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(54) Title: PRECISION/CONTEXT-DEPENDENT ACTIVATABLE ANTIBODIES, AND METHODS OF MAKING AND USING THE SAME

(57) Abstract: Provided herein are libraries containing synthetic polynucleotides that encode activatable binding polypeptides. Further provided herein are activatable binding polypeptides and polypeptide libraries containing such activatable binding polypeptides. Also provided herein are vectors, vector libraries, cells, kits, and methods of making and using activatable polypeptide libraries.

PRECISION/CONTEXT-DEPENDENT ACTIVATABLE ANTIBODIES, AND METHODS OF MAKING AND USING THE SAME

REREFERENCE TO SEQUENCE LISTING

[0001] The content of the following submission on ASCII text file is incorporated herein by reference in its entirety: a computer readable form (CRF) of the Sequence Listing (file name: 695402000640SEQLIST.txt, date recorded: January 8, 2018, size: 35 KB).

FIELD OF THE INVENTION

[0002] The present disclosure relates to polynucleotides and polynucleotide libraries useful for screening for and/or identifying one or more precision/context-dependent activatable binding polypeptides (*e.g.,* activatable antibodies), as well as polypeptides and polypeptide libraries useful for screening for and/or identifying precision/context-dependent activatable binding polypeptides (*e.g.,* activatable antibodies capable of binding to CTLA4 or CD137 when in active form), cells, methods, and kits related thereto.

BACKGROUND

[0003] Activatable binding polypeptides exhibit an "activatable" conformation such that an antigen binding moiety contained therein is less accessible to bind to its target when uncleaved than after cleavage in the presence of one or more specific proteases. These activatable binding polypeptides thus provide antigen-specific binding proteins that are only capable of binding their targets in certain contexts (*e.g.,* in the protease-rich tumor microenvironment). While a number of interesting activatable binding polypeptides have been developed, the process of developing such proteins is slow, labor intensive, and costly. Accordingly, there exists a need for improved methods and products useful for identifying self-blocking peptides for activatable binding polypeptides.

[0004] All references cited herein, including patent applications, patent publications, non-patent literature, and UniProtKB/Swiss-Prot/GenBank Accession numbers are herein

incorporated by reference in their entirety, as if each individual reference were specifically and individually indicated to be incorporated by reference.

BRIEF SUMMARY

[0005] To meet the above and other needs, disclosed herein are libraries of polynucleotides *e.g.,* that are useful for screening for and/or identifying activatable binding polypeptides (*i.e.,* activatable antibodies). The present disclosure is based, at least in part, on the finding that polypeptides described herein show a significantly improved masking efficiency before activation, allowing for better design, screening and/or identification of activatable binding polypeptides (*i.e.,* activatable antibodies) with superior therapeutic indexes and safety profiles. The present disclosure is further based, at least in part, on the surprising finding that the polynucleotide libraries described herein may be successfully constructed and screened to identify activatable binding polypeptides, (*see* Examples 1 and 2 below). Disclosed herein are precision/context-dependent activatable binding polypeptides that bind to human CTLA4 (*see* Example 3) or human CD137 (*see* Example 5) when in active form but not in inactive form, *i.e.,* they bind their target (when in active form) only after cleavage of the cleavable moiety (CM) to remove the first peptide (FP) (*i.e.,* a masking moiety (MM) or self-blocking peptide). The discovered first peptides (FPs) (*e.g.,* masking moieties) described herein are capable of efficiently masking antibody activity and/or reducing or completely inhibiting antigen binding, while in some embodiments being devoid of the chemically labile residues methionine and/or tryptophan. Furthermore, activatable antibodies identified using the polynucleotide libraries described herein are as efficient at treating multiple cancer types as their parental antibody, while having significantly reduced cytotoxicity even in susceptible animals (NOD mice, *see* Example 4).

[0006] Accordingly, in one aspect, provided herein is a library comprising polynucleotides, wherein at least one of the polynucleotides encodes a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D,

E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, the polynucleotides in the library encode at least two, at least three, at least four, at least five, or at least ten unique polypeptides and each unique polypeptide comprise, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments that may be combined with any of the preceding embodiments, each of the polynucleotides in the library encodes a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments that may be combined with any of the preceding embodiments, the FP is encoded by a polynucleotide sequence comprising a nucleic acid sequence according to Formula (XIV): $(NNK)_mTGY(NNK)_nTGY(NNK)_o$ (SEQ ID NO: 87), wherein each N is independently A, G, T, or C, wherein each K is independently T or G, and wherein each Y is independently T or C.

[0007] In some embodiments that may be combined with any of the preceding embodiments, each X is not M, W, or C. In some embodiments that may be combined with any of the preceding embodiments, each X in X_m of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_n of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y,

S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_o of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, m is 6. In some embodiments that may be combined with any of the preceding embodiments, n is from 6-8. In some embodiments that may be combined with any of the preceding embodiments, n is 6. In some embodiments that may be combined with any of the preceding embodiments, o is from 1-2. In some embodiments that may be combined with any of the preceding embodiments, o is 2. In some embodiments that may be combined with any of the preceding embodiments, the FP further comprises, at its N-terminus, an additional amino acid sequence. In some embodiments, the additional amino acid sequence comprises the amino acid sequence of SEQ ID NO: 16.

[0008] In some embodiments that may be combined with any of the preceding embodiments, the first cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. In some embodiments that may be combined with any of the preceding embodiments, the CM further comprises a first linker (L_1) C-terminal to the first cleavage site. In some embodiments, the L_1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 17-24. In some embodiments that may be combined with any of the preceding embodiments, the CM further comprises a second cleavage site. In some embodiments, the second cleavage site is C-terminal to the L_1. In some embodiments, the second cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-

13, Caspase-14, and TACE. In some embodiments, the first and second cleavage sites are different. In some embodiments that may be combined with any of the preceding embodiments, the CM further comprises a second linker (L_2) C-terminal to the second cleavage site. In some embodiments, the L_2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 17-24.

[0009] In some embodiments that may be combined with any of the preceding embodiments, the polypeptide encoded by one or more polynucleotides in the library comprises a first peptide (FP) and a cleavable moiety (CM) comprising an amino acid sequence according to Formula (III): $EVGSYX_1X_2X_3X_4X_5X_6CX_7X_8X_9X_{10}X_{11}X_{12}CX_{13}X_{14}SGRSAGGGGTENLYFQGSGGS$ (SEQ ID NO: 3), wherein X1 is A, D, I, N, P, or Y, x2 is A, F, N, S, or V, X3 is A, H, L, P, S, V, or Y, X4 is A, H, S, or Y, X5 is A, D, P, S, V, or Y, X6 is A, D, L, S, or Y, X7 is D, P, or V, X8 is A, D, H, P, S, or T, X9 is A, D, F, H, P, or Y, X10 is L, P, or Y, X11 is F, P, or Y, X12 is A, P, S, or Y, X13 is A, D, N, S, T, or Y, and X14 is A, S, or Y. In some embodiments, each of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence according to Formula (III). In some embodiments that may be combined with any of the preceding embodiments, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 25-46.

[0010] In some embodiments that may be combined with any of the preceding embodiments, the TBM comprises an antibody light chain variable region. In some embodiments, the TBM further comprises a heavy chain variable region C-terminal to the light chain variable region. In some embodiments, the library further comprises polynucleotides that encode one or more antibody heavy chain variable regions. In some embodiments, the heavy chain variable region and light chain variable region forms an antigen binding site that is capable of binding to a target in the absence of a masking moiety (MM).

[0011] In some embodiments that may be combined with any of the preceding embodiments, the TBM comprises an antibody heavy chain variable region. In some embodiments, the TBM further comprises a light chain variable region C-terminal to the heavy chain variable region. In some embodiments, the library further comprises polynucleotides that

encode one or more antibody light chain variable regions. In some embodiments, the heavy chain variable region and light chain variable region forms an antigen binding site that is capable of binding to a target in the absence of a masking moiety (MM).

[0012] In some embodiments that may be combined with any of the preceding embodiments, at least one of the polynucleotides encoding the polypeptide is in a vector. In some embodiments, the vector is an expression vector or a display vector. In some embodiments that may be combined with any of the preceding embodiments, at least one of the polynucleotides encoding the polypeptide is in a cell. In some embodiments, the cell is a bacterial cell, a yeast cell, an insect cell, or a mammalian cell.

[0013] Other aspects of the present disclosure relate to a method of producing an activatable antibody comprising culturing any of the cells described herein under conditions suitable for producing the activatable antibody. In some embodiments, the method further comprises recovering the activatable antibody produced by the cell. In some embodiments, the method further comprises testing the activatable antibody for the ability to maintain an activatable phenotype while soluble.

[0014] Other aspects of the present disclosure relate to a method of using any of the libraries described herein to screen for an activatable antibody that binds to a target, comprising the steps of a) contacting the expression products of the library with the target before the CM is cleaved, b) contacting the expression products of the library with the target after the CM is cleaved, and c) isolating one or more of the expression products that binds to the target after the CM is cleaved, but does not bind to the target before the CM is cleaved. In some embodiments, the CM comprises at least a first protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. In some embodiments, the target is CTLA4, CD137, PD-1, PD-L1, PD-L2, LAG3, TIM3, B7-H3, OX40, CD3, CD19, CD20, CD40, CD95, CD120a,

BTLA, VISTA, ICOS, BCMA, Her1, Her2, Her3, and/or B7-H4. In some embodiments, the target is CTLA4 or CD137.

[0015] Other aspects of the present disclosure relate to a polypeptide encoded by one or more polynucleotides of any of the libraries described herein.

[0016] Other aspects of the present disclosure relate to a kit comprising any of the libraries described herein.

[0017] Other aspects of the present disclosure relate to a library comprising antigen binding domains, wherein at least one of the antigen binding domains comprises a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, at least two, at least three, at least four, at least five, or at least ten of the antigen binding domains comprise a unique polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments that may be combined with any of the preceding embodiments, each of the antigen binding domains comprises a unique polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D,

E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments that may be combined with any of the preceding embodiments, the TBM comprises an antibody light chain variable region and the antigen binding domain further comprises an antibody heavy chain variable region. In some embodiments that may be combined with any of the preceding embodiments, the TBM comprises an antibody heavy chain variable region and the antigen binding domain further comprises an antibody light chain variable region. In some embodiments that may be combined with any of the preceding embodiments, each X is not M, W, or C. In some embodiments that may be combined with any of the preceding embodiments, each X in X_m in formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_n of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_o of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0018] Other aspects of the present disclosure relate to an antibody light chain comprising a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region. Other aspects of the present disclosure relate to an antibody comprising a heavy chain and a light chain, wherein the light chain is any of the antibody light chains described herein.

[0019] Other aspects of the present disclosure relate to an antibody heavy chain comprising a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable

moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody heavy chain variable region. Other aspects of the present disclosure relate to an antibody comprising a heavy chain and a light chain, wherein the heavy chain is any of the antibody heavy chains described herein.

[0020] Other aspects of the present disclosure relate to a cell comprising at least one polypeptide displayed on its surface, wherein the at least polypeptide comprises, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the FP comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, the cell is a bacterial cell, a yeast cell, an insect cell, or a mammalian cell. In some embodiments that may be combined with any of the preceding embodiments, each X is not M, W, or C. In some embodiments that may be combined with any of the preceding embodiments, each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0021] Other aspects of the present disclosure relate to an activatable antibody comprising: a) a polypeptide comprising, from N-terminus to C-terminus, a masking moiety (MM), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the MM comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from

3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; wherein the MM inhibits the binding of the activatable antibody to human CTLA4 when the CM is not cleaved; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region (VL); and b) an antibody heavy chain variable region (VH); and wherein the activatable antibody binds to human CTLA4 when the CM is cleaved. In some embodiments, the CM comprises at least a first protease cleavage site and is cleaved with one or more proteases selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. In some embodiments that may be combined with any of the preceding embodiments, each X is not M, W, or C. In some embodiments that may be combined with any of the preceding embodiments, each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, the MM comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 72-78. In some embodiments that may be combined with any of the preceding embodiments, the VL comprises an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 62, an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 63, and an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 64. In some embodiments that may be combined with any of the preceding embodiments, the VL comprises the amino acid sequence of SEQ ID NO: 48. In some embodiments that may be combined with any of the preceding embodiments, the VH comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 59, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 60, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 61. In some

embodiments that may be combined with any of the preceding embodiments, the VH comprises the amino acid sequence of SEQ ID NO: 47.

[0022] Other aspects of the present disclosure relate to an activatable antibody comprising: a) a polypeptide comprising, from N-terminus to C-terminus, a masking moiety (MM), a cleavable moiety (CM), and a target binding moiety (TBM), wherein the MM comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; wherein the MM inhibits the binding of the activatable antibody to human CD137 when the CM is not cleaved; wherein the CM comprises at least a first cleavage site; and wherein the TBM comprises an antibody light chain variable region (VL); and b) an antibody heavy chain variable region (VH); and wherein the activatable antibody binds to human CD137 when the CM is cleaved. In some embodiments, the CM comprises at least a first protease cleavage site and is cleaved with one or more proteases selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. In some embodiments that may be combined with any of the preceding embodiments, each X is not M, W, or C. In some embodiments that may be combined with any of the preceding embodiments, each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments that may be combined with any of the preceding embodiments, the MM comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 79-85. In some embodiments that may be combined with any of the preceding embodiments, the VL comprises an HVR-L1 comprising the amino acid

sequence of SEQ ID NO: 68, an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 69, and an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 70. In some embodiments that may be combined with any of the preceding embodiments, the VL comprises the amino acid sequence of SEQ ID NO: 50. In some embodiments that may be combined with any of the preceding embodiments, the VH comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 65, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 66, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 67. In some embodiments that may be combined with any of the preceding embodiments, the VH comprises the amino acid sequence of SEQ ID NO: 49.

[0023] Other aspects of the present disclosure relate to a polynucleotide encoding any of the activatable antibodies described herein. In other aspects, the present disclosure relates to a vector comprising any of the polynucleotides described herein (*e.g.,* a polynucleotide encoding an activatable antibody). In some embodiments, the vector is an expression vector and/or a display vector. In other aspects, the present disclosure relates to a host cell comprising any of the polynucleotides and/or vectors described herein (*e.g.,* a polynucleotide and/or vector encoding an activatable antibody). In some embodiments, the host cell is a eukaryotic cell. In some embodiments, the host cell is a Chinese Hamster Ovary (CHO) cell. In other aspects, the present disclosure relates to a method of making an activatable antibody comprising culturing any of the host cells described herein under conditions suitable for producing the antibody or activatable antibody. In some embodiments, the method further comprises recovering the antibody or activatable antibody produced by the cell.

[0024] Other aspects of the present disclosure relate to a method of treating or delaying progression of cancer in a subject in need thereof, the method comprising administering to the subject an effective amount of a polypeptide encoded by one or more polynucleotides from any of the libraries described herein and/or any of the activatable antibodies described herein. In some embodiments, the method further comprises administering to the subject an effective amount of at least one additional therapeutic agent. In some embodiments, the at least one additional therapeutic agent is selected from the group consisting of viral gene therapy, immune checkpoint inhibitors, target therapies, radiation therapies, and chemotherapies. In some embodiments, the at least one additional therapeutic agent is selected from the group

consisting of pomalyst, revlimid, lenalidomide, pomalidomide, thalidomide, a DNA-alkylating platinum-containing derivative, cisplatin, 5-fluorouracil, cyclophosphamide, an anti-CD137 antibody, an anti-CTLA4 antibody, an anti-PD-1 antibody, an anti-PD-L1 antibody, an anti-CD20 antibody, an anti-CD40 antibody, an anti-DR5 antibody, an anti-CD1d antibody, an anti-TIM3 antibody, an anti-SLAMF7 antibody, an anti-KIR receptor antibody, an anti-OX40 antibody, an anti-HER2 antibody, an anti-ErbB-2 antibody, an anti-EGFR antibody, cetuximab, rituximab, trastuzumab, pembrolizumab, radiotherapy, single dose radiation, fractionated radiation, focal radiation, whole organ radiation, IL-12, IFNα, GM-CSF, a chimeric antigen receptor, adoptively transferred T cells, an anti-cancer vaccine, and an oncolytic virus.

[0025] It is to be understood that one, some, or all of the properties of the various embodiments described above and herein may be combined to form other embodiments of the present disclosure. These and other aspects of the present disclosure will become apparent to one of skill in the art. These and other embodiments of the present disclosure are further described by the detailed description that follows.

BRIEF DESCRIPTION OF THE DRAWINGS

[0026] **FIG. 1** shows a schematic of an exemplary selection process for self-blocking peptides using the Fab fragment of the target antibody displayed on yeast surface.

[0027] **FIG. 2** shows a schematic of an exemplary selection process for self-blocking peptide using the scFv fragment of the target antibody displayed on yeast surface.

[0028] **FIGS. 3A-B** show functional display of Fabs and scFvs targeting CTLA4 on yeast, as determined by flow cytometry. **FIG. 3A** shows functional display of Fabs targeting CTLA4 on the surface of yeast. **FIG. 3B** shows functional display of scFvs targeting CTLA4 on the surface of yeast.

[0029] **FIG. 4** shows an exemplary selection process for activatable antibodies targeting human CTLA4. A yeast library displaying fusion proteins were subjected to several rounds of FACS-based screening.

