 18, 20, 22, 24, 26, or 28.
30. The dimeric antigen receptor (DAR) construct of claim 27, wherein the antibody heavy chain constant region comprises the amino acid sequence of SEQ ID NO:7 or 29.
31. The dimeric antigen receptor (DAR) construct of claim 27, wherein the antibody light chain variable region comprises the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30.
32. The dimeric antigen receptor (DAR) construct of claim 27, wherein the antibody light chain constant region comprises the amino acid sequence of 11 or 31.
33. The dimeric antigen receptor (DAR) construct of claim 27, wherein the hinge region comprises the amino acid sequence of SEQ ID NO:34, 35 or 36.
34. The dimeric antigen receptor (DAR) construct of claim 27, wherein the transmembrane region comprises the amino acid sequence of SEQ ID NO:37, 38, 39 or 40.
35. The dimeric antigen receptor of claim 27, wherein the intracellular region comprises:
  - i) a CD3zeta having ITAM 1, 2 and 3 comprising the amino acid sequence of SEQ ID NO:44,
  - ii) a CD3zeta ITAM 1 comprising the amino acid sequence of SEQ ID NO:45,

- iii) a CD3zeta ITAM 2 comprising the amino acid sequence of SEQ ID NO:46, or
  - iv) a CD3zeta having ITAM 3 comprising the amino acid sequence of SEQ ID NO:47.
36. The dimeric antigen receptor of claim 27, wherein the intracellular region comprises:
- i) intracellular sequences from CD28 and from CD3zeta having ITAM 1, 2 and 3, comprising the amino acid sequence of SEQ ID NO:48 or 50, or
  - ii) intracellular sequences from 4-1BB and from CD3zeta having ITAM 1, 2 and 3, comprising the amino acid sequence of SEQ ID NO:49, or
  - iii) intracellular sequences from CD28, from 4-1BB and from CD3zeta having ITAM 1, 2 and 3, comprising the amino acid sequence of SEQ ID NO:51 or 88, or
  - iv) intracellular sequences from 4-1BB and from CD3zeta having ITAM 3, comprising the amino acid sequence of SEQ ID NO:52, or
  - v) intracellular sequences from CD28 (SEQ ID NO:42) and from CD3zeta having ITAM 3 (SEQ ID NO:47), or
  - vi) intracellular sequences from CD28, from 4-1BB and from CD3zeta having ITAM 3, comprising the amino acid sequence of SEQ ID NO:53 or 89.
37. The dimeric antigen receptor (DAR) construct of claim 27, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:64, 67, 70, 73, 76, 79, 82 or 85.
38. The dimeric antigen receptor (DAR) construct of claim 27, wherein the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:65, 68, 71, 74, 77, 80, 83, or 86.
39. The precursor polypeptide of any one of claims 1-18, wherein upon cleavage of the self-cleaving sequence, the heavy chain variable region and the light chain variable region are capable of forming an antigen-binding domain that binds a BMCA (B-cell maturation antigen) protein, optionally wherein the BMCA (B-cell maturation antigen) protein comprises the amino acid sequence of SEQ ID NO:1, 2 or 3.

40. The dimeric antigen receptor (DAR) construct of claim 27, wherein
- a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region ; (iii) a hinge region comprising a CD8 and CD28 hinge region; (iv) a CD28 transmembrane region; and (v) an intracellular region comprising a CD28 co-stimulatory sequence and CD3zeta ITAM 1, 2 and 3 intracellular sequences; and wherein
  - b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,  
wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and  
wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein, optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V1 construct.
41. The dimeric antigen receptor (DAR) construct of claim 27, wherein
- a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO:6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a hinge region comprising a CD28 hinge region; (iv) a CD28 transmembrane region; and (v) an intracellular region comprising a 4-1BB co-stimulatory sequence and CD3zeta ITAM 1, 2 and 3 intracellular sequences; and wherein
  - b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain

variable region comprising the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,

wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and

wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein, optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V2a construct.