[0030] **FIGS. 5A-B** show CTLA4 binding affinity of exemplary CTLA4 activatable antibody clones, as determined by flow cytometry. **FIG. 5A** shows binding affinity of CTLA4 activatable antibody clones in the scFv format, including the CTLA4 activatable antibody clone B13287 with the masking peptide intact, or with the masking peptide cleaved by the TEV protease, as compared to the scFv fragment of the target antibody with no masking peptide. **FIG. 5B** shows CTLA4 binding affinity of CTLA4 activatable antibody clones in the Fab format, including the CTLA4 activatable antibody clone B13189 with the masking peptide intact, or with the masking peptide cleaved by the TEV protease, as compared to the Fab fragment of the target antibody with no masking peptide.

[0031] **FIGS. 6A-B** show the masking efficiency of exemplary CTLA4 activatable antibodies TY22401, TY22403, TY22402, and TY22404, as compared to the parental antibody TY21580. **FIG. 6A** shows the association and dissociation curves of the indicated activatable antibodies as compared to the parental antibody TY21580, as determined by the ForteBio system. **FIG. 6B** shows a graph of the relative ratio of bound activatable antibodies, as compared to the parental antibody TY21580.

[0032] **FIGS. 7A-C** show the masking efficiency of exemplary CTLA4 activatable antibodies against recombinant human CTLA4-Fc, as determined by ELISA. **FIG. 7A** shows a first batch of ELISA data indicating binding of CTLA4 activatable antibodies TY22401, TY22402, TY22403, TY22404 to recombinant human CTLA4-Fc, as compared to the parental antibody TY21580. **FIG. 7B** shows a second batch of ELISA data indicating binding of CTLA4 activatable antibodies TY22401, TY22402, TY22403, TY22404 to recombinant human CTLA4-Fc, as compared to the parental antibody TY21580. **FIG. 7C** shows binding of CTLA4 activatable antibodies TY22563, TY22564, TY22565, TY22566 to recombinant human CTLA4-Fc, as compared to the parental antibody TY21580.

[0033] **FIGS. 8A-B** show activity of CTLA4 activatable antibody TY22404 upon removal of the masking peptide. **FIG. 8A** shows SDS-PAGE results of activatable antibody TY22404 with no treatment, treated with the protease uPA, or treated with 5 or 10 units of the protease MMP-9. **FIG. 8B** shows binding of activatable antibody TY22404 with no treatment, treated

with the protease uPA, or treated with the protease MMP-9, as compared to the parental antibody TY21580, determined by ELISA.

[0034] **FIGS. 9A-C** show the size-exclusion chromatography (SEC) profiles of exemplary activatable antibodies under accelerated stress conditions. **FIG. 9A** shows the SEC profiles of activatable antibody TY22402 after six cycles of freezing and thawing, as compared to the control condition. **FIG. 9B** shows the SEC profiles of activatable antibody TY22402 after seven days at 50°C, as compared to the control condition. **FIG. 9C** shows the percentages of SEC main peak area of the exemplary activatable antibodies after seven days at 50°C, after storage at 40°C for up to 28 days, or after six cycles of freezing and thawing, as compared to the control condition.

[0035] **FIG. 10** shows the percentages of SEC main peak area of activatable antibodies TY22401 and TY22402 after storage at approximately 8mg/mL or at >150mg/mL.

[0036] **FIG. 11** shows the masking efficiency of untreated activatable antibodies TY21580, TY22401, TY22402 and TY22566 incubated at pH 3.7 for 30 minutes, or incubated at pH 3.7 for an hour, as determined by the ForteBio System.

[0037] **FIGS. 12A-B** show human peripheral blood mononuclear cell (PBMC) activation by isotype control antibody, parental antibody TY21580, or exemplary CTLA4 activatable antibodies TY22401, TY22402, or TY22404, as measured by ELISA. **FIG. 12A** shows the effect on IL-2 secretion from CD3-primed human PBMCs stimulated with isotype control antibody, parental antibody TY21580, and exemplary CTLA4 activatable antibodies TY22401, TY22402, or TY22404. **FIG. 12B** shows the effect on IFNγ secretion from CD3-primed human PBMCs stimulated with isotype control antibody, parental antibody TY21580, and exemplary CTLA4 activatable antibodies TY22401, TY22402, or TY22404.

[0038] **FIG. 13** shows the antibody-dependent cell-mediated cytotoxicity (ADCC) activity of isotype control antibody, the parental antibody TY21580, or exemplary activatable antibodies TY22401, TY21580, or TY22404 on HEK293F cells transiently overexpressing human CTLA4, as determined by an ADCC reporter gene assay.

[0039] **FIGS. 14A-B** show the *in vivo* anti-tumor efficacy of parental antibody TY21580, isotype control antibody, or exemplary CTLA4 activatable antibodies TY22401, TY22402, or TY22566 in an MC38 syngeneic mouse colorectal tumor model. **FIG. 14A** shows the tumor growth curves of different treatment groups of female C57BL/6 mice bearing MC38-established tumors. Data points represent group mean; error bars represent SEM. **FIG. 14B** shows individual tumor growth curves for the groups treated with TY21580, TY22401, TY22402, and TY22566.

[0040] **FIG. 15** shows the *in vivo* anti-tumor efficacy of isotype control antibody, parental antibody TY21580, or one of three activatable antibodies, in a CT26 syngeneic mouse colorectal tumor model. Tumor growth curves of different treatment groups of female C57BL/6 mice bearing CT26-established tumors are shown. Data points represent group mean; error bars represent SEM.

[0041] **FIG. 16** shows the *in vivo* anti-tumor efficacy of isotype control antibody, parental antibody TY21580, or one of three activatable antibodies, in an H22 syngeneic mouse liver tumor model. Tumor growth curves of different treatment groups of female C57BL/6 mice bearing H22-established tumors are shown. Data points represent group mean; error bars represent SEM.

[0042] **FIGS. 17A-B** show the *in vivo* anti-tumor efficacy of parental antibody TY21580, isotype control antibody, and exemplary activatable antibodies TY22401, TY22402, or TY22566 in a 3LL syngeneic mouse lung tumor model. **FIG.17A** shows the tumor growth curves of different treatment groups of female C57BL/6 mice bearing 3LL-established tumors. Data points represent group mean; error bars represent SEM. **FIG. 17B** shows individual tumor growth curves for the groups treated with TY21580, TY22401, TY22402, and TY22566.

[0043] **FIGS. 18A-C** show time courses of the blood concentrations of the test articles (TAs) intravenously administered at a concentration of 10 mg/kg to female BALB/c mice, as determined by ELISA. **FIG. 18A** shows a time course of the blood concentrations of the activatable antibody TY22401 intravenously administered at a concentration of 10 mg/kg to female BALB/c mice, as compared to the parental antibody TY21580. **FIG. 18B** shows a time course of the blood concentrations of the activatable antibody TY22402 intravenously

administered at a concentration of 10 mg/kg to female BALB/c mice, as compared to the parental antibody TY21580. **FIG. 18C** shows a time course of the blood concentrations of the activatable antibody TY22404 intravenously administered at a concentration of 10 mg/kg to female BALB/c mice, as compared to the parental antibody TY21580.

[0044] **FIG.19** shows the repeated dosing toxicity of isotype control antibody, parental antibody TY21580, and exemplary activatable antibodies TY22566, TY22401, and TY22402 using the NOD mouse model. Percent survival rate over 20 days were shown for each treatment group.

[0045] **FIGS. 20A-B** show functional display of Fabs and scFvs targeting human CD137 on yeast, as determined by flow cytometry. **FIG. 20A** shows scFvs targeting CD137 on the surface of yeast. **FIG. 20B** shows Fabs targeting CD137 on the surface of yeast.

[0046] **FIG. 21** shows an exemplary selection process for activatable antibodies targeting human CD137. A yeast library displaying fusion proteins were subjected to several rounds of FACS-based screening.

[0047] **FIGS. 22A-B** show CD137 binding affinity of exemplary CD137 activatable antibody clones, as determined by flow cytometry. **FIG. 22A** shows binding affinity of CD137 activatable antibody clones in the scFv format, including the CD137 activatable antibody clone B13428 with the masking peptide intact, or with the masking peptide cleaved by the TEV protease, as compared to the scFv fragment of the target antibody with no masking peptide. **FIG. 22B** shows CD137 binding affinity of CD137 activatable antibody clones in the scFv format, including the CD137 activatable antibody clone B13439 with the masking peptide intact, or with the masking peptide cleaved by the TEV protease, as compared to the scFv fragment of the target antibody with no masking peptide.

[0048] **FIG. 23** shows masking efficiency of exemplary activatable antibodies against human CD137, as compared to the parental antibody TY21242, determined by flow cytometry.

DETAILED DESCRIPTION

I. General techniques

[0049] The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized methodologies described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 3d edition (2001) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.; *Current Protocols in Molecular Biology* (F.M. Ausubel, et al. eds., (2003)); the series *Methods in Enzymology* (Academic Press, Inc.): *PCR 2: A Practical Approach* (M.J. MacPherson, B.D. Hames and G.R. Taylor eds. (1995)), Harlow and Lane, eds. (1988) *Antibodies, A Laboratory Manual*, and *Animal Cell Culture* (R.I. Freshney, ed. (1987)); *Oligonucleotide Synthesis* (M.J. Gait, ed., 1984); *Methods in Molecular Biology*, Humana Press; *Cell Biology: A Laboratory Notebook* (J.E. Cellis, ed., 1998) Academic Press; *Animal Cell Culture* (R.I. Freshney), ed., 1987); *Introduction to Cell and Tissue Culture* (J.P. Mather and P.E. Roberts, 1998) Plenum Press; *Cell and Tissue Culture: Laboratory Procedures* (A. Doyle, J.B. Griffiths, and D.G. Newell, eds., 1993-8) J. Wiley and Sons; *Handbook of Experimental Immunology* (D.M. Weir and C.C. Blackwell, eds.); *Gene Transfer Vectors for Mammalian Cells* (J.M. Miller and M.P. Calos, eds., 1987); *PCR: The Polymerase Chain Reaction*, (Mullis et al., eds., 1994); *Current Protocols in Immunology* (J.E. Coligan et al., eds., 1991); *Short Protocols in Molecular Biology* (Wiley and Sons, 1999); *Immunobiology* (C.A. Janeway and P. Travers, 1997); *Antibodies* (P. Finch, 1997); *Antibodies: A Practical Approach* (D. Catty., ed., IRL Press, 1988-1989); *Monoclonal Antibodies: A Practical Approach* (P. Shepherd and C. Dean, eds., Oxford University Press, 2000); *Using Antibodies: A Laboratory Manual* (E. Harlow and D. Lane (Cold Spring Harbor Laboratory Press, 1999); *The Antibodies* (M. Zanetti and J. D. Capra, eds., Harwood Academic Publishers, 1995); and *Cancer: Principles and Practice of Oncology* (V.T. DeVita et al., eds., J.B. Lippincott Company, 1993).

II. Definitions

[0050] Before describing the present disclosure in detail, it is to be understood that this present disclosure is not limited to particular compositions or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

[0051] As used herein, the singular forms "a", "an" and "the" include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to "a molecule" optionally includes a combination of two or more such molecules, and the like.

[0052] The term "about" as used herein refers to the usual error range for the respective value readily known to the skilled person in this technical field. Reference to "about" a value or parameter herein includes (and describes) embodiments that are directed to that value or parameter per se.

[0053] It is understood that aspects and embodiments of the present disclosure described herein include "comprising," "consisting," and "consisting essentially of" aspects and embodiments.

[0054] The term "and/or" as used herein a phrase such as "A and/or B" is intended to include both A and B; A or B; A (alone); and B (alone). Likewise, the term "and/or" as used herein a phrase such as "A, B, and/or C" is intended to encompass each of the following embodiments: A, B, and C; A, B, or C; A or C; A or B; B or C; A and C; A and B; B and C; A (alone); B (alone); and C (alone).

[0055] The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.,* hydroxyproline, gamma-carboxyglutamate, and O-phosphoserine. The term "amino acid analogs" refers to compounds that have the same basic chemical structure as a naturally occurring amino acid but the C-terminal carboxy group, the N-terminal amino group, or side chain functional group has been chemically modified to another functional group. The term "amino acid mimetics" refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

[0056] As used herein, the twenty conventional amino acids and their abbreviations follow conventional usage. *See e.g., Immunology—A Synthesis* (2nd Edition, E. S. Golub and D. R. Gren, Eds., Sinauer Associates, Sunderland, Mass. (1991)).

[0057] The terms "polypeptide," "protein," and "peptide" are used interchangeably herein and may refer to polymers of two or more amino acids.

[0058] "Polynucleotide," or "nucleic acid," as used interchangeably herein, refer to polymers of nucleotides of any length, and include DNA and RNA. The nucleotides can be deoxyribonucleotides, ribonucleotides, modified nucleotides or bases, and/or their analogs, or any substrate that can be incorporated into a polymer by DNA or RNA polymerase or by a synthetic reaction. A polynucleotide may comprise modified nucleotides, such as methylated nucleotides and their analogs. If present, modification to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may comprise modification(s) made after synthesis, such as conjugation to a label. Other types of modifications include, for example, "caps," substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, *etc.*) and with charged linkages (*e.g.*, phosphorothioates, phosphorodithioates, *etc.*), those containing pendant moieties, such as, for example, proteins (*e.g.*, nucleases, toxins, antibodies, signal peptides, ply-L-lysine, *etc.*), those with intercalators (*e.g.*, acridine, psoralen, *etc.*), those containing chelators (*e.g.*, metals, radioactive metals, boron, oxidative metals, *etc.*), those containing alkylators, those with modified linkages (*e.g.*, alpha anomeric nucleic acids, *etc.*), as well as unmodified forms of the polynucleotides(s). Further, any of the hydroxyl groups ordinarily present in the sugars may be replaced, for example, by phosphonate groups, phosphate groups, protected by standard protecting groups, or activated to prepare additional linkages to additional nucleotides, or may be conjugated to solid or semi-solid supports. The 5' and 3' terminal OH can be phosphorylated or substituted with amines or organic capping group moieties of from 1 to 20 carbon atoms. Other hydroxyls may also be derivatized to standard protecting groups. Polynucleotides can also contain analogous forms of ribose or deoxyribose sugars that are generally known in the art, including, for example, 2'-O-methyl-, 2'-O-allyl-, 2'-fluoro- or 2'-azido-ribose, carbocyclic sugar analogs, α-anomeric sugars, epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, sedoheptuloses, acyclic analogs, and basic nucleoside analogs such as methyl riboside. One or more

phosphodiester linkages may be replaced by alternative linking groups. These alternative linking groups include, but are not limited to, embodiments wherein phosphate is replaced by P(O)S ("thioate"), P(S)S ("dithioate"), (O)NR2 ("amidate"), P(O)R, P(O)OR', CO, or CH2 ("formacetal"), in which each R or R' is independently H or substituted or unsubstituted alkyl (1-20 C) optionally containing an ether (-O-) linkage, aryl, alkenyl, cycloalkyl, cycloalkenyl or araldyl. Not all linkages in a polynucleotide need be identical. The preceding description applies to all polynucleotides referred to herein, including RNA and DNA.

[0059] The term "isolated nucleic acid" refers to a nucleic acid molecule of genomic, cDNA, or synthetic origin, or a combination thereof, which is separated from other nucleic acid molecules present in the natural source of the nucleic acid. For example, with regard to genomic DNA, the term "isolated" includes nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5′ and 3′ ends of the nucleic acid of interest.

[0060] As used herein, "library" refers to a set of two or more entities having a shared class. For example, a library containing polynucleotides may refer to a set of two or more polynucleotides. The term "library" is used herein in the broadest sense and specifically covers sub-libraries that may or may not be combined.

[0061] As used herein, "unique" refers to a member of a set that is different from other members of the set. For example, a unique activatable antibody in a library may refer to an activatable antibody having a particular sequence not shared by other activatable antibodies in the library. As a practical matter, it is to be understood that a "unique" member of a physical realization of a library may be present in more than one copy. For example, a library may contain a plurality of "unique" activatable antibodies, with one or more of the "unique" activatable antibody molecules occurring in more than one copy.

[0062] As used herein, "diversity" refers to a variety and/or heterogeneity. For example, a diversity of antibodies in a library may refer to a variety of antibodies with unique sequences present in the library.

[0063] The term "antibody" is used herein in the broadest sense and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies, trispecific antibodies), and antibody fragments (*e.g.*, Fab, Fab', Fab'-SH, F(ab')2, Fv and/or a single-chain variable fragment or scFv) so long as they exhibit the desired biological activity.

[0064] In some embodiments, the term "antibody" refers to an antigen-binding protein (*i.e.*, immunoglobulin) having a basic four-polypeptide chain structure consisting of two identical heavy (H) chains and two identical light (L) chains. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each heavy chain has, at the N-terminus, a variable region (abbreviated herein as V_H) followed by a constant region. The heavy chain constant region is comprised of three domains, C_{H1}, C_{H2} and C_{H3}. Each light chain has, at the N-terminus, a variable region (abbreviated herein as V_I) followed by a constant region at its other end. The light chain constant region is comprised of one domain, C_L. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (CH1). The pairing of a V_H and V_L together forms a single antigen-binding site. An IgM antibody consists of 5 of the basic heterotetramer units along with an additional polypeptide called J chain, and therefore contains 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain.

[0065] The V_H and V_L regions can be further subdivided into regions of hypervariability, termed hyper-variable regions (HVR) based on structural and sequence analysis. HVRs are interspersed with regions that are more conserved, termed framework regions (FW) (*see e.g.*, Chen *et al.* (1999) J. Mol. Biol. (1999) 293, 865-881). Each V_H and V_L is composed of three HVRs and four FWs, arranged from amino-terminus to carboxy-terminus in the following order: FW-1_HVR-1_FW-2_HVR-2_FW-3_HVR-3_FW4. Throughout the present disclosure, the three HVRs of the heavy chain are referred to as HVR-H1, HVR-H2, and HVR-H3. Similarly, the three HVRs of the light chain are referred to as HVR-L1, HVR-L2, and HVR-L3.