42. The dimeric antigen receptor (DAR) construct of claim 27, wherein

a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a hinge region; (iv) a CD28 transmembrane region; and (v) an intracellular region comprising a CD28 co-stimulatory sequence and CD3zeta ITAM 1, 2 and 3 intracellular sequences; and wherein

b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,

wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and

wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein, optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V2b construct.

43. The dimeric antigen receptor (DAR) construct of claim 27, wherein

a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain

variable region comprising the amino acid sequence of SEQ ID NO: 6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a hinge region comprising a CD28 hinge region; (iv) a CD28 transmembrane region; and (v) an intracellular region comprising a 4-1BB co-stimulatory sequence, a CD28 co-stimulatory sequence, and CD3zeta ITAM 1, 2 and 3 intracellular sequences; and wherein

- b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,

wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and

wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein, optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V2c construct.

44. The dimeric antigen receptor (DAR) construct of claim 27, wherein

- a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence selected from a group consisting of SEQ ID NO: 6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a hinge region comprising a CD28 hinge region; (iv) a CD28 transmembrane region; and (v) an intracellular region comprising a 4-1BB co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence, wherein the intracellular region optionally includes an intracellular CD28 co-stimulatory sequence; and wherein
- b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,

wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and  
wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein,  
optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V3 construct.

45. The dimeric antigen receptor (DAR) construct of claim 27, wherein
- a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO:6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a CD28 transmembrane region; and (iv) an intracellular region comprising a 4-1BB co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence; and wherein
  - b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO:8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,  
wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and  
wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein,  
optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V4 construct.
46. The dimeric antigen receptor (DAR) construct of claim 27, wherein
- a) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence selected from a group consisting of SEQ ID NO:6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a hinge region comprising a CD28

hinge region; (iv) a CD28 transmembrane region; and (v) an intracellular region comprising a CD28 co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence, wherein the intracellular region optionally includes an intracellular CD28 and 4-1BB co-stimulatory sequence; and wherein

- b) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO:8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,  
wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and  
wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein, optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V3c construct.

47. The dimeric antigen receptor (DAR) construct of claim 27, wherein

- c) the first polypeptide chain comprises a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO:6, 12, 14, 16, 18, 20, 22, 24, 26, or 28; (ii) an antibody heavy chain constant region; (iii) a CD28 transmembrane region; and (iv) an intracellular region comprising a 4-1BB co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence; and wherein
- d) the second polypeptide chain comprising a plurality of regions ordered from the amino terminus to the carboxyl terminus: (i) a BCMA antibody light chain variable region comprising the amino acid sequence of SEQ ID NO:8, 9, 10, 13, 15, 17, 19, 21, 23, 25, 27 or 30; and (ii) an antibody light chain constant region,  
wherein the antibody heavy chain constant region and the antibody light chain constant region form a dimerization domain, and  
wherein the antibody heavy chain variable region and the antibody light chain variable region form an antigen binding domain that binds a BCMA protein,

optionally wherein the dimeric antigen receptor (DAR) construct is a DAR V4 construct.

48. The DAR construct of claim 41, wherein the intracellular region comprising the 4-1BB co-stimulatory sequence and CD3zeta ITAM 1, 2 and 3 intracellular sequences comprises the amino acid sequence of SEQ ID NO:49.
49. The DAR construct of claim 42, wherein the intracellular region comprising the CD28 co-stimulatory sequence and CD3zeta ITAM 1, 2 and 3 intracellular sequences comprises the amino acid sequence of SEQ ID NO:50.
50. The DAR construct of claim 43, wherein the intracellular region comprising the 4-1BB co-stimulatory sequence, a CD28 co-stimulatory sequence, and CD3zeta ITAM 1, 2 and 3 intracellular sequences comprises the amino acid sequence of SEQ ID NO:51 or 88.
51. The DAR construct of claim 44, wherein the intracellular region comprising the 4-1BB co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence comprises the amino acid sequence of SEQ ID NO:52, or the intracellular region comprising a 4-1BB co-stimulatory sequence, a CD28 co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence comprises the amino acid sequence of SEQ ID NO:53 or 89.
52. The DAR construct of claim 45, wherein the intracellular region comprising the 4-1BB co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence comprises the amino acid sequence of SEQ ID NO:52.
53. The DAR construct of claim 46, wherein the intracellular region comprising the CD28 co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence comprises the amino acid sequence of SEQ ID NO:87.
54. The DAR construct of claim 47, wherein the intracellular region comprising the 4-1BB co-stimulatory sequence and a CD3zeta ITAM 3 intracellular sequence comprises the amino acid sequence of SEQ ID NO:52.