[0066] The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (*e.g.,* effector cells) and the first component (Clq) of the classical complement system. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 or more amino acids (*see e.g.,* Fundamental Immunology Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y). (1989)).

[0067] The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (CH), antibodies can be assigned to different classes or isotypes. There are five classes of antibodies: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α (alpha), δ (delta), ε (epsilon), γ (gamma), and μ (mu), respectively. The IgG class of antibody can be further classified into four subclasses IgG1, IgG2, IgG3, and IgG4 by the gamma heavy chains, Y1-Y4, respectively.

[0068] The term "antigen-binding fragment" or "antigen binding portion" of an antibody refers to one or more portions of an antibody that retain the ability to bind to the antigen that the antibody bonds to. Examples of "antigen-binding fragments" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the V_L, V_H, C_L and C_{H1} domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and C_{H1} domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a dAb fragment (Ward *et al., Nature* 341:544-546 (1989)), which consists of a V_H domain; and (vi) an isolated complementarity determining region (CDR).

[0069] The term "CTLA4" is used in the present application, and includes the human CTLA4 (*e.g.,* UniProt accession number P16410), as well as variants, isoforms, and species homologs thereof (*e.g.,* mouse CTLA4 (UniProt accession number P09793), rat CTLA4 (UniProt accession number Q9Z1A7), dog CTLA4 (UniProt accession number Q9XSI1),

cynomolgus monkey CTLA4 (UniProt accession number G7PL88), *etc.*). Accordingly, a binding molecule (*e.g.,* an activatable antibody) may also bind CTLA4 from species other than human. In other cases, a binding molecule may be completely specific for the human CTLA4 and may not exhibit species or other types of cross-reactivity.

[0070] The term "CD137" is used in the present application, and includes the human CD137 (*e.g.,* GenBank Accession No. NM_001561; NP_001552), as well as variants, isoforms, and species homologs thereof (*e.g.,* mouse CD137 (GenBank Gene ID 21942), rat CD137 (GenBank Gene ID 500590), dog CD137 (GenBank Gene ID 608274), cynomolgus monkey CTLA4 (GenBank Gene ID 102127961), *etc.*). Accordingly, a binding molecule (*e.g.,* an activatable antibody) may also bind CD137 from species other than human. In other cases, a binding molecule may be completely specific for the human CD137 and may not exhibit species or other types of cross-reactivity.

[0071] The term "chimeric antibody" refers to an antibody that comprises amino acid sequences derived from different animal species, such as those having a variable region derived from a human antibody and a murine immunoglobulin constant region.

[0072] The term "compete for binding" refers to the interaction of two antibodies in their binding to a binding target. A first antibody competes for binding with a second antibody if binding of the first antibody with its cognate epitope is detectably decreased in the presence of the second antibody compared to the binding of the first antibody in the absence of the second antibody. The alternative, where the binding of the second antibody to its epitope is also detectably decreased in the presence of the first antibody, can, but need not, be the case. That is, a first antibody can inhibit the binding of a second antibody to its epitope without that second antibody inhibiting the binding of the first antibody to its respective epitope. However, where each antibody detectably inhibits the binding of the other antibody with its cognate epitope, whether to the same, greater, or lesser extent, the antibodies are said to "cross-compete" with each other for binding of their respective epitope(s).

[0073] The term "epitope" refers to a part of an antigen to which an antibody (or antigen-binding fragment thereof) binds. Epitopes can be formed both from contiguous amino acids or noncontiguous amino acids juxtaposed by tertiary folding of a protein. Epitopes formed from

contiguous amino acids are typically retained on exposure to denaturing solvents whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope can include various numbers of amino acids in a unique spatial conformation. Methods of determining spatial conformation of epitopes include, for example, x-ray crystallography, 2-dimensional nuclear magnetic resonance, deuterium and hydrogen exchange in combination with mass spectrometry, or site-directed mutagenesis, or all methods used in combination with computational modeling of antigen and its complex structure with its binding antibody and its variants (*see e.g.*, Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, G. E. Morris, Ed. (1996)). Once a desired epitope of an antigen is determined, antibodies to that epitope can be generated, *e.g.,* using the techniques described herein. The generation and characterization of antibodies may also elucidate information about desirable epitopes. From this information, it is then possible to competitively screen antibodies for binding to the same epitope. An approach to achieve this is to conduct cross-competition studies to find antibodies that competitively bind with one another, *i.e.,* the antibodies compete for binding to the antigen. A high throughput process for "binning" antibodies based upon their cross-competition is described in PCT Publication No. WO 03/48731.

[0074] The term "germline" refers to the nucleotide sequences of the antibody genes and gene segments as they are passed from parents to offspring via the germ cells. The germline sequence is distinguished from the nucleotide sequences encoding antibodies in mature B cells which have been altered by recombination and hypermutation events during the course of B cell maturation.

[0075] The term "glycosylation sites" refers to amino acid residues which are recognized by a eukaryotic cell as locations for the attachment of sugar residues. The amino acids where carbohydrate, such as oligosaccharide, is attached are typically asparagine (N-linkage), serine (O-linkage), and threonine (O-linkage) residues. The specific site of attachment is typically signaled by a sequence of amino acids, referred to herein as a "glycosylation site sequence". The glycosylation site sequence for N-linked glycosylation is: -Asn-X-Ser- or -Asn-X-Thr-, where X may be any of the conventional amino acids, other than proline. The terms "N-linked" and "O-linked" refer to the chemical group that serves as the attachment site between the sugar molecule and the amino acid residue. N-linked sugars are attached through an amino group; O-

linked sugars are attached through a hydroxyl group. The term "glycan occupancy" refers to the existence of a carbohydrate moiety linked to a glycosylation site (*i.e.*, the glycan site is occupied). Where there are at least two potential glycosylation sites on a polypeptide, either none (0-glycan site occupancy), one (1-glycan site occupancy) or both (2-glycan site occupancy) sites can be occupied by a carbohydrate moiety.

[0076] The term "host cell" refers to a cellular system which can be engineered to generate proteins, protein fragments, or peptides of interest. Host cells include, without limitation, cultured cells, *e.g.*, mammalian cultured cells derived from rodents (rats, mice, guinea pigs, or hamsters) such as CHO, BHK, NSO, SP2/0, YB2/0; human cells (*e.g.*, HEK293F cells, HEK293T cells; or human tissues or hybridoma cells, yeast cells, insect cells (*e.g.*, S2 cells), bacterial cells (*e.g.*, E. coli cells) and cells comprised within a transgenic animal or cultured tissue. The term encompasses not only the particular subject cell but also the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not be identical to the parent cell, but are still included within the scope of the term "host cell."

[0077] A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human or a human cell or derived from a non-human source that utilizes human antibody repertoires or other human antibody-encoding sequences. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues.

[0078] The term "humanized antibody" refers to a chimeric antibody that contains amino acid residues derived from human antibody sequences. A humanized antibody may contain some or all of the CDRs or HVRs from a non-human animal or synthetic antibody while the framework and constant regions of the antibody contain amino acid residues derived from human antibody sequences.

[0079] The term "illustrative antibody" refers to any one of the antibodies described herein. These antibodies may be in any class (*e.g.*, IgA, IgD, IgE, IgG, and IgM). Thus, each antibody identified above encompasses antibodies in all five classes that have the same amino acid sequences for the V_L and V_H regions. Further, the antibodies in the IgG class may be in any

subclass (*e.g.,* IgG1 IgG2, IgG3, and IgG4). Thus, each antibody identified above in the IgG subclass encompasses antibodies in all four subclasses that have the same amino acid sequences for the V_L and V_H regions. The amino acid sequences of the heavy chain constant regions of human antibodies in the five classes, as well as in the four IgG subclasses, are known in the art. The amino acid sequence of the full length heavy chain and light chain for the IgG4 subclass of each of the illustrative antibodies shown in in Table 1b is provided in the disclosure.

[0080] An "isolated" antibody or binding molecule is one which has been separated from a component of its natural environment. In some embodiments, an antibody is purified to greater than 95% or 99% purity as determined by, for example, electrophoretic (*e.g.,* SDS-PAGE, isoelectric focusing (IEF), capillary electrophoresis) or chromatographic (*e.g.,* ion exchange or reverse phase HPLC). For review of methods for assessment of antibody purity, *see e.g.,* Flatman et al., J. Chromatogr. B 848:79-87 (2007).

[0081] The term "k_a" refers to the association rate constant of a particular antibody -antigen interaction, whereas the term "k_d" refers to the dissociation rate constant of a particular antibody -antigen interaction.

[0082] The term "K_D" refers to the equilibrium dissociation constant of a particular antibody-antigen interaction. It is obtained from the ratio of k_d to k_a (*i.e.,* k_d/k_a) and is expressed as a molar concentration (M). K_D is used as a measure for the affinity of an antibody's binding to its binding partner. The smaller the K_D, the more tightly bound the antibody is, or the higher the affinity between antibody and the antigen. For example, an antibody with a nanomolar (nM) dissociation constant binds more tightly to a particular antigen than an antibody with a micromolar (μM) dissociation constant. K_D values for antibodies can be determined using methods well established in the art. One method for determining the K_D of an antibody is by using an ELISA. For example, an assay procedure using an ELISA is described in at least Example 3 of the present disclosure.

[0083] The term "mammal" refers to any animal species of the Mammalia class. Examples of mammals include: humans; laboratory animals such as rats, mice, hamsters, rabbits, non-

human primates, and guinea pigs; domestic animals such as cats, dogs, cattle, sheep, goats, horses, and pigs; and captive wild animals such as lions, tigers, elephants, and the like.

[0084] The term "prevent" or "preventing," with reference to a certain disease condition in a mammal, refers to preventing or delaying the onset of the disease, or preventing the manifestation of clinical or subclinical symptoms thereof.

[0085] As used herein, "sequence identity" between two polypeptide sequences indicates the percentage of amino acids that are identical between the sequences. The amino acid sequence identity of polypeptides can be determined conventionally using known computer programs such as Bestfit, FASTA, or BLAST (*see e.g.*, Pearson, *Methods Enzymol.* 183:63-98 (1990); Pearson, *Methods Mol. Biol.* 132:185-219 (2000); Altschul *et al., J. Mol. Biol.* 215:403-410 (1990); Altschul *et al., Nucleic Acids Res.* 25:3389-3402 (1997)). When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference amino acid sequence, the parameters are set such that the percentage of identity is calculated over the full length of the reference amino acid sequence and that gaps in homology of up to 5% of the total number of amino acid residues in the reference sequence are allowed. This aforementioned method in determining the percentage of identity between polypeptides is applicable to all proteins, fragments, or variants thereof disclosed herein.

[0086] As used herein, the term "binds", "binds to", "specifically binds" "specifically binds to" or is "specific for" refers to measurable and reproducible interactions such as binding between a target and an antibody, which is determinative of the presence of the target in the presence of a heterogeneous population of molecules including biological molecules. For example, an antibody that binds to or specifically binds to a target (which can be an epitope) is an antibody that binds this target with greater affinity, avidity, more readily, and/or with greater duration than it binds to other targets. In one embodiment, the extent of binding of an antibody to an unrelated target is less than about 10% of the binding of the antibody to the target as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that specifically binds to a target has a dissociation constant (Kd) of $\leq 1\mu M$, ≤ 100 nM, ≤ 10 nM, ≤ 1 nM, or ≤ 0.1 nM. In certain embodiments, an antibody specifically binds to an epitope

on a protein that is conserved among the protein from different species. In another embodiment, specific binding can include, but does not require exclusive binding.

[0087] The term "treat", "treating", or "treatment", with reference to a certain disease condition in a mammal, refers causing a desirable or beneficial effect in the mammal having the disease condition. The desirable or beneficial effect may include reduced frequency or severity of one or more symptoms of the disease (*i.e.,* tumor growth and/or metastasis, or other effect mediated by the numbers and/or activity of immune cells, and the like), or arrest or inhibition of further development of the disease, condition, or disorder. In the context of treating cancer in a mammal, the desirable or beneficial effect may include inhibition of further growth or spread of cancer cells, death of cancer cells, inhibition of reoccurrence of cancer, reduction of pain associated with the cancer, or improved survival of the mammal. The effect can be either subjective or objective. For example, if the mammal is human, the human may note improved vigor or vitality or decreased pain as subjective symptoms of improvement or response to therapy. Alternatively, the clinician may notice a decrease in tumor size or tumor burden based on physical exam, laboratory parameters, tumor markers or radiographic findings. Some laboratory signs that the clinician may observe for response to treatment include normalization of tests, such as white blood cell count, red blood cell count, platelet count, erythrocyte sedimentation rate, and various enzyme levels. Additionally, the clinician may observe a decrease in a detectable tumor marker. Alternatively, other tests can be used to evaluate objective improvement, such as sonograms, nuclear magnetic resonance testing and positron emissions testing.

[0088] The term "vector" refers to a nucleic acid molecule capable of transporting a foreign nucleic acid molecule. The foreign nucleic acid molecule is linked to the vector nucleic acid molecule by a recombinant technique, such as ligation or recombination. This allows the foreign nucleic acid molecule to be multiplied, selected, further manipulated or expressed in a host cell or organism. A vector can be a plasmid, phage, transposon, cosmid, chromosome, virus, or virion. One type of vectors can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome (*e.g.,* non-episomal mammalian vectors). Another type of vector is capable of autonomous replication in a host cell into which it is introduced (*e.g.,* bacterial vectors having a bacterial

origin of replication and episomal mammalian vectors). Another specific type of vector capable of directing the expression of expressible foreign nucleic acids to which they are operatively linked is commonly referred to as "expression vectors." Expression vectors generally have control sequences that drive expression of the expressible foreign nucleic acids. Simpler vectors, known as "transcription vectors," are only capable of being transcribed but not translated: they can be replicated in a target cell but not expressed. The term "vector" encompasses all types of vectors regardless of their function. Vectors capable of directing the expression of expressible nucleic acids to which they are operatively linked are commonly referred to "expression vectors." Other examples of "vectors" may include display vectors (*e.g.,* vectors that direct expression and display of an encoded polypeptide on the surface of a virus or cell (such as a bacterial cell, yeast cell, insect cell, and/or mammalian cell).

[0089] As used herein, a "subject", "patient", or "individual" may refer to a human or a non-human animal. A "non-human animal" may refer to any animal not classified as a human, such as domestic, farm, or zoo animals, sports, pet animals (such as dogs, horses, cats, cows, *etc.*), as well as animals used in research. Research animals may refer without limitation to nematodes, arthropods, vertebrates, mammals, frogs, rodents (*e.g.,* mice or rats), fish (*e.g.,* zebrafish or pufferfish), birds (*e.g.,* chickens), dogs, cats, and non-human primates (*e.g.,* rhesus monkeys, cynomolgus monkeys, chimpanzees, *etc.*). In some embodiments, the subject, patient, or individual is a human.

[0090] An "effective amount" refers to at least an amount effective, at dosages and for periods of time necessary, to achieve one or more desired or indicated effects, including a therapeutic or prophylactic result. An effective amount can be provided in one or more administrations. For purposes of the present disclosure, an effective amount of antibody, drug, compound, or pharmaceutical composition is an amount sufficient to accomplish prophylactic or therapeutic treatment either directly or indirectly. As is understood in the clinical context, an effective amount of a drug, compound, or pharmaceutical composition may or may not be achieved in conjunction with another drug, compound, or pharmaceutical composition (*e.g.,* an effective amount as administered as a monotherapy or combination therapy). Thus, an "effective amount" may be considered in the context of administering one or more therapeutic

agents, and a single agent may be considered to be given in an effective amount if, in conjunction with one or more other agents, a desirable result may be or is achieved.

III. Activatable binding polypeptide libraries and generation of libraries

[0091] Certain aspects of the present disclosure relate to polynucleotides (*e.g.,* encoding any of the polypeptides described herein) and/or libraries of polynucleotides *e.g.,* that encode polypeptides useful for screening for and/or identifying one or more activatable binding polypeptides (*i.e.,* one or more activatable antibodies), including activatable antibodies, activatable antigen binding fragments thereof, or derivatives of activatable antibodies.

[0092] The term "activatable binding polypeptide", "ABP", or "activatable antibody" includes a polypeptide that comprises a target binding moiety (TBM), a cleavable moiety (CM), and a masking moiety (MM). In some embodiments, the TBM comprises an amino acid sequence that binds to a target. In some embodiments, the TBM comprises an antigen binding domain (ABD) of an antibody or antibody fragment thereof. In some embodiments, the TBM comprises an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH), wherein the VH and VL forms a binding domain that binds to the target in the absence of the MM. In some embodiments, the VH and VL are covalently linked, *e.g.,* in an scFv. In some embodiments, the VH and VL form a Fab fragment. In some embodiments, the VH is linked to an antibody heavy chain constant region, and the VL is linked to an antibody light chain constant region.

[0093] In some embodiments, the activatable antibody comprises a polypeptide comprising the structure, from N-terminus to C-terminus, of: masking moiety (MM)-cleavable moiety (CM)-VL, and the activatable antibody further comprises a second polypeptide comprising a VH (*e.g.,* a Fab fragment). In some embodiments, the activatable antibody comprises a polypeptide comprising the structure, from N-terminus to C-terminus, of: masking moiety (MM)-cleavable moiety (CM)-VL-VH (*e.g.,* an scFv). In some embodiments, the activatable antibody comprises a polypeptide comprising the structure, from N-terminus to C-terminus, of: masking moiety (MM)-cleavable moiety (CM)-VH, and the activatable antibody further comprises a second polypeptide comprising a VL (*e.g.,* a Fab fragment). In some embodiments, the activatable antibody comprises a polypeptide comprising the structure, from

N-terminus to C-terminus, of: masking moiety (MM)-cleavable moiety (CM)-VH-VL (*e.g.,* an scFv).

[0094] The CM generally includes an amino acid sequence that is cleavable, for example, serves as the substrate for an enzyme and/or a cysteine-cysteine pair capable of forming a reducible disulfide bond. As such, when the terms "cleavage," "cleavable," "cleaved" and the like are used in connection with a CM, the terms encompass enzymatic cleavage, e.g., by a protease, as well as disruption of a disulfide bond between a cysteine-cysteine pair via reduction of the disulfide bond that can result from exposure to a reducing agent.

[0095] The MM refers to an amino acid sequence that, when the CM of the activatable antibody is intact (*e.g.,* uncleaved by a corresponding enzyme, and/or containing an unreduced cysteine-cysteine disulfide bond), the MM interferes with or inhibits binding of the TBM to its target. In some embodiments, the MM interferes with or inhibits binding of the TBM to its target so efficiently that binding of the TBM to its target is extremely low and/or below the limit of detection (*e.g.,* binding cannot be detected in an ELISA or flow cytometry assay). The amino acid sequence of the CM may overlap with or be included within the MM. It should be noted that for sake of convenience "ABP" or “activatable antibody” are used herein to refer to an ABP or activatable antibody in both their uncleaved (or "native") state, as well as in their cleaved state. It will be apparent to the ordinarily skilled artisan that in some embodiments a cleaved ABP may lack an MM due to cleavage of the CM, e.g., by a protease, resulting in release of at least the MM (e.g., where the MM is not joined to the ABP by a covalent bond (e.g., a disulfide bond between cysteine residues)). Exemplary ABPs are described in more detail below.

[0096] A library of the present disclosure may contain one or more polynucleotides encoding any of the polypeptides described herein (*e.g.,* one or more of the activatable binding polypeptides described herein). In some embodiments, one or more (*i.e.,* one, some, or all) of the polynucleotides of a library described herein encode(s) a polypeptide comprising full length antibody light and/or heavy chain(s). In some embodiments, one or more (*i.e.,* one, some, or all) of the polynucleotides of a library described herein encode(s) a polypeptide comprising light and/or heavy chain Fab fragment(s). In some embodiments, one or more (*i.e.,* one, some,

or all) of the polynucleotides of a library described herein encode(s) a polypeptide comprising single-chain variable fragment(s) (scFvs).

[0097] Other aspects of the present disclosure relate to polypeptides (*e.g.*, any of the polypeptides described herein) and/or libraries of polypeptides useful for screening for and/or identifying one or more activatable binding polypeptides (*i.e.*, one or more activatable antibodies), including activatable antibodies, activatable antigen binding fragments thereof, or derivatives of activatable antibodies. A library of the present disclosure may contain one or more of the polypeptides described herein (*e.g.*, one or more activatable binding polypeptides). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise full length antibody light and/or heavy chain(s). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise light and/or heavy chain Fab fragment(s). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise single-chain variable fragment(s) (scFvs). In some embodiments, the polypeptides are expressed on a cell surface (*e.g.*, yeast or mammalian cell display).

[0098] In some embodiments, a polypeptide of the present disclosure comprises: (a) a first peptide (FP); (b) a cleavable moiety (CM); and (c) a target binding moiety (TBM). In some embodiments, the FP is any of the first peptides described herein (*e.g.*, a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y). In some embodiments, X is not W, M, and/or C. In some embodiments, each X in X_m of formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P, each X in X_n of formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P, and/or each X in X_o of formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments, the FP is any of the first peptides described herein (*e.g.*, a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T,

V, W, and Y, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P). In some embodiments, X is not W, M, and/or C. In some embodiments, each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P and/or each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments, the FP is any of the first peptides described herein (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (XII): $Z_mCZ_nCZ_o$ (SEQ ID NO: 71), where m is from 3-10, n is from 3-10, and o is from 1-10, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P). In some embodiments, the CM is any of the cleavable moieties described herein (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site). In some embodiments, the CM is any of the cleavable moieties described herein (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site). In some embodiments, the TBM is any of the target binding moieties described herein (*e.g.,* a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region).

[0099] In some embodiments, the first peptide (FP) interferes with, obstructs, reduces the ability of, prevents, inhibits, or competes with the target binding moiety for binding to its target (*e.g.,* an "inactive activatable antibody). In some embodiments, the first peptide (FP) interferes with, obstructs, reduces, prevents, inhibits, or competes with the target binding moiety for binding to its target only when the polypeptide has not been activated (*e.g.,* activated by a change in pH (increased or decreased), activated by a temperature shift (increased or decreased), activated after being contacted with a second molecule (such as a small molecule or a protein ligand), *etc.*). In some embodiments, activation induces cleavage of the polypeptide within the cleavage moiety. In some embodiments, activation induces conformation changes in the polypeptide (*e.g.,* displacement of the first peptide (FP)), leading to the first peptide no longer preventing the activatable antibody from binding to its target. In some embodiments, the first peptide (FP) interferes with, obstructs, reduces the ability of, prevents, inhibits, or competes with the target binding moiety for binding to its target only when the cleavable moiety (CM) has not been cleaved by one or more proteases that cleave

within the cleavable moiety (CM). In some embodiments, the first peptide (FP) has a masking efficiency of at least about 2.0 (*e.g.*, at least about 2.0, at least about 3.0, at least about 4.0, at least about 5.0, at least about 6.0, at least about 7.0, at least about 8.0, at least about 9.0, at least about 10, at least about 25, at least about 50, at least about 75, at least about 100, at least about 150, at least about 200, at least about 300, at least about 400, at least about 500, *etc.*) prior to activation. In some embodiments, masking efficiency is measured as the difference in affinity of an activatable antibody comprising the first peptide (FP) for binding its target (before activation) relative to the affinity of a polypeptide lacking the first peptide for binding its target (*e.g.*, the difference in affinity for a target antigen (such as CTLA4) of an activatable antibody comprising a first peptide (FP) (before activation) relative to a parental antibody lacking the first peptide (FP), or the difference in affinity for a target antigen (such as CTLA4) of an activatable antibody comprising a first peptide (FP) (before activation) relative to the affinity for the target antigen of the activatable antibody after activation). In some embodiments, the masking efficiency is measured by dividing the EC_{50} for binding of an activatable antibody comprising a first peptide (FP) (before activation) by the EC_{50} of the parental antibody (*e.g.*, by measuring EC_{50} by ELISA; *see e.g.*, the methods of Example 3). In some embodiments, masking efficiency is measured as the difference in affinity of an activatable antibody comprising the first peptide (FP) for binding its target before activation relative to the affinity of the activatable antibody comprising the first peptide (FP) for binding its target after activation (*e.g.*, the difference in affinity for a target antigen (such as CTLA4) of an activatable antibody before activation relative to the activatable antibody after activation). In some embodiments, the first peptide (FP) binds to the target binding moiety (TBM), and prevents the activatable antibody from binding to its target (*e.g.*, an "inactive" activatable antibody). In some embodiments, the first peptide (FP) has a dissociation constant for binding to the target binding moiety (TBM) that is greater than the dissociation constant of the target binding moiety (TBM) for its target. In some embodiments, the first peptide (FP) is a masking moiety (MM).

[0100] In some embodiments, the first peptide (FP) does not interfere with, obstruct, reduce the ability of, prevent, inhibit, or compete with the target binding moiety (TBM) for binding to its target after the polypeptide has been activated (*e.g.*, activated by treatment with

one or more proteases that cleave within the cleavable moiety (CM), activated by a change in pH (increased or decreased), activated by a temperature shift (increased or decreased), activated after being contacted with a second molecule (such as an enzyme), *etc.*). In some embodiments, the first peptide (FP) does not interfere with, obstruct, reduce the ability of, prevent, inhibit, or compete with the target binding moiety (TBM) for binding to its target after the cleavable moiety (CM) has been cleaved by one or more proteases that cleave within the cleavable moiety (CM). In some embodiments, the first peptide (FP) has a masking efficiency of at most about 1.75 (*e.g.*, at most about 1.75, at most about 1.5, at most about 1.4, at most about 1.3, at most about 1.2, at most about 1.1, at most about 1.0, at most about 0.9, at most about 0.8, at most about 0.7, at most about 0.6, or at most about 0.5, *etc.*) after to activation (*e.g.*, the relative affinity of the activatable antibody after activation as compared to the affinity of a parental antibody).

[0101] In some embodiments, a polypeptide of the present disclosure comprises the structure, from N-terminus to C-terminus, of: the first peptide (FP)-the cleavable moiety (CM)-the target binding moiety (TBM). Libraries of the present disclosure may be used to screen for one or more activatable binding polypeptides (*i.e.*, activatable antibodies) that, when in active form, bind to any target of interest, including, for example, CTLA4, CD137, PD-1, PD-L1, PD-L2, LAG3, TIM3, B7-H3, OX40, CD3, CD19, CD20, CD40, CD95, CD120a, BTLA, VISTA, ICOS, BCMA, Her1, Her2, Her3, and/or B7-H4.

[0102] In some embodiments, a library of the present disclosure contains a plurality of polynucleotides that encodes at least one, at least 50, at least 100, at least 250, at least 500, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19} unique polypeptides comprising: (a) a first peptide (FP); (b) a cleavable moiety (CM); and (c) a target binding moiety (TBM), as described herein.

[0103] In some embodiments, a library of the present disclosure: 1) encodes and/or contains a smaller number of unique peptides (*e.g.*, FPs comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86) or Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1)) than are found in typical random peptide libraries; 2) encodes and/or contains peptides (*e.g.*, FPs comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86)

or Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1)) comprising a pair of cysteine residues at fixed positions to ensure that the display peptides had constrained conformations; and/or 3) encodes and/or contains peptides (*e.g.*, FPs comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86) or Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1)) harboring few or no chemically labile residues (such as methionine or tryptophan). Advantageously, libraries of the present disclosure have dramatically reduced library size relative to random peptide libraries, enabling the construction of libraries with much better coverage of the peptides (*e.g.*, FPs comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86) or Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1)). Moreover, the inclusion of a pair of cysteine residues at fixed positions ensured that the display peptides had constrained conformations, tending to exhibit increased binding affinity and/or specificity. Furthermore, libraries of the present disclosure have peptides (*e.g.*, FPs comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86) or Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1)) including few to no unfavorable residues for manufacturing processes, such as methionine or tryptophan.

[0104] In some embodiments, a library of the present disclosure contains a plurality of polynucleotides, with at least one of the polynucleotides in the library encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.*, at least a first protease cleavage site); and c) a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.*, an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.*, an expression vector or display vector). In some embodiments, a library of the present disclosure contains a plurality of polynucleotides, with at least one of the polynucleotides in the library encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an

amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.*, at least a first protease cleavage site); and c) a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.*, an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.*, an expression vector or display vector).

[0105] In some embodiments, at least one of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence according to Formula (III), $EVGSYX_1X_2X_3X_4X_5X_6CX_7X_8X_9X_{10}X_{11}X_{12}CX_{13}X_{14}SGRSAGGGGTENLYFQGSGGS$ (SEQ ID NO: 3), where X1 is A, D, I, N, P, or Y, x2 is A, F, N, S, or V, X3 is A, H, L, P, S, V, or Y, X4 is A, H, S, or Y, X5 is A, D, P, S, V, or Y, X6 is A, D, L, S, or Y, X7 is D, P, or V, X8 is A, D, H, P, S, or T, X9 is A, D, F, H, P, or Y, X10 is L, P, or Y, X11 is F, P, or Y, X12 is A, P, S, or Y, X13 is A, D, N, S, T, or Y, and X14 is A, S, or Y. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.*, an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.*, an expression vector or display vector).

[0106] In some embodiments, at least one of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence selected from SEQ ID NOS: 25-46. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.*, an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.*, an expression vector or display vector).

[0107] In some embodiments, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 250, at least 500, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19} of

the polynucleotides in the library encodes a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); and c) a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 250, at least 500, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19} of the polynucleotides in the library encodes a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); and c) a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.,* an expression vector or display vector).

[0108] In some embodiments, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 250, at least 500, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19} of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence

according to Formula (III), EVGSYX$_1$X$_2$X$_3$X$_4$X$_5$X$_6$CX$_7$X$_8$X$_9$X$_{10}$X$_{11}$X$_{12}$CX$_{13}$X$_{14}$SGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 3), where X1 is A, D, I, N, P, or Y, x2 is A, F, N, S, or V, X3 is A, H, L, P, S, V, or Y, X4 is A, H, S, or Y, X5 is A, D, P, S, V, or Y, X6 is A, D, L, S, or Y, X7 is D, P, or V, X8 is A, D, H, P, S, or T, X9 is A, D, F, H, P, or Y, X10 is L, P, or Y, X11 is F, P, or Y, X12 is A, P, S, or Y, X13 is A, D, N, S, T, or Y, and X14 is A, S, or Y. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.,* an expression vector or display vector).

[0109] In some embodiments, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 250, at least 500, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19} of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence selected from SEQ ID NOS: 25-46. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.,* an expression vector or display vector).

[0110] In some embodiments, each of the polynucleotides in the library encode a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); and c) a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, each of the polynucleotides in the library encode a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is

independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); and c) a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.,* an expression vector or display vector).

[0111] In some embodiments, each of the polynucleotides in the library encode a polypeptide comprising an amino acid sequence according to Formula (III), $EVGSYX_1X_2X_3X_4X_5X_6CX_7X_8X_9X_{10}X_{11}X_{12}CX_{13}X_{14}SGRSAGGGGTENLYFQGSGGS$ (SEQ ID NO: 3), where X1 is A, D, I, N, P, or Y, x2 is A, F, N, S, or V, X3 is A, H, L, P, S, V, or Y, X4 is A, H, S, or Y, X5 is A, D, P, S, V, or Y, X6 is A, D, L, S, or Y, X7 is D, P, or V, X8 is A, D, H, P, S, or T, X9 is A, D, F, H, P, or Y, X10 is L, P, or Y, X11 is F, P, or Y, X12 is A, P, S, or Y, X13 is A, D, N, S, T, or Y, and X14 is A, S, or Y. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.,* an expression vector or display vector).

[0112] In some embodiments, each of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence selected from SEQ ID NOS: 25-46. In some embodiments, at least one of the polynucleotides in the library encodes an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, one or more polynucleotides of the library are in a vector (*e.g.,* an expression vector or display vector).

[0113] In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-

10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody light chain variable region; and d) an antibody heavy chain variable region. In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody light chain variable region; and d) an antibody heavy chain variable region. In some embodiments, the polypeptide comprising the structure, from N-terminus to C-terminus, of: first peptide (FP)-cleavable moiety (CM)-VL-VH. In some embodiments, at least one of the polypeptides is an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, a linker sequence separates the VL and VH (*i.e.,* the structure VL-linker-VH). The inker sequence may be any linker sequence known in the art, *e.g.,* any of the linker sequences described herein. In some embodiments, the linker sequence is any copy number of GGGGS (SEQ ID NO: 17) (*e.g.,* repeated 2 times, repeated 3 times, *etc.*).

[0114] In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM)

comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody light chain variable region, and the library further comprises one or more polynucleotides encoding an antibody heavy chain variable region. In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody light chain variable region, and the library further comprises one or more polynucleotides encoding an antibody heavy chain variable region. In some embodiments, the polynucleotide encoding the polypeptide comprising a target binding moiety (TBM) comprising an antibody light chain variable region, and the polynucleotide encoding an antibody heavy chain variable region are on the same vector (*e.g.,* expressed from their own promoters) or on different vectors. In some embodiments, at least one of the polypeptides forms an activatable binding polypeptide (*i.e.,* an activatable antibody) when coupled with the antibody heavy chain variable region.

[0115] In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target

binding moiety (TBM) comprising an antibody heavy chain variable region; and d) an antibody light chain variable region. In some embodiments, the activatable binding polypeptide comprises a polypeptide comprising the structure, from N-terminus to C-terminus, of: first peptide (FP)-cleavable moiety (CM)-VH-VL In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody heavy chain variable region; and d) an antibody light chain variable region. In some embodiments, the activatable binding polypeptide comprises a polypeptide comprising the structure, from N-terminus to C-terminus, of: first peptide (FP)-cleavable moiety (CM)-VH-VL. In some embodiments, at least one of the polypeptides is an activatable binding polypeptide (*i.e.,* an activatable antibody). In some embodiments, a linker sequence separates the VH and VL (*i.e.,* the structure VH-linker-VL). The inker sequence may be any linker sequence known in the art, *e.g.,* any of the linker sequences described herein. In some embodiments, the linker sequence is any copy number of GGGGS (SEQ ID NO: 17) (*e.g.,* repeated 2 times, repeated 3 times, *etc.*).