55. The DAR construct of claim 40 or 51, wherein the CD8 and CD28 hinge region comprises the amino acid sequence of SEQ ID NO:36.
56. The DAR construct of any one of claims 41-44, 46-49, or 54, wherein the hinge region comprises a CD28 hinge any one of claims region comprising the amino acid sequence of SEQ ID NO:35.
57. The DAR construct of any one of claims 40, 45, or 50, wherein the CD28 transmembrane region comprises the amino acid sequence of SEQ ID NO:37.
58. The DAR construct of any one of claims 40-55, wherein the heavy chain constant region comprises:
- a) a human IgG, IgA, IgD, IgE, or IgM CH1 domain;
  - b) a human IgG1, IgG2, IgG3, or IgG4 CH1 domain;
  - c) a human IgG1 domain;
  - d) an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:7 or 29; or
  - e) the amino acid sequence of SEQ ID NO:7 or 29.
59. The DAR construct of any one of claims 40-56, wherein the light chain constant region comprises:
- a) a human Ig kappa constant domain;
  - b) a human Ig lambda constant domain;
  - c) an amino acid sequence having at least 95% sequence identity to the amino acid sequence of SEQ ID NO:11 or 31; or
  - d) the amino acid sequence of SEQ ID NO:11 or 31.
60. A nucleic acid encoding the precursor polypeptide of any one of claims 1-18.
61. An expression vector comprising the nucleic acid of claim 60 operably linked to a promoter.

62. A host cell, or a population of host cells, harboring the nucleic acid of claim 60 operably linked to a promoter, optionally wherein the nucleic acid is present in an expression vector.
63. The host cell or the population of host cells of claim 62, wherein the host cell is a T lymphocyte (e.g., regulatory T cell, gamma-delta T cell or cytotoxic T cell), a NK (natural killer) cell, a macrophages, a dendritic cell, a mast cell, an eosinophil, a B lymphocyte, or a monocyte, or the population of host cells comprises T lymphocytes (e.g., regulatory T cells, gamma-delta T cells or cytotoxic T cells), NK (natural killer) cells, macrophages, dendritic cells, mast cells, eosinophils, B lymphocytes or monocytes.
64. The host cell or the population of host cells of claim 62, wherein the host cell is an autologous host cell or the population comprises autologous host cells.
65. The host cell or the population of host cells of claim 62, wherein the host cell is an allogeneic host cell or the population comprises allogeneic host cells.
66. A method for preparing a population of host cells expressing a plurality of a dimeric antigen receptor (DAR), comprising: culturing the population of host cells of any one of claims 62-65 under conditions suitable for expressing a plurality of the precursor polypeptide by the population of host cells, and suitable for processing the plurality of precursor polypeptides into a plurality of dimeric antigen receptors (DARs) by the population of host cells, wherein the processing by the population of host cells comprises cleaving the plurality of precursor polypeptide into a plurality of first and second polypeptide chains, assembling the plurality of first and second polypeptide chains with each other to form a plurality of dimeric antigen receptors (DARs), and anchoring the plurality of dimeric antigen receptors (DARs) in the cellular membrane of the population of host cells.
67. The method of claim 66, wherein the expression vector directs transient introduction of the nucleic acid encoding the precursor polypeptide into the host cell or the population of host cells.

68. The method of claim 66, wherein the expression vector directs stable insertion of the nucleic acid encoding the precursor polypeptide into the host cells' genome.
69. The method of claim 66, wherein the expression vector directs transcription and/or translation of the nucleic acid encoding the precursor polypeptide in the host cell or the population of host cells.
70. The method of claim 66, wherein the expression vector directs expression of the nucleic acid encoding the precursor polypeptide in the host cell or the population of host cells, wherein expression includes transcription and/or translation of the nucleic acid encoding the precursor polypeptide.
71. A population of host cells comprising a plurality of dimeric antigen receptors (DARs) anchored in the cellular membrane of the population of host cells prepared by the method of any one of claims 66-70.
72. A population of host cells expressing a plurality of a dimeric antigen receptor (DAR) construct according to any one of claims 19-59, wherein the DAR construct is anchored in the cellular membrane of the population of the host cells.
73. A pharmaceutical composition comprising the population of host cells of claim 71 or 72 and a pharmaceutically-acceptable excipient.
74. A method for treating a subject having a disease, disorder or condition associated with detrimental expression of a tumor antigen in the subject, comprising: administering to the subject the population of host cells of claim 71 or 72 or the pharmaceutical composition of claim 73.
75. The method of claim 74, wherein the disease is a hematologic cancer selected from the group consisting of non-Hodgkin's lymphoma (NHL), Burkitt's lymphoma (BL), B chronic lymphocytic leukemia (B-CLL), B and T acute lymphocytic leukemia (ALL), T cell lymphoma (TCL), acute myeloid leukemia (AML), hairy cell leukemia (HCL), Hodgkin's Lymphoma (HL), chronic myeloid leukemia (CML) and multiple myeloma (MM).

- 76. A first nucleic acid encoding the first polypeptide of any one of claims 19-59.
- 77. A second nucleic acid encoding the second polypeptide of any one of claims 19-59.
- 78. A first nucleic acid encoding the first polypeptide and a second nucleic acid encoding the second polypeptide of any one of claims 19-59.
- 79. A first expression vector comprising the first nucleic acid of claim 78 operably linked to a promoter and a second expression vector comprising the second nucleic acid of claim 78 operably linked to a promoter.
- 80. An expression vector comprising the first and second nucleic acid of claim 78 operably linked to a promoter.
- 81. A first host cell, or a first population of host cells, harboring the first expression vector of claim 79.
- 82. A second host cell, or a second population of host cells, harboring the second expression vector of claim 79.
- 83. A first host cell, or a first population of host cells, harboring the first expression vector of claim 79, and a second host cell, or a second population of host cells, harboring the second expression vector of claim 79.
- 84. A host cell, or a population of host cells, harboring the first and second expression vectors of claim 79.
- 85. A host cell, or a population of host cells, harboring the expression vector of claim 80.
- 86. The host cell or the population of host cells of any one of claims 81-84, wherein the host cell is a T lymphocyte (e.g., regulatory T cell, gamma-delta T cell or cytotoxic T cell), a NK (natural killer) cell, a macrophages, a dendritic cell, a mast cell, an

eosinophil, a B lymphocyte, or a monocyte or the population comprises T lymphocytes (e.g., regulatory T cells, gamma-delta T cells or cytotoxic T cells), NK (natural killer) cells, macrophages, dendritic cells, mast cells, eosinophils, B lymphocytes or monocytes.

87. The host cell or the population of host cells of any one of claims 81-84, wherein the host cell is an autologous host cell or the population comprises autologous host cells.
88. The host cell or the population of host cells of any one of claims 81-84, wherein the host cell is an allogeneic host cell or the population comprises allogeneic host cells.
89. A method for preparing a plurality of a dimeric antigen receptor (DAR), comprising: culturing the first and second population of host cells of claim 83 under conditions suitable for expressing a plurality of the first and second polypeptide chains.
90. A method for preparing a plurality of a dimeric antigen receptor (DAR), comprising: culturing the population of host cells of claim 84 under conditions suitable for expressing a plurality of the first and second polypeptide chains by the population of host cells, and suitable for processing the plurality of first and second polypeptides into a plurality of dimeric antigen receptors (DARs) by the population of host cells, wherein the processing by the population of host cells comprises assembling the plurality of first and second polypeptide chains with each other to form a plurality of dimeric antigen receptors (DARs), and anchoring the plurality of dimeric antigen receptors (DARs) in the cellular membrane of the population of host cells.
91. A method for preparing a plurality of a dimeric antigen receptor (DAR), comprising: culturing the population of host cells of claim 85 under conditions suitable for expressing a plurality of the first and second polypeptide chains by the population of host cells, and suitable for processing the plurality of first and second polypeptides into a plurality of dimeric antigen receptors (DARs) by the population of host cells, wherein the processing by the population of host cells comprises assembling the plurality of first and second polypeptide chains with each other to form a plurality of dimeric antigen receptors (DARs), and anchoring the plurality of dimeric antigen receptors (DARs) in the cellular membrane of the population of host cells.