[0116] In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; (b) a cleavable moiety (CM)

comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody heavy chain variable region, and the library further comprises one or more polynucleotides encoding an antibody light chain variable region. In some embodiments, a library of the present disclosure contains at least one (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) polynucleotide encoding a polypeptide comprising: (a) a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P; (b) a cleavable moiety (CM) comprising at least a first cleavage site (*e.g.,* at least a first protease cleavage site); c) a target binding moiety (TBM) comprising an antibody heavy chain variable region, and the library further comprises one or more polynucleotides encoding an antibody light chain variable region. In some embodiments, the polynucleotide encoding the polypeptide comprising a target binding moiety (TBM) comprising an antibody heavy chain variable region, and the polynucleotide encoding an antibody light chain variable region are on the same vector (*e.g.,* expressed from their own promoters) or on different vectors. In some embodiments, at least one of the polypeptides forms an activatable binding polypeptide (*i.e.,* an activatable antibody) when coupled with the antibody light chain variable region.

[0117] Polynucleotides and/or polynucleotide libraries described herein may incorporate any of the HVR sequences (*e.g.,* one, two, or three of the heavy chain variable region HVR sequences, and/or one, two, or three of the light chain variable region HVR sequences), heavy chain variable region sequences, and/or light chain variable region sequences of any of the antibodies described herein (*e.g.,* an anti-CTLA4 antibody, an anti-CD137 antibody). Polynucleotides and/or polynucleotide libraries described herein may also incorporate any of the HVR sequences (*e.g.,* one, two, or three of the heavy chain variable region HVR sequences, and/or one, two, or three of the light chain variable region HVR sequences), heavy chain variable region sequences, light chain variable region sequences, heavy chains, and/or light chains

described in PCT application number PCT/CN2017/098333 (incorporated herein by reference in its entirety), and/or PCT application number PCT/CN2017/098299 (incorporated herein by reference in its entirety).

[0118] In some embodiments, a library of the present disclosure includes one or more vectors (*e.g.,* an expression vector and/or display vector) encoding one or more polynucleotides (e.g., synthetic polynucleotides) of the present disclosure.

[0119] Further provided herein is a method of preparing a library, *e.g.*, by providing and assembling the polynucleotide sequences (*e.g.*, synthetic polynucleotide(s)) of a library of the present disclosure. Also provided herein is a method of making a library, *e.g.*, by selecting multiple (*e.g.,* at least one, at least two, at least 5, at least 10, at least 100, at least 10^3, at least 10^4, at least 10^5, at least 10^6, at least 10^7, at least 10^8, at least 10^9, at least 10^{10}, at least 10^{11}, at least 10^{12}, at least 10^{13}, at least 10^{14}, at least 10^{15}, at least 10^{16}, at least 10^{17}, at least 10^{18}, or at least 10^{19}) first peptide (FP) sequences, cleavable moiety (CM) sequences, and/or target binding moiety (TBM) sequences (*e.g.*, any one or more of the FP, CM, and TBM sequences described herein), and assembling polynucleotide sequences encoding these sequences to produce a library of polynucleotides (*e.g.,* synthetic polynucleotides) encoding a plurality of polypeptides. In some embodiments, at least one of the polypeptides encoded by the assembled library is an activatable binding polypeptide (*i.e.,* an activatable antibody).

[0120] Polynucleotides encoding polypeptides as described herein can be cloned into any suitable vector for expression of a portion or the entire polypeptide sequence. In some embodiments, the polynucleotide is cloned into a vector allowing for production of a portion or the entire polypeptide fused to all or a portion of a protein (*e.g.,* a viral coat protein, a bacterial surface protein, a yeast surface protein, an insect cell surface protein, a mammalian cell surface protein) (*i.e.*, creating a fusion protein) and displayed on the surface of a particle or cell. Several types of vectors are available and may be used to practice the present disclosure, for example, phagemid vectors. Phagemid vectors generally contain a variety of components including promoters, signal sequences, phenotypic selection genes, origin of replication sites, and other necessary components as are known to those of ordinary skill in the art. In some embodiments, the polynucleotides encoding the polypeptide regions can be cloned into vectors for expression

in bacterial cells for bacterial display or in yeast cells for yeast display. Exemplary vectors are described in US PG Pub. No. US20160145604. In some embodiments, the vector is a display vector comprising, from 5' to 3', a polynucleotide encoding an amino acid sequence to be displayed on a surface (*e.g.*, a surface of phage, bacteria, yeast, insect, or mammalian cells), a restriction site, a second polynucleotide encoding a surface peptide capable of being displayed on the surface, and a second restriction site. In some embodiments, the second polynucleotide encodes a phage coat protein, a yeast outer wall protein (such as Aga2), a bacterial outer membrane protein, a cell surface tether domain, or an adapter, or a truncation or derivative thereof. In some embodiments, the surface peptide is for phage display, yeast display, bacterial display, insect display, or mammalian display, or shuttling display there between. In some embodiments, when expressed, the amino acid sequence and the surface peptide are displayed as a fusion protein on the surface. In some embodiments, the vector further comprises a fusion tag 5' to the first restriction site or 3' to the second restriction site.

[0121] Certain aspects of the present disclosure relate to a population of cells containing vector(s) described herein. Polypeptides encoded by polynucleotides generated by any of the techniques described herein, or other suitable techniques, can be expressed and screened to identify activatable binding polypeptides having desired structure and/or activity. Expression of the polypeptides can be carried out, for example, using cell-free extracts (*e.g.*, ribosome display), phage display, prokaryotic cells (*e.g.*, bacterial display), or eukaryotic cells (*e.g.*, yeast display). In some embodiments, the cells are bacterial cells, yeast cells, insect cells, or mammalian cells (such as Chinese Hamster Ovary (CHO) cells). Methods for transfecting bacterial cells, yeast cells, or mammalian cells are known in the art and described in the references cited herein. Expression (*e.g.*, from a library of the present disclosure) of polypeptides (*e.g.*, one or more activatable binding polypeptides) in these cell types, as well as screening for activatable binding polypeptides of interest, are described in more detail below.

[0122] Alternatively, the polynucleotides can be expressed in an *E. coli* expression system, such as that described by Pluckthun and Skerra. (Meth. Enzymol., 1989, 178: 476; Biotechnology, 1991, 9: 273). The mutant proteins can be expressed for secretion in the medium and/or in the cytoplasm of the bacteria, as described by Better and Horwitz, Meth. Enzymol., 1989, 178: 476. In some embodiments, the polypeptides are attached to the 3′ end of a sequence

encoding a signal sequence, such as the ompA, phoA or pelB signal sequence (Lei et al., J. Bacteriol., 1987, 169: 4379). These gene fusions are assembled in a dicistronic construct, so that they can be expressed from a single vector and secreted into the periplasmic space of *E. coli* where they will refold and can be recovered in active form. (Skerra et al., Biotechnology, 1991, 9: 273). For example, a gene encoding a polypeptide comprising a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM) comprising an antibody light chain can be concurrently expressed with an antibody heavy chain gene to produce a polypeptide of interest.

[0123] In other embodiments, the polypeptide sequences of the present disclosure are expressed on the membrane surface of a prokaryote, *e.g., E. coli*, using a secretion signal and lipidation moiety as described, e.g., in US20040072740; US20030100023; and US20030036092.

[0124] Alternatively, polypeptide sequences of the present disclosure can be expressed and screened by anchored periplasmic expression (APEx 2-hybrid surface display), as described, for example, in Jeong *et al.,* PNAS, 2007, 104: 8247 or by other anchoring methods as described, for example, in Mazor *et al.,* Nature Biotechnology, 2007, 25: 563.

[0125] Higher eukaryotic cells, such as mammalian cells, for example myeloma cells (*e.g.,* NS/0 cells), hybridoma cells, Chinese hamster ovary (CHO) cells, and human embryonic kidney (HEK) cells, can also be used for expression of the polypeptides of the present disclosure. Polypeptides (*e.g.,* activatable binding polypeptides) expressed in mammalian cells may be designed to be secreted into the culture medium, or expressed on the surface of the cell.

[0126] In other embodiments, polypeptides (*e.g.,* activatable binding polypeptides) can be selected using mammalian cell display (Ho et al., PNAS, 2006, 103: 9637). In some embodiments, as described above and exemplified below, polypeptides (*e.g.,* activatable binding polypeptides) can be selected after production of a portion or the entire polypeptide sequence fused to all or a portion of a viral coat protein (*i.e.*, creating a fusion protein) and displayed on the surface of a particle or cell, *e.g.*, using phage display.

[0127] Certain aspects of the present disclosure relate to a non-human animal comprising a polynucleotide or polynucleotide library of the present disclosure. For example, a non-human animal of the present disclosure may be modified such that its genome includes a polynucleotide

encoding a polypeptide (*e.g.*, an activatable binding polypeptide) of the present disclosure. In some embodiments, the transgenic animal (*e.g.*, mouse) expresses polypeptides encoded by the polynucleotides. Techniques for modifying the genome of a non-human animal are known in the art (*e.g.*, methods used to generate Xenomouse™).

[0128] The screening for activatable binding polypeptides derived from the libraries of the present disclosure can be carried out by any appropriate means (*e.g.*, determining target binding before and after activation (such as treatment of a polypeptide with one or more proteases that cleave a sequence within the cleavable moiety (CM))). For example, binding activity can be evaluated by standard immunoassay and/or affinity chromatography. Screening of the polypeptides of the present disclosure for catalytic function, *e.g.*, proteolytic function can be accomplished using a standard assays, *e.g.*, a hemoglobin plaque assay. Determining binding affinity of a polypeptide (*e.g.*, an activatable binding polypeptide) to a target can be assayed *in vitro* using a variety of well-known techniques, *e.g.*, an ELISA, a BIACORE™ instrument, which measures binding rates of an protein to a given target based on surface plasmon resonance, or Bio-Layer Interferometry (BLI), as exemplified below using the ForteBio Octet® RED96 platform (Pall Life Sciences). *In vivo* assays can be conducted using any of a number of animal models and then subsequently tested, as appropriate, in humans. Cell-based biological assays are also contemplated. The polypeptides (*e.g.*, activatable binding polypeptides) can be further selected for functional activity, for example, antagonist or agonist activity. For example, in some embodiments, affinity of binding between a polypeptide comprising fab fragment(s) and one or more target(s) is measured using BLI by tagging antigens with human IgG1-Fc tag and capture by Anti-hIgG-Fc Capture (AHC) Biosensor (*e.g.*, before and after activation). Polypeptides can be tagged at the C-terminus of the CH1 domain with a His6 tag, over-expressed in a host cell such as *E. coli,* and purified, *e.g.*, using a Ni-NTA resin. Affinity can then be measured using AHC sensors (anti-human IgG-Fc capture dip and read biosensors) dipped into wells containing the purified polypeptides comprising the Fabs diluted, *e.g.*, to 5-10 μg/mL with kinetic buffer (*e.g.*, before and after activation).

[0129] After binders are identified (*e.g.*, by determining that the polypeptide is capable of binding to a target or antigen when "active" (*e.g.*, after treatment with protease), but not when "inactive" (*e.g.*, before treatment with protease)), the nucleic acid can be extracted. Extracted

DNA can then be used directly to transform *E. coli* host cells or alternatively, the encoding sequences can be amplified, for example using PCR with suitable primers, and sequenced by any typical sequencing method. DNA sequences of the binders can be restriction enzyme digested and then inserted into a vector for protein expression.

First peptides (FPs)

[0130] In some embodiments, the present disclosure relates to polynucleotides and/or polynucleotide libraries encoding one or more polypeptides comprising a first peptide (FP). In some embodiments, the present disclosure relates to polypeptides and/or polypeptide libraries comprising at least one polypeptide comprising a first peptide (FP). In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y. In some embodiments, X is not W, M, and/or C. In some embodiments, each X in X_m of formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P, each X in X_n of formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P, and/or each X in X_o of formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments, the FP comprises a polypeptide encoded by a polynucleotide sequence according to Formula (XIV): $(NNK)_mTGY(NNK)_nTGY(NNK)_o$ (SEQ ID NO: 87), where each N is independently A, G, T, or C, where each K is independently T or G, and where each Y is independently T or C, and wherein each H is independently A, T, or C.

[0131] In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments, X is not W, M, and/or C. In some embodiments, each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S,

T, N, I, L, F, V, H, and P and each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P. In some embodiments, the FP comprises a polypeptide encoded by a polynucleotide sequence according to Formula (II): $(NNK)_mTGY(NNK)_nTGY(NHC)_o$ (SEQ ID NO: 2), wherein each N is independently A, G, T, or C, wherein each K is independently T or G, wherein each Y is independently T or C, and wherein each H is independently A, T, or C.

[0132] In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (XII): $Z_mCZ_nCZ_o$ (SEQ ID NO: 71), where m is from 3-10, n is from 3-10, and o is from 1-10, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0133] In some embodiments, m is from 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-10, 5-9, 5-8, 5-7, 5-6, 6-10, 6-9, 6-8, 6-7, 7-10, 7-9, 7-8, 8-10, 8-9, or 9-10. In some embodiments, m is from 6-8. In some embodiments, m is 3, 4, 5, 6, 7, 8, 9, or 10. In some embodiments, m is 6.

[0134] In some embodiments, n is from 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-10, 5-9, 5-8, 5-7, 5-6, 6-10, 6-9, 6-8, 6-7, 7-10, 7-9, 7-8, 8-10, 8-9, or 9-10. In some embodiments, n is from 6-8. In some embodiments, n is 3, 4, 5, 6, 7, 8, 9, or 10. In some embodiments, n is 6. In some embodiments, n is 8.

[0135] In some embodiments, o is from 1-10, 1-9, 1-8, 1-7, 1-6, 1-5, 1-4, 1-3, 1-2, 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, 2-3, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-10, 5-9, 5-8, 5-7, 5-6, 6-10, 6-9, 6-8, 6-7, 7-10, 7-9, 7-8, 8-10, 8-9, or 9-10. In some embodiments, o is from 1-2. In some embodiments, o is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. In some embodiments, o is 2.

[0136] In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (IV): Z6CX6CZ2 (SEQ ID NO: 55), where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0137] In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (V): Z6CX8CZ2 (SEQ ID NO: 56) where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0138] In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (VI): (Z6)C(Z6)C(Z2) (SEQ ID NO: 57), where each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0139] In some embodiments, the first peptide (FP) comprises an amino acid sequence according to Formula (VII): (Z6)C(Z8)C(Z2) (SEQ ID NO: 58), where each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0140] In some embodiments, the first peptide (FP) comprises an amino acid sequence selected from SEQ ID NOS: 72-85.

[0141] In some embodiments, any of the first peptides (FPs) described herein may further comprise one or more additional amino acid sequences (*e.g.,* one or more polypeptide tags). Examples of suitable additional amino acid sequence may include, without limitation, purification tags (such as his-tags, flag-tags, maltose binding protein and glutathione-S-transferase tags), detection tags (such as tags that may be detected photometrically (*e.g.,* red or green fluorescent protein, *etc.*)), tags that have a detectable enzymatic activity (*e.g.,* alkaline phosphatase, *etc.*), tags containing secretory sequences, leader sequences, and/or stabilizing sequences, protease cleavage sites (*e.g.,* furin cleavage sites, TEV cleavage sites, Thrombin cleavage sites), and the like. In some embodiments, the one or more additional amino acid sequences are at the N-terminus of the first peptide (FP). In some embodiments, the additional amino acid sequence comprises or consists of the sequence EVGSY (SEQ ID NO: 16).

[0142] In some embodiments, the first peptide is a masking peptide that binds to the target binding moiety (TBM) and inhibits the polypeptide from binding to its target before activation (*e.g.,* before treatment with one or more proteases that cleave within the cleavable moiety (CM), before undergoing a (local) change in pH (increased or decreased), before a temperature shift

(increased or decreased), before being contacted with a second molecule (such as a small molecule or a protein ligand), *etc.*), but does not bind to the TBM and/or inhibit the polypeptide from binding to its target after activation (*e.g.*, after treatment with one or more proteases that cleave within the cleavable moiety (CM), after undergoing a (local) change in pH (increased or decreased), after a temperature shift (increased or decreased), after being contacted with a second molecule (such as a small molecule or a protein ligand), *etc.*). In some embodiments, the first peptide (FP) (*e.g.*, a masking moiety) inhibits binding of a polypeptide (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)) to its target when the CM is not cleaved, but does not inhibit binding of a polypeptide (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)) to its target when the CM is cleaved. In some embodiments, the first peptide (FP) (*e.g.*, a masking moiety) has a dissociation constant for binding to the TBM that is greater (*e.g.*, at least about 1.5-fold greater, at least about 2-fold greater, at least about 2.5-fold greater, at least about 3-fold greater, at least about 3.5-fold greater, at least about 4-fold greater, at least about 4.5-fold greater, at least about 5-fold greater, at least about 10-fold greater, at least about 100-fold greater, at least about 500-fold greater, *etc.*) than the dissociation constant of the polypeptide (*e.g.*, an activatable polypeptide (*i.e.*, activatable antibody)) for its target.

Cleavable moieties (CMs)

[0143] In some embodiments, the present disclosure relates to polynucleotides and/or polynucleotide libraries encoding one or more polypeptides comprising a cleavable moiety (CM). In some embodiments, the present disclosure relates to polypeptides and/or polypeptide libraries comprising at least one polypeptide comprising a cleavable moiety (CM).