92. The method of claim 89, wherein the first expression vector directs transient introduction of the nucleic acid encoding the first polypeptide chain into the first host cell or the first population of host cells, and wherein the second expression vector directs transient introduction of the nucleic acid encoding the second polypeptide chain into the second host cell or the second population of host cells.
93. The method of claim 89, wherein the first expression vector directs stable insertion of the nucleic acid encoding the first polypeptide chain into the first host cells' genome, and wherein the second expression vector directs stable insertion of the nucleic acid encoding the second polypeptide chain into the second host cells' genome.
94. The method of claim 89, wherein the first expression vector directs transcription and/or translation of the nucleic acid encoding the first polypeptide chain in the first host cell or the first population of host cells, and wherein the second expression vector directs transcription and/or translation of the nucleic acid encoding the second polypeptide chain in the second host cell or the second population of host cells.
95. The method of claim 90, wherein the first expression vector directs transient introduction of the nucleic acid encoding the first polypeptide chain into the host cell or the population of host cells, and wherein the second expression vector directs transient introduction of the nucleic acid encoding the second polypeptide chain into the host cell or the population of host cells.
96. The method of claim 90, wherein the first expression vector directs stable insertion of the nucleic acid encoding the first polypeptide chain into the host cells' genome, and wherein the second expression vector directs stable insertion of the nucleic acid encoding the second polypeptide chain into the host cells' genome.
97. The method of claim 90, wherein the first expression vector directs transcription and/or translation of the nucleic acid encoding the first polypeptide chain in the host cell or the population of host cells, and wherein the second expression vector directs transcription and/or translation of the nucleic acid encoding the second polypeptide chain in the host cell or the population of host cells.

98. The method of claim 91, wherein the expression vector directs transient introduction of the nucleic acid encoding the first and second polypeptide chains into the host cell or the population of host cells.
99. The method of claim 91, wherein the expression vector directs stable insertion of the nucleic acid encoding the first and second polypeptide chains into the host cells' genome.
100. The method of claim 91, wherein the expression vector directs transcription and/or translation of the nucleic acid encoding the first and second polypeptide chains in the host cell or the population of host cells.
101. A population of host cells comprising a plurality of dimeric antigen receptors (DARs) anchored in the cellular membrane of the population of host cells prepared by the method of any one of claims 90-100.
102. A population of host cells expressing a plurality of a dimeric antigen receptor (DAR) construct according to any one of claims 19-59 anchored in the cellular membrane of the population of the host cells.
103. A pharmaceutical composition comprising the population of host cells of claim 101 or 102 and a pharmaceutically-acceptable excipient.
104. A method for treating a subject having a disease, disorder or condition associated with detrimental expression or over-expression of a tumor antigen in the subject, comprising: administering to the subject the population of host cells of claim 101 or 102 or the pharmaceutical composition of claim 103.
105. The method of claim 104, wherein the disease is a hematologic cancer selected from the group consisting of non-Hodgkin's lymphoma (NHL), Burkitt's lymphoma (BL), B chronic lymphocytic leukemia (B-CLL), B and T acute lymphocytic leukemia (ALL), T cell lymphoma (TCL), acute myeloid leukemia (AML), hairy cell leukemia (HCL), Hodgkin's Lymphoma (HL), chronic myeloid leukemia (CML) and multiple myeloma (MM).