[0144] In some embodiments, the cleavable moiety (CM) comprises at least a first cleavage site (CS_1) (*e.g.*, a first protease cleavage site). In some embodiments, the first cleavage site is a first protease cleavage site. Any suitable protease cleavage site recognized and/or cleaved by any protease (*e.g.*, a protease that is known to be co-localized with a target of a polypeptide comprising the CM) known in the art may be used, including, for example, a protease cleavage site recognized and/or cleaved by urokinase-type plasminogen activator (uPA); matrix metalloproteinases (*e.g.*, MMP-1, MMP-2, MMP-3, MMP-7, MMP-8, MMP-9, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-16, MMP-17, MMP-19, MMP-20, MMP-23,

MMP-24, MMP-26, and/or MMP-27); Tobacco Etch Virus (TEV) protease; plasmin; Thrombin; PSA; PSMA; ADAMS/ADAMTS (*e.g.,* ADAM 8, ADAM 9, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAMDEC1, ADAMTS1, ADAMTS4, and/or ADAMTS5); caspases (*e.g.,* Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, and/or Caspase-14); aspartate proteases (*e.g.,* RACE and/or Renin); aspartic cathepsins (*e.g.,* Cathepsin D and/or Cathepsin E); cysteine cathepsins (*e.g.,* Cathepsin B, Cathepsin C, Cathepsin K, Cathepsin L, Cathepsin S, Cathepsin V/L2, and/or Cathepsin X/Z/P); cysteine proteinases (*e.g.,* Cruzipain, Legumain, and/or Otubain-2); KLKs (*e.g.,* KLK4, KLK5, KLK6, KLK7, KLK8, KLK10, KLK11, KLK13, and/or KLK14); metallo proteainases (*e.g.,* Meprin, Neprilysin, PSMA, and/or BMP-1); serine proteases (*e.g.,* activated protein C, Cathepsin A, Cathepsin G, Chymase, and/or coagulation factor proteases (such as FVIIa, FIXa, FXa, FXIa, FXIIa)); elastase; granzyme B; guanidinobenzoatase; HtrA1; human neutrophil elastase; lactoferrin; marapsin; NS3/4A; PACE4; tPA; tryptase; type II transmembrane serine proteases (TTSPs) (*e.g.,* DESC1, DPP-4, FAP, Hepsin, Matriptase-2, MT-SP1/Matriptase, TMPRSS2, TMPRSS3 and/or TMPRSS4); *etc.* In some embodiments, the first protease cleavage site is a cleavage site for a protease selected from uPA, MMP-1, MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, TEV protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE. In some embodiments, the first protease cleavage site is a cleavage site for a protease selected from uPA, MMP-2, MMP-9, and/or TEV protease. In some embodiments, the protease cleavage comprises an amino acid sequence selected from SGRSA (SEQ ID NO: 13), PLGLAG (SEQ ID NO: 14), and ENLYFQG (SEQ ID NO: 15).

[0145] In some embodiments, a polypeptide comprising a first peptide (FP) and a cleavable moiety (CM) comprises an amino acid sequence according to Formula (VIII): EVGSY(Z6)C(Z6)C(Z2)SGRSA (SEQ ID NO: 4), where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P.

[0146] In some embodiments, a polypeptide comprising a first peptide (FP) and a cleavable moiety (CM) comprises an amino acid sequence according to Formula (IX):

EVGSY(Z6)C(X6)C(Z2)SGRSA (SEQ ID NO: 5), where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and where each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0147] In some embodiments, a polypeptide comprising a first peptide (FP) and a cleavable moiety (CM) comprises an amino acid sequence according to Formula (X): EVGSY(Z6)C(Z8)C(Z2)SGRSA (SEQ ID NO: 6), where each Z is independently an amino acid selected from D, A, Y, S, T, N, I, L, F, V, H, and P.

[0148] In some embodiments, a polypeptide comprising a first peptide (FP) and a cleavable moiety (CM) comprises an amino acid sequence according to Formula (XI): EVGSY(Z6)C(X8)C(Z2)SGRSA (SEQ ID NO: 7), where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

[0149] In some embodiments, the cleavable moiety (CM) further comprises a first linker (L_1). In some embodiments, the first linker (L_1) is C-terminal to the first cleavage site (CS_1) (*e.g.*, a first protease cleavage site). In some embodiments, the cleavable moiety (CM) comprises a structure, from N-terminus to C-terminus, of: (CS_1)-L_1.

[0150] Any suitable linker (*e.g.*, a flexible linker) known in the art may be used, including, for example: glycine polymers (G)n, where n is an integer of at least 1 (*e.g.*, at least one, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, *etc.*); glycine-serine polymers (GS)n, where n is an integer of at least 1 (*e.g.*, at least one, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, *etc.*) such as GGGGS (SEQ ID NO: 17), SGGS (SEQ ID NO: 18), GGSG (SEQ ID NO: 19), GGSGG (SEQ ID NO: 20), GSGSG (SEQ ID NO: 21), GSGGG (SEQ ID NO: 22), GGGSG (SEQ ID NO: 23), and/or GSSSG (SEQ ID NO: 24)); glycine-alanine polymers; alanine-serine polymers; and the like. Linker sequences may be of any length, such as from about 1 amino acid (*e.g.*, glycine or serine) to about 20 amino acids (*e.g.*, 20 amino acid glycine polymers or glycine-serine polymers), about 1 amino acid to about 15 amino acids, about 3 amino acids to about 12 amino

acids, about 4 amino acids to about 10 amino acids, about 5 amino acids to about 9 amino acids, about 6 amino acids to about 8 amino acids, *etc.* In some embodiments, the linker is any of about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids in length. In some embodiments, the linker comprises an amino acid sequence selected from SEQ ID NOS: 17-24. In some embodiments, the linker comprises an amino acid sequence of SEQ ID NO: 17 or 18.

[0151] In some embodiments, the cleavable moiety (CM) further comprises at least a second cleavage site (*e.g.,* at least a second, at least a third, at least a fourth, at least a fifth, *etc.*). In some embodiments, the cleavable moiety (CM) further comprises a second cleavage site (CS_2). In some embodiments, the second cleavage site is a second protease cleavage site. The second protease cleavage site may be any suitable protease cleavage site recognized and/or cleaved by any of the proteases described above. In some embodiments, the first (CS_1) and second (CS_2) cleavage sites are protease cleavage sites recognized and/or cleaved by the same protease. In some embodiments, the first (CS_1) and second (CS_2) cleavage sites are protease cleavage sites recognized and/or cleaved by different proteases (*e.g.,* the first protease cleavage site is recognized and/or cleaved by uPA, and the second protease cleavage site is recognized and/or cleaved by MMP-2; the first protease cleavage site is recognized and/or cleaved by uPA, and the second protease cleavage site is recognized and/or cleaved by MMP-9; the first protease cleavage site is recognized and/or cleaved by uPA, and the second protease cleavage site is recognized and/or cleaved by TEV protease; *etc.*). In some embodiments, the at least second cleavage site (CS_2) is C-terminal to the first linker (L_1). In some embodiments, the cleavable moiety (CM) comprises a structure, from N-terminus to C-terminus, of: (CS_1)-L_1-(CS_2).

[0152] In some embodiments, the cleavable moiety (CM) further comprises at least a second linker (*e.g.,* at least a second, at least a third, at least a fourth, at least a fifth, *etc.*). In some embodiments, the cleavable moiety (CM) further comprises a second linker (L_2). The second linker (L_2) may be any suitable linker described above. In some embodiments, the second linker comprises an amino acid sequence selected from SEQ ID NO: 17-24. In some embodiments, the first (L_1) and second (L_2) linkers are the same (*e.g.,* both linkers comprise the sequence of SEQ ID NO: 17 or 18). In some embodiments, the first (L_1) and second (L_2) linkers are different (*e.g.,* the first linker (L_1) comprises the amino acid sequence of SEQ ID NO: 17, and the second linker (L_2) comprises the amino acid sequence of SEQ ID NO: 18, *etc.*). In some embodiments, the at

least second linker (L_2) is C-terminal to the second cleavage site (CS_2). In some embodiments, the cleavable moiety (CM) comprises a structure, from N-terminus to C-terminus, of: (CS_1)-L_1-(CS_2)-L_2.

Exemplary FP-CM sequences

[0153] In some embodiments, a polypeptide of the present disclosure comprises the structure, from N-terminus to C-terminus, of: (FP)-(PCS_1)-L_1-(PCS_2)-L_2. In some embodiments, a polypeptide of the present disclosure comprises the amino acid sequence of: EVGSYDALHYACPPDYYACYYSGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 25); EVGSYNSYHAYCPHPLYPCTASGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 26); EVGSYASSAVLCVTAYFSCNSSGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 27); EVGSYNFVADSCPDHPYPCSASGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 28); EVGSYNFVADSCPDHPYPCSASGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 29); EVGSYIVHHSDCDAFYPYCDSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 30); EVGSYIVHHSDCDAFYPYCDSSGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 31); EVGSYYSAYPACDSHYPYCNSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 32); EVGSYYSAYPACDSHYPYCNSSGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 33); EVGSYPNPSSDCVPYYYACAYSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 34); EVGSYPNPSSDCVPYYYACAYSGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 35); EVGSYYSAYPACDSHYPYCQSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 36); EVGSYYSAYPACDSHYPYCNSAGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 37); EVGSYPQPSSDCVPYYYACAYSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 38); EVGSYPNPASDCVPYYYACAYSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 39); EVGSYPTDLDACADAPNHCHFSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 40); EVGSYSSTHAHCHHSPANCISSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 41); EVGSYDTDYDFCPILRHRCDSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 42); EVGSYNDYNYHCKWRPSRCHNSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 43); EVGSYYHDYDDCRVLPRRCFNSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 44); EVGSYSNNFASCLWRHRSCADSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 45); and/or EVGSYTDNYDYCPRLRRKCYHSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 46). In some

embodiments, a polypeptide of the present disclosure comprises the structure, from N-terminus to C-terminus, of: (FP)-(PCS_1)-L_1-(PCS_2)-L_2-(TBM).

Target binding moieties (TBMs)

[0154] In some embodiments, the present disclosure relates to polynucleotides and/or polynucleotide libraries encoding one or more polypeptides comprising a target binding moiety (TBM). In some embodiments, the present disclosure relates to polypeptides and/or polypeptide libraries comprising at least one polypeptide comprising a target binding moiety (TBM). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region and/or an antibody heavy chain variable region. In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region. In some embodiments, the target binding moiety (TBM) comprises an antibody heavy chain variable region. In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region and an antibody heavy chain variable region. In some embodiments, the antibody heavy chain variable region is C-terminal to the antibody light chain variable region. In some embodiments, the antibody light chain variable region is C-terminal to the antibody heavy chain variable region. In some embodiments, a target binding moiety (TBM) of the present disclosure comprises an antibody light chain variable region and/or an antibody heavy chain variable region with specificity for any target of interest, including, for example, CTLA4, CD137, PD-1, PD-L1, PD-L2, LAG3, TIM3, B7-H3, OX40, CD3, CD19, CD20, CD40, CD95, CD120a, BTLA, VISTA, ICOS, BCMA, Her1, Her2, Her3, and/or B7-H4.

[0155] In some embodiments, the target binding moiety (TBM) comprises a full length antibody light chain and/or a full length antibody heavy chain. The antibody light chain may be a kappa or lambda light chain. The antibody heavy chain may be in any class, such as IgG, IgM, IgE, IgA, or IgD. In some embodiments, the antibody heavy chain is in the IgG class, such as IgG1, IgG2, IgG3, or IgG4 subclass. An antibody heavy chain described herein may be converted from one class or subclass to another class or subclass using methods known in the art.

[0156] Any one or more of the target binding moieties (TBMs) described herein may incorporate any of the HVR sequences (*e.g.,* one, two, or three of the heavy chain variable region HVR sequences, and/or one, two, or three of the light chain variable region HVR sequences),

heavy chain variable region sequences, and/or light chain variable region sequences of any of the antibodies described in PCT application number PCT/CN2017/098333 (incorporated herein by reference in its entirety), PCT application number PCT/CN2017/098299 (incorporated herein by reference in its entirety), PCT application number PCT/CN2017/098332 (incorporated herein by reference in its entirety), and/or the PCT application titled "Compositions Comprising Cross-reactive Anti-CTLA4 Antibodies, and Methods of Making and Using the Same", filed concurrently herewith under Attorney Docket No. 69540-2000540 (incorporated herein by reference in its entirety).

[0157] Any one or more of the target binding moieties (TBMs) described herein may incorporate any of the HVR sequences (*e.g.*, one, two, or three of the heavy chain variable region HVR sequences, and/or one, two, or three of the light chain variable region HVR sequences), heavy chain variable region sequences, and/or light chain variable region sequences of any of the antibodies described herein (*e.g.*, an anti-CTLA4 antibody, an anti-CD137 antibody).

[0158] In some embodiments, the target binding moiety (TBM) comprises a sequence of one or more of the anti-CTLA4 antibodies described herein, including antibodies described with reference to specific amino acid sequences of HVRs, variable regions (VL, VH), and/or light and heavy chains (*e.g.*, IgG1, IgG2, IgG4). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region comprising an HVR-L1 comprising the amino acid sequence RASQSVRGRFLA (SEQ ID NO: 62), an HVR-L2 comprising the amino acid sequence DASNRATGI (SEQ ID NO: 63), and/or an HVR-L3 comprising the amino acid sequence YCQQSSSWPPT (SEQ ID NO: 64). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 48. In some embodiments, the target binding moiety (TBM) comprises an antibody heavy chain variable region comprising an HVR-H1 comprising the amino acid sequence YSISSGYHWSWI (SEQ ID NO: 59), an HVR-H2 comprising the amino acid sequence LARIDWDDDKYYSTSLKSRL (SEQ ID NO: 60), and/or an HVR-H3 comprising the amino acid sequence ARSYVYFDY (SEQ ID NO: 61). In some embodiments, the target binding moiety (TBM) comprises an antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 47. In some embodiments, the target binding moiety (TBM) comprises: a) an antibody light chain variable region comprising an HVR-L1 comprising the amino acid

sequence RASQSVRGRFLA (SEQ ID NO: 62), an HVR-L2 comprising the amino acid sequence DASNRATGI (SEQ ID NO: 63), and/or an HVR-L3 comprising the amino acid sequence YCQQSSSWPPT (SEQ ID NO: 64); and b) an antibody heavy chain variable region comprising an HVR-H1 comprising the amino acid sequence YSISSGYHWSWI (SEQ ID NO: 59), an HVR-H2 comprising the amino acid sequence LARIDWDDDKYYSTSLKSRL (SEQ ID NO: 60), and/or an HVR-H3 comprising the amino acid sequence ARSYVYFDY (SEQ ID NO: 61). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 48, and an antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 47.

[0159] In some embodiments, the target binding moiety (TBM) comprises a sequence of one or more of the anti-CD137 antibodies described herein, including antibodies described with reference to specific amino acid sequences of HVRs, variable regions (VL, VH), and/or light and heavy chains (*e.g.,* IgG1, IgG2, IgG4). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region comprising an HVR-L1 comprising the amino acid sequence RASQSIGSYLA (SEQ ID NO: 68), an HVR-L2 comprising the amino acid sequence DASNLETGV (SEQ ID NO: 69), and/or an HVR-L3 comprising the amino acid sequence YCQQGYYLWT (SEQ ID NO: 70). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 50. In some embodiments, the target binding moiety (TBM) comprises an antibody heavy chain variable region comprising an HVR-H1 comprising the amino acid sequence FSLSTGGVGVGWI (SEQ ID NO: 65), an HVR-H2 comprising the amino acid sequence LALIDWADDKYYSPSLKSRL (SEQ ID NO: 66), and/or an HVR-H3 comprising the amino acid sequence ARGGSDTVIGDWFAY (SEQ ID NO: 67). In some embodiments, the target binding moiety (TBM) comprises an antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 49. In some embodiments, the target binding moiety (TBM) comprises: a) an antibody light chain variable region comprising an HVR-L1 comprising the amino acid sequence RASQSIGSYLA (SEQ ID NO: 68), an HVR-L2 comprising the amino acid sequence DASNLETGV (SEQ ID NO: 69), and/or an HVR-L3 comprising the amino acid sequence YCQQGYYLWT (SEQ ID NO: 70); and b) an antibody heavy chain variable region comprising an HVR-H1 comprising the amino acid sequence FSLSTGGVGVGWI (SEQ ID NO:

65), an HVR-H2 comprising the amino acid sequence LALIDWADDKYYSPSLKSRL (SEQ ID NO: 66), and/or an HVR-H3 comprising the amino acid sequence ARGGSDTVIGDWFAY (SEQ ID NO: 67). In some embodiments, the target binding moiety (TBM) comprises an antibody light chain variable region comprising the amino acid sequence of SEQ ID NO: 50, and an antibody heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 49.

V. Polypeptides and polypeptide libraries

[0160] Other aspects of the present disclosure relate to polypeptides (*e.g.*, any of the polypeptides described herein) and/or libraries of polypeptides useful for screening for, identifying, and/or selecting one or more activatable binding polypeptides (*i.e.*, one or more activatable antibodies), including activatable antibodies, activatable antigen binding fragments thereof, or derivatives of activatable antibodies. A library of the present disclosure may contain one or more of the polypeptides described herein (*e.g.*, one or more activatable binding polypeptides). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise antigen binding domain(s). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise full length antibody light and/or heavy chain(s). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise light and/or heavy chain Fab fragment(s). In some embodiments, one or more (*e.g.*, one, some, or all) of the polypeptides of a library described herein comprise single-chain variable fragment(s) (scFvs). In some embodiments, the polypeptides are expressed on a cell surface (*e.g.*, yeast or mammalian cell display).

[0161] In some embodiments, a polypeptide of the present disclosure (*e.g.*, in a library) comprises: (a) a first peptide (FP); (b) a cleavable moiety (CM); and (c) a target binding moiety (TBM). In some embodiments, the FP is any of the first peptides described herein (*e.g.*, a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y). In some embodiments, the FP is any of the first peptides described herein (*e.g.*, a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID

NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P). In some embodiments, the CM is any of the cleavable moieties described herein (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site). In some embodiments, the TBM is any of the target binding moieties described herein (*e.g.,* a target binding moiety (TBM) comprising an antibody light chain variable region and/or an antibody heavy chain variable region).

[0162] In some embodiments, provided herein is an antigen binding domain and/or a library comprising antigen binding domains, wherein at least one (*e.g.,* one, some, or all) of the antigen binding domains comprises a polypeptide of the present disclosure. In some embodiments, at least one (*e.g.,* one, some, or all) of the antigen binding domains comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety comprising an antibody light chain variable region. In some embodiments, at least one (*e.g.,* one, some, or all) of the antigen binding domains comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety comprising an antibody light chain variable region. In some embodiments, the antigen binding domain further comprises an antibody heavy chain variable region. In some embodiments, at least one (*e.g.,* one, some, or all) of the antigen binding domains comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence

according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety comprising an antibody heavy chain variable region. In some embodiments, at least one (*e.g.,* one, some, or all) of the antigen binding domains comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety comprising an antibody heavy chain variable region. In some embodiments, the antigen binding domain further comprises an antibody light chain variable region.

[0163] In some embodiments, further provided herein is an antibody fragment or scFv comprising any of the polypeptides described herein. In some embodiments, the antibody fragment or scFv comprises a polypeptide comprising a target binding moiety (TBM) comprising an antibody light chain variable region. In some embodiments, the antibody fragment or scFv comprises a polypeptide comprising a target binding moiety (TBM) comprising an antibody heavy chain variable region. In some embodiments, provided herein is a library of antibody fragments or scFvs, wherein at least one of the antibody fragments or scFvs comprises any of the polypeptides described herein. In some embodiments, at least one (*e.g.,* one, some, or all) of the antibody fragments or scFvs in the library comprises a polypeptide comprising a target binding moiety (TBM) comprising an antibody light chain variable region. In some embodiments, at least one (*e.g.,* one, some, or all) of the antibody fragments or scFvs in the library comprises a polypeptide comprising a target binding moiety (TBM) comprising an antibody heavy chain variable region. Further provided herein are cells and/or a library of cells expressing one or more of the antibody fragments and/or scFvs described herein on their surface.

[0164] In some embodiments, the present disclosure relates to an antibody light chain comprising a polypeptide of the present disclosure. In some embodiments, the antibody light chain comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety (TBM) comprising an antibody light chain variable region. In some embodiments, the antibody light chain comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety (TBM) comprising an antibody light chain variable region. In some embodiments, the present disclosure relates to a library comprising antibody light chains, where at least one (*e.g.,* one, some, or all) of the antibody light chains in the library are antibody light chains as described above). In some embodiments, the present disclosure relates to an antibody comprising an antibody light chain and an antibody heavy chain, wherein the antibody light chain is an antibody light chain as described above. In some embodiments, the antibody heavy chain is any antibody heavy chain known in the art (including any of the antibody heavy chains described herein). In some embodiments, the present disclosure relates to a library comprising antibodies, where at least one (*e.g.,* one, some, or all) of the antibodies are antibodies as described above).

[0165] In some embodiments, the present disclosure relates to an antibody heavy chain comprising a polypeptide of the present disclosure. In some embodiments, the antibody heavy chain comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), where m is from 3-10, n is from 3-10, and o is from 1-10, and

where each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety (TBM) comprising an antibody heavy chain variable region. In some embodiments, the antibody heavy chain comprises a polypeptide comprising, from N-terminus to C-terminus: (a) a first peptide (FP) (*e.g.,* a first peptide (FP) comprising an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, each X is independently an amino acid selected from A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P); (b) a cleavable moiety (*e.g.,* a cleavable moiety (CM) comprising at least a first protease cleavage site); and (c) a target binding moiety (TBM) comprising an antibody heavy chain variable region. In some embodiments, the present disclosure relates to a library comprising antibody heavy chains, where at least one (*e.g.,* one, some, or all) of the antibody heavy chains in the library are antibody heavy chains as described above). In some embodiments, the present disclosure relates to an antibody comprising an antibody heavy chain and an antibody light chain, wherein the antibody heavy chain is an antibody heavy chain as described above. In some embodiments, the antibody light chain is any antibody light chain known in the art (including any of the antibody light chains described herein). In some embodiments, the present disclosure relates to a library comprising antibodies, where at least one (*e.g.,* one, some, or all) of the antibodies are antibodies as described above).

[0166] Polypeptides (*e.g.,* any of the antibodies described above) of the present disclosure may be produced using recombinant methods and compositions, *e.g.,* as described in U.S. Patent No. 4,816,567. In some embodiments, isolated nucleic acids encoding any or the polypeptides (*e.g.,* any of the antibodies described above) are provided. Such nucleic acids may encode an amino acid sequence comprising the V_L and/or an amino acid sequence comprising the V_H of the antibodies (*e.g.,* the light and/or heavy chains of the antibodies). In some embodiments, one or more vectors (*e.g.,* expression vectors) comprising such nucleic acids are provided herein. In some embodiments, a host cell comprising such nucleic acids is provided. In one such embodiment, a host cell comprises (*e.g.,* has been transformed with): (1) a vector comprising a nucleic acid that encodes an amino acid sequence comprising a polypeptide of the present

disclosure comprising a V_L and an amino acid sequence comprising a V_H (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)), (2) a vector comprising a nucleic acid that encodes an amino acid sequence comprising a polypeptide of the present disclosure comprising a V_H and an amino acid sequence comprising the V_L (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)), (3) a first vector comprising a nucleic acid that encodes an amino acid sequence comprising a polypeptide of the present disclosure comprising a V_L and a second vector comprising a nucleic acid that encodes an amino acid sequence comprising the V_H (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)), or (4). a first vector comprising a nucleic acid that encodes an amino acid sequence comprising a polypeptide of the present disclosure comprising a V_H and a second vector comprising a nucleic acid that encodes an amino acid sequence comprising the V_L (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)). In some embodiments, the host cell is eukaryotic, *e.g.* a yeast cell, an insect cell, a Chinese Hamster Ovary (CHO) cell or lymphoid cell (e.g., Y0, NS0, Sp20 cell). In some embodiments, a method of making a polypeptide (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)) is provided, wherein the method comprises culturing a host cell comprising a nucleic acid encoding the polypeptide (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)), as provided above, under conditions suitable for expression of the polypeptide, and optionally recovering the polypeptide (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)) from the host cell (or host cell culture medium).

[0167] For recombinant production of polypeptides (*e.g.*, activatable binding polypeptides (*i.e.*, activatable antibodies)) of the present disclosure, nucleic acid encoding a polypeptide (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)), *e.g.*, as described above, is isolated and inserted into one or more vectors for further cloning and/or expression in a host cell. Such nucleic acid may be readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the polypeptide(s)).

[0168] Suitable host cells for cloning or expression of polypeptide-encoding (*e.g.*, activatable binding polypeptide (*i.e.*, an activatable antibody)-encoding) vectors include prokaryotic or eukaryotic cells. For example, polypeptides (*e.g.*, an activatable binding polypeptide (*i.e.*, an activatable antibody)) may be produced in bacteria, in particular when glycosylation and Fc

effector function are not needed (*see, e.g.,* U.S. Patent Nos. 5,648,237, 5,789,199, and 5,840,523; See also Charlton, *Methods in Molecular Biology, Vol. 248* (B.K.C. Lo, ed., Humana Press, Totowa, NJ, 2003), pp. 245-254, describing expression of antibody fragments in *E. coli*.). After expression, the polypeptide may be isolated from the bacterial cell paste in a soluble fraction and may be further purified.

[0169] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for polypeptide-encoding (*e.g.,* activatable binding polypeptide (*i.e.,* activatable antibody)-encoding) vectors, including fungi and yeast strains whose glycosylation pathways have been "humanized," resulting in the production of a polypeptide with a partially or fully human glycosylation pattern. *See* Gerngross, *Nat. Biotech.* 22:1409-1414 (2004), and Li et al., *Nat. Biotech.* 24:210-215 (2006).

[0170] Suitable host cells for the expression of glycosylated polypeptides are also derived from multicellular organisms (invertebrates and vertebrates). Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of *Spodoptera frugiperda* cells.

[0171] Plant cell cultures can also be utilized as hosts. *See, e.g.,* US Patent Nos. 5,959,177, 6,040,498, 6,420,548, 7,125,978, and 6,417,429 (describing PLANTIBODIES™ technology for producing antibodies in transgenic plants).

[0172] Vertebrate cells may also be used as hosts. For example, mammalian cell lines that are adapted to grow in suspension may be useful. Other examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7); human embryonic kidney line (293 or 293 cells as described, *e.g.,* in Graham *et al., J. Gen Virol.* 36:59 (1977)); baby hamster kidney cells (BHK); mouse sertoli cells (TM4 cells as described, *e.g.,* in Mather, *Biol. Reprod.* 23:243-251 (1980)); monkey kidney cells (CV1); African green monkey kidney cells (VERO-76); human cervical carcinoma cells (HELA); canine kidney cells (MDCK; buffalo rat liver cells (BRL 3A); human lung cells (W138); human liver cells (Hep G2); mouse mammary tumor (MMT 060562); TRI cells, as described, e.g., in Mather *et al., Annals N.Y. Acad. Sci.* 383:44-68 (1982); MRC 5 cells; and FS4 cells. Other useful mammalian host cell lines include Chinese hamster ovary (CHO) cells, including $DHFR^-$ CHO cells (Urlaub *et al., Proc. Natl. Acad. Sci.*

USA 77:4216 (1980)); and myeloma cell lines such as Y0, NS0 and Sp2/0. For a review of certain mammalian host cell lines suitable for antibody production, *see, e.g.*, Yazaki and Wu, *Methods in Molecular Biology, Vol. 248* (B.K.C. Lo, ed., Humana Press, Totowa, NJ), pp. 255-268 (2003).

VI. Activatable binding polypeptides and their production

[0173] In some embodiments, provided herein are activatable binding polypeptides (*e.g.*, activatable antibodies) screened for, identified and/or selected from any of the polynucleotide and/or polypeptide libraries described herein.

[0174] In some embodiments, activatable antibodies of the present disclosure are context-dependent (*e.g.*, are activated (are only capable of binding their targets) in certain contexts (such as in the protease-rich tumor microenvironment)). In some embodiments, the activatable antibodies of the present disclosure provide improved safety over more traditional, non-activatable antibodies (*e.g.*, show reduced toxicity, do not induce significant alterations to the weights of many organs, do not alter liver histopathology, hematology, and/or blood biochemistry, *etc.*). In some embodiments, activatable antibodies of the present disclosure have improved pharmacokinetic properties as compared to more traditional, non-activatable antibodies (*e.g.*, have longer *in vivo* half-lives).

[0175] In some embodiments, an activatable binding polypeptide of the present disclosure comprises: (a) a first peptide (FP) (*e.g.*, a masking moiety), (b) a cleavable moiety, and (c) a target binding moiety. In some embodiments, the first peptide (FP) binds to the target binding moiety (TBM) of the activatable binding domain and reduces or inhibits binding of the activatable binding moiety to its target (*e.g.*, human CTLA4 or human CD137), as compared to the binding of a corresponding binding polypeptide lacking the masking moiety to the target and/or as compared to the binding of a parental antibody to the target.

[0176] In some embodiments, an "activatable" binding polypeptides refers to a binding polypeptide that exhibits a first level of binding to a target when in an inhibited, masked, and/or uncleaved state, and exhibits a second level of binding to the target in an uninhibited, unmasked, and/or cleaved state, where the second level of target binding is greater than the first level of

target binding. In some embodiments, access to the target by the activatable binding polypeptide is greater after cleavage within the cleavable moiety (*e.g.,* by one or more proteases.

[0177] In some embodiments, a polypeptide of the present disclosure is generally considered to be an "activatable" binding polypeptide when binding affinity of the polypeptide to its target (*e.g.,* human CTLA4 or CD137) increases by at least about 2-fold (*e.g.,* at least about 2-fold, at least about 2.5-fold, at least about 3, at least about 3.5-fold, at least about 4-fold, at least about 4.5-fold, at least about 5-fold, at least about 5.5-fold, at least about 6-fold, at least about 6.5-fold, at least about 7-fold, at least about 7.5-fold, at least about 8-fold, at least about 8.5-fold, at least about 9-fold, at least about 9.5-fold, at least about 10-fold, at least about 25-fold, at least about 50-fold, at least about 75-fold, at least about 100-fold, at least about 250-fold, at least about 500-fold, at least about 750-fold, or at least about 1000-fold, or more) after activation of the polypeptide as compared to prior to activation of the polypeptide (*e.g.,* after activation by treatment with one or more proteases that cleave within the cleavable moiety (CM), after activation by a change in pH (increased or decreased), after activation by a temperature shift (increased or decreased), after activation by being contacted with a second molecule (such as a small molecule or a protein ligand), *etc.*). In some embodiments, a polypeptide of the present disclosure is generally considered "activatable" if the EC_{50} of the polypeptide increases by at least about 2-fold (*e.g.,* at least about 2-fold, at least about 2.5-fold, at least about 3, at least about 3.5-fold, at least about 4-fold, at least about 4.5-fold, at least about 5-fold, at least about 5.5-fold, at least about 6-fold, at least about 6.5-fold, at least about 7-fold, at least about 7.5-fold, at least about 8-fold, at least about 8.5-fold, at least about 9-fold, at least about 9.5-fold, at least about 10-fold, at least about 25-fold, at least about 50-fold, at least about 75-fold, at least about 100-fold, at least about 250-fold, at least about 500-fold, at least about 750-fold, or at least about 1000-fold, or more) after "activation" (*e.g.,* as measured by an ELISA or FACS assay; *see* the examples below). In some embodiments, a polypeptide of the present disclosure is generally considered "activatable" if the EC_{50} of the polypeptide increases by at least about 2-fold after treatment with a protease that cleaves within the cleavable moiety (*e.g.,* as measured by an ELISA or FACS assay; *see* the examples below)

[0178] In some embodiments, when the masking moiety is bound to the target binding moiety of the activatable binding polypeptide, the K_D of the activatable binding polypeptide for

its target is about 2 (*e.g.,* about 2, about 2.5, about 3, about 3.5 about 4, about 4.5, about 5, about 5.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10, about 25, about 50, about 75, about 100, about 250, about 500, about 750, or about 1000 or more) times greater than when the masking moiety is not bound to the target binding moiety (*e.g.,* after "activation" of the activatable binding polypeptide (such as after protease treatment to cleave within the cleavable moiety)) and/or than the K_D of the parental antibody for the target. Methods of measuring affinity are known in the art, including, for example, by the methods described in Example 3 below).

[0179] In some embodiments, when the masking moiety is bound to the target binding moiety of the activatable binding polypeptide, the K_D of the activatable binding polypeptide for its target is reduced by at least about 25% (*e.g.,* at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 99%) relative to when the masking moiety is not bound to the target binding moiety (*e.g.,* after "activation" of the activatable binding polypeptide (such as after protease treatment to cleave within the cleavable moiety)) and/or relative to the K_D of the parental antibody for the target. Methods of measuring affinity are known in the art, including, for example, by the methods described in Example 3 below).

[0180] In some embodiments, the masking moiety sterically hinders binding of the activatable binding polypeptide to its target and/or allosterically hinders binding of the activatable binding polypeptide to its target. In some embodiments, the masking moiety does not comprise an amino acid sequence of a natural binding partner of activatable binding polypeptide.

[0181] In some embodiments, the dissociation constant of the masking moiety for the target binding moiety is greater than the dissociation constant for the activatable binding polypeptide for the target (when in active activate form). In some embodiments, the dissociation constant of the masking moiety for the target binding moiety is about 2 (*e.g.,* about 2, about 2.5, about 3, about 3.5 about 4, about 4.5, about 5, about 5.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10, about 25, about 50, about 75, about 100, about 250, about 500, about 750, or about 1000 or more) times greater than the dissociation constant for the activatable binding polypeptide for the target (when in activate form). In some embodiments, the

dissociation constant of the masking moiety for the target binding moiety is about equal to the dissociation constant for the activatable binding polypeptide for the target (when in activate form). In some embodiments, the first peptide (FP) binds to the target binding moiety (TBM), and prevents the polypeptide from binding to its target only when the polypeptide has not been activated (*e.g.,* activated by treatment with one or more proteases that cleave within the cleavable moiety (CM), activated by a change in pH (increased or decreased), activated by a temperature shift (increased or decreased), activated after being contacted with a second molecule (such as a small molecule or a protein ligand), *etc.*). In some embodiments, activation induces cleavage of the polypeptide within the cleavage moiety. In some embodiments, activation induces conformation changes in the polypeptide (*e.g.,* displacement of the first peptide (FP)), leading to the first peptide no longer preventing the polypeptide from binding to its target.

[0182] The activatable binding polypeptides (*i.e.,* activatable antibodies) described herein may be further modified. In some embodiments, the activatable binding polypeptides are linked to an additional molecular entity. Examples of additional molecular entities include pharmaceutical agents, peptides or proteins, detection agent or labels, and antibodies.

[0183] In some embodiments, an activatable binding polypeptide of the present disclosure is linked to a pharmaceutical agent. Examples of pharmaceutical agents include cytotoxic agents or other cancer therapeutic agents, and radioactive isotopes. Specific examples of cytotoxic agents include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents also include, for example, antimetabolites (*e.g.,* methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.,* mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.,* daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.,* dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.,* vincristine and vinblastine). Examples of radioactive isotopes that can be conjugated to antibodies for use

diagnostically or therapeutically include, but are not limited to, iodine^{131}, indium^{111}, yttrium^{90} and lutetium^{177}. Methods for linking a polypeptide to a pharmaceutical agent are known in the art, such as using various linker technologies. Examples of linker types include hydrazones, thioethers, esters, disulfides and peptide-containing linkers. For further discussion of linkers and methods for linking therapeutic agents to antibodies *see e.g.,* Saito *et al.*, *Adv. Drug Deliv. Rev.* 55:199-215 (2003); Trail, *et al.*, *Cancer Immunol. Immunother.* 52:328-337 (2003); Payne, *Cancer Cell* 3:207-212 (2003); Allen, *Nat. Rev. Cancer* 2:750-763 (2002); Pastan and Kreitman, *Curr. Opin. Investig. Drugs* 3:1089-1091 (2002); Senter and Springer (2001) *Adv. Drug Deliv. Rev.* 53:247-264.

Activatable binding polypeptides targeting CTLA4

[0184] In some embodiments, the present disclosure relates to activatable binding polypeptides (*i.e.,* activatable antibodies) that bind to human CTLA4, including activatable anti-CTLA4 antibodies, antigen binding fragments of the activatable anti-CTLA4 antibodies, and/or derivatives of the activatable anti-CTLA4 antibodies. In some embodiments, the activatable antibody comprises: (a) a polypeptide comprising, from N-terminus to C-terminus, a masking moiety (MM), a cleavable moiety (CM), and a target binding moiety (TBM), where the MM comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; where the CM comprises at least a first cleavage site (*e.g.,* at least a first protease cleavage site); and where the TBM comprises an antibody light chain variable region (VL); and (b) an antibody heavy chain variable region (VH). In some embodiments, the MM inhibits the binding of the activatable antibody to human CTLA4 when the CM is not cleaved. In some embodiments, the activatable antibody is capable of binding to human CTLA4 when the CM is cleaved. In some embodiments, the MM comprises an amino acid sequence selected from SEQ ID NOS: 72-78.

[0185] In some embodiments, the activatable binding polypeptides comprise any of the anti-CTLA4 antibodies described herein, including antibodies described with reference to specific

amino acid sequences of HVRs, variable regions (VL, VH), and/or light and heavy chains (*e.g.*, IgG1, IgG2, IgG4). In some embodiments, the anti-CTLA4 antibodies are human antibodies. In some embodiments, the anti-CTLA4 antibodies are humanized antibodies and/or chimeric antibodies.

[0186] In some embodiments, the activatable binding polypeptide comprises: a) an HVR-H1 comprising the amino acid sequence YSISSGYHWSWI (SEQ ID NO: 59), an HVR-H2 comprising the amino acid sequence LARIDWDDDKYYSTSLKSRL (SEQ ID NO: 60), and an HVR-H3 comprising the amino acid sequence ARSYVYFDY (SEQ ID NO: 61); and/or b) an HVR-L1 comprising the amino acid sequence RASQSVRGRFLA (SEQ ID NO: 62), an HVR-L2 comprising the amino acid sequence DASNRATGI (SEQ ID NO: 63), and an HVR-L3 comprising the amino acid sequence YCQQSSSWPPT (SEQ ID NO: 64). In some embodiments, the activatable binding polypeptide comprises: a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 47; and/or b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 48.

[0187] In some embodiments, the present disclosure relates to activatable binding polypeptides that bind to human CTLA4 when in active form (*e.g.*, the activatable binding polypeptides are active after cleavage in the cleavable moiety (*e.g.*, with one or more proteases), but inactive prior to cleavage in the cleavable moiety (*e.g.*, with one or more proteases)), and have at least one (*e.g.*, at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, or all nine) of the following functional properties: (a) bind to human, cynomolgus monkey, mouse, rat, and/or dog CTLA4 with a K_D of 500 nM or less; (b) have antagonist activity on human CTLA4; (c) do not bind to human PD-1, PD-L1, PD-L2, LAG3, TIM3, B7-H3, CD95, CD120a, OX40, CD40, BTLA, VISTA, ICOS, and/or B7-H4 at concentration up to 100 nM; (d) are cross-reactive with monkey, mouse, rat, and/or dog CTLA4; (e) induces ADCC effects (*e.g.*, on Tregs); (f) activates human PBMCs (*e.g.*, stimulates secretion of IL-2 and/or IFNγ); (g) are capable of inhibiting tumor cell growth; (h) have therapeutic effect on a cancer; and (i) inhibit binding of human CTLA4 to human CD80 and/or human CD86. Also provided herein are one or more activatable binding polypeptides that cross-compete for binding to human CTLA4 with one or more of the CTLA4-targeting activatable binding polypeptides and/or anti-CTLA4 antibodies described herein.

[0188] In some embodiments, the activatable binding polypeptides bind to human, cynomolgus monkey, mouse, rat, and/or dog CTLA4 with a K_D of about 500 nM or more when in inactive form. In some embodiments, the activatable binding polypeptides bind to human, cynomolgus monkey, mouse, rat, and/or dog CTLA4 with a K_D of about 500 nM or less when in active form (*e.g.,* about 500 nM or less, about 450 nM or less, about 400 nM or less, about 350 nM or less, about 300 nM or less, about 250 nM or less, about 200 nM or less, about 150 nM or less, about 100 nM or less, about 90 nM or less, about 80 nM or less, about 70 nM or less, about 60 nM or less, about 50 nM or less, about 40 nM or less, about 30 nM or less, about 25 nM or less, about 20 nM or less, about 10 nM or less, about 1 nM or less, about 0.1 nM or less, *etc.*) In some embodiments, the activatable binding polypeptides bind to human, cynomolgus monkey, mouse, rat, and/or dog CTLA4 with a K_D of about 350 nM or less when in active form. In some embodiments, the activatable binding polypeptides bind to human CTLA4 with a K_D of about 100 nM or less when in active form. In some embodiments, the activatable binding polypeptides bind to human CTLA4 with a K_D of about 50 nM or less when in active form. In some embodiments, the activatable binding polypeptides bind to human CTLA4 with a K_D of about 10 nM or less when in active form. Methods of measuring the K_D of an activatable binding polypeptide may be carried out using any method known in the art, including for example, by surface plasmon resonance, an ELISA, isothermal titration calorimetry, a filter binding assay, an EMSA, *etc.* In some embodiments, the K_D is measured by an ELISA (*see e.g.,* Example 3 below).

[0189] In some embodiments, the activatable binding polypeptides do not have antagonist activity on human CTLA4 when in inactive form. In some embodiments, the activatable binding polypeptides have antagonist activity on human CTLA4 when in active form (*e.g.,* induces ADCC effects (such as on Tregs), activates PBMCs (such as by activating, inducing, and/or stimulating IL-2 and/or IFNγ secretion), bocks binding of human CTLA4 to human CD80 and/or human CD86, *etc.*). In some embodiments, the activatable binding polypeptides repress one or more activities of human CTLA4 when in active form (*e.g.,* repress one or more activities of human CTLA4 when a cell (such as a human cell) expressing human CTLA4 is contacted by an activated activatable binding polypeptide).

[0190] In some embodiments, when in inactive form, the activatable binding polypeptides are not cross-reactive with monkey (*e.g.,* cynomolgus monkey), mouse, rat, and/or dog CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross-reactive with monkey (*e.g.,* cynomolgus monkey), mouse, rat, and/or dog CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross-reactive with monkey CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross-reactive with mouse CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross-reactive with rat CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross-reactive with dog CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross reactive with monkey and mouse CTLA4; monkey and rat CTLA4; monkey and dog CTLA4; mouse and rat CTLA4; mouse and dog CTLA4; rat and dog CTLA4; monkey, mouse, and rat CTLA4; monkey, mouse, and dog CTLA4; monkey, rat, and dog CTLA4; mouse, rat, and dog CTLA4; or monkey, mouse, rat, and dog CTLA4. In some embodiments, when in active form, the activatable binding polypeptides are cross-reactive at about 350 nM (*e.g.,* at about 1nM, at about 10nM, at about 25nM, at about 50nM, at about 75nM, at about 100nM, at about 150 nM, at about 200 nM, at about 250 nM, at about 300 nM, at about 350 nM). Methods of measuring cross-reactivity are known in the art, including, without limitation, surface plasmon resonance, an ELISA, isothermal titration calorimetry, a filter binding assay, an EMSA, *etc.*

[0191] In some embodiments, the activatable binding polypeptides do not induce ADCC effects (*e.g.,* on human cells such as Tregs) when in inactive form. In some embodiments, the activatable binding polypeptides have reduced ADCC effects (*e.g.,* on human cells such as Tregs) when in inactive form as compared to a control binding polypeptide (*e.g.,* a parental antibody lacking the first peptide (FP) and cleavable moiety (CM)). In some embodiments, the activatable antibodies induce ADCC effects (*e.g.,* on human cells such as Tregs) when in active form. Methods of measuring ADCC effects (*e.g., in vitro* methods) are known in the art, including, without limitation, via the methods described in Example 4 below. In some embodiments, when in inactive form, the activatable binding polypeptides induce ADCC effects by less than about 10% (*e.g.,* induce ADCC by less than about 10%, less than about 5%, less than about 1%, *etc.*) relative to a control (*e.g.,* a parental antibody lacking the first peptide (FP)

and cleavable moiety (CM)). In some embodiments, when in active form, the activatable binding polypeptides induce ADCC effects by more than about 10% (*e.g.*, induce ADCC by more than about 10%, more than about 15%, more than about 20%, more than about 25%, more than about 30%, more than about 35%, more than about 40%, *etc.*) relative to a control (*e.g.*, an isotype control).

[0192] In some embodiments, the activatable binding polypeptides are capable of inhibiting tumor cell growth and/or proliferation. In some embodiments, the tumor cell growth and/or proliferation is inhibited by at least about 5% (*e.g.*, at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 99%) when contacted with the activatable binding polypeptides relative to corresponding tumor cells not contacted with the activatable binding polypeptides (or relative to corresponding tumor cells contacted with an isotype control antibody). In some embodiments, the activatable binding polypeptides are capable of reducing tumor volume in a subject when the subject is administered the activatable binding polypeptides. In some embodiments, the activatable binding polypeptides are capable of reducing tumor volume in a subject by at least about 5% (*e.g.*, at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 99%) relative to the initial tumor volume in the subject (*e.g.*, prior to administration of the activatable binding polypeptides; as compared to a corresponding tumor in a subject administered an isotype control antibody). Methods of monitoring tumor cell growth/proliferation, tumor volume, and/or tumor inhibition are known in the art, including, for example, via the methods described in Example 4 below.

[0193] In some embodiments, the activatable binding polypeptides have therapeutic effect on a cancer. In some embodiments, the activatable binding polypeptides reduce one or more signs or symptoms of a cancer. In some embodiments, a subject suffering from a cancer goes into partial or complete remission when administered the activatable binding polypeptides.

[0194] In some embodiments, the present disclosure provides isolated activatable binding polypeptides that, when in active form, compete or cross-compete for binding to human CTLA4

with an antibody comprising: a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 59; an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 60; and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 61; and/or b) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 62; an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 63; and an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 54. In some embodiments, the present disclosure provides isolated activatable binding polypeptides that, when in active form, compete or cross-compete for binding to human CTLA4 with an antibody comprising: a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 47; and/or b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 48. The ability of an activatable binding polypeptide to compete or cross-compete for binding with an antibody can be determined using standard binding assays known in the art, such as BIAcore analysis, ELISA assays, or flow cytometry. For example, one can allow an antibody (*e.g.,* as described above) to bind to human CTLA4 under saturating conditions and then measure the ability of the test activatable binding polypeptide (when in active form) to bind to the CTLA4. If the test activatable binding polypeptide is able to bind to the CTLA4 at the same time as the antibody, then the test activatable binding polypeptide binds to a different epitope then the antibody. However, if the test activatable binding polypeptide is not able to bind to the CTLA4 at the same time, then the test activatable binding polypeptide binds to the same epitope, an overlapping epitope, or an epitope that is in close proximity to the epitope bound by the antibody. This experiment can be performed using various methods, such as ELISA, RIA, FACS or surface plasmon resonance.

[0195] In some embodiments, the activatable binding polypeptides (when in inactive form) do not inhibit the binding between CTLA4 and one or more of its binding partners (*e.g.,* human CTLA4 and human CD80, human CTLA4 and human CD86). In some embodiments, the activatable binding polypeptides (when in active form) inhibit the binding between CTLA4 and one or more of its binding partners (*e.g.,* human CTLA4 and human CD80, human CTLA4 and human CD86). In some embodiments, the activatable binding polypeptides inhibit the binding between CTLA4 and its ligand *in vitro*. In some embodiments, the activatable binding polypeptides have a half maximal inhibitory concentration (IC_{50}) of about 500 nM or less (*e.g.,* about 500 nM or less, about 400nM or less, about 300nM or less, about 200nM or less, about

100nM or less, about 50nM or less, about 25nM or less, about 10nM or less, about 1nM or less, *etc.*) for inhibiting binding of CTLA4 to CD80 and/or CD86. In some embodiments, the activatable binding polypeptides have a half maximal inhibitory concentration (IC_{50}) of about 100 nM or less for inhibiting binding of CTLA4 to CD80 and/or CD86. In some embodiments, the activatable binding polypeptides completely inhibit binding of human CTLA4 to CD80 and/or CD86 when provided at a concentration of about 100 nM or greater (*e.g.,* about 100nM or greater, about 500nM or greater, about 1μM or greater, about 10μM or greater, *etc.*). As used herein, the term "complete inhibiting" or "completely inhibits" refers to the activatable binding polypeptide's ability to reduce binding between a first protein and a second protein by at least about 80% (*e.g.,* at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 99%, *etc.*). Methods of measuring the ability of an a polypeptide to inhibit binding of a first protein (*e.g.,* human CTLA4) and a second protein (*e.g.,* human CD80 or human CD86) are known in the art, including, without limitation, via BIAcore analysis, ELISA assays, and flow cytometry.

Activatable binding polypeptides targeting CD137

[0196] In some embodiments, the present disclosure relates to activatable binding polypeptides (*i.e.,* activatable antibodies) that bind to human CD137, including activatable anti-CD137 antibodies, antigen binding fragments of the activatable anti- CD137 antibodies, and/or derivatives of the activatable anti- CD137 antibodies. In some embodiments, the activatable antibody comprises: (a) a polypeptide comprising, from N-terminus to C-terminus, a masking moiety (MM), a cleavable moiety (CM), and a target binding moiety (TBM), where the MM comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), where m is from 3-10, n is from 3-10, and o is from 1-10, where each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; where the CM comprises at least a first cleavage site (*e.g.,* at least a first protease cleavage site); and where the TBM comprises an antibody light chain variable region (VL); and (b) an antibody heavy chain variable region (VH). In some embodiments, the MM inhibits the binding of the activatable antibody to human CD137 when the CM is not cleaved. In some embodiments, the activatable antibody is capable of binding to

human CD137 when the CM is cleaved. In some embodiments, the MM comprises an amino acid sequence selected from SEQ ID NOS: 79-85.

[0197] In some embodiments, the activatable binding polypeptides comprise any of the anti-CD137 antibodies described herein, including antibodies described with reference to specific amino acid sequences of HVRs, variable regions (VL, VH), and/or light and heavy chains (*e.g.*, IgG1, IgG2, IgG4). In some embodiments, the anti-CD137 antibodies are human antibodies. In some embodiments, the anti-CD137 antibodies are humanized antibodies and/or chimeric antibodies.

[0198] In some embodiments, the activatable binding polypeptide comprises: a) an HVR-H1 comprising the amino acid sequence FSLSTGGVGVGWI (SEQ ID NO: 65), an HVR-H2 comprising the amino acid sequence LALIDWADDKYYSPSLKSRL (SEQ ID NO: 66), and an HVR-H3 comprising the amino acid sequence ARGGSDTVIGDWFAY (SEQ ID NO: 67); and/or b) an HVR-L1 comprising the amino acid sequence RASQSIGSYLA (SEQ ID NO: 68), an HVR-L2 comprising the amino acid sequence DASNLETGV (SEQ ID NO: 69), and an HVR-L3 comprising the amino acid sequence YCQQGYYLWT (SEQ ID NO: 70). In some embodiments, the activatable binding polypeptide comprises: a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 49; and/or b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 50.

[0199] In some embodiments, the present disclosure relates to activatable binding polypeptides that bind to human CD137 when in active form (*e.g.*, the activatable binding polypeptides are active after cleavage in the cleavable moiety (*e.g.*, with one or more proteases), but inactive prior to cleavage in the cleavable moiety (*e.g.*, with one or more proteases)) and have at least one (e.g., at least one, at least two, at least three, at least four, at least five, at least six, at least seven, or all eight) of the following functional properties: (a) bind to human CD137 with a K_D of 500 nM or less; (b) have agonist activity on human CD137; (c) do not bind to human OX40, CD40, GITR and/or CD27 receptor at concentration up to 1000 nM; (d) are cross-reactive with monkey, mouse, rat, and/or dog CD137; (e) do not induce ADCC effects; (f) are capable of inhibiting tumor cell growth; (g) have therapeutic effect on a cancer; and (h) inhibit binding between CD137 and CD137L. In some embodiments, the activatable binding

polypeptides disclosed herein can also inhibit, *e.g.,* completely inhibit, the binding between CD137 and its ligand CD137L. Also provided herein are one or more activatable binding polypeptides anti-CD137 antibodies or antigen-binding fragments that cross-compete for binding to human CD137 with one or more of the CD137-targeting activatable binding polypeptides and/or anti-CD137 antibodies described herein.

[0200] In some embodiments, the activatable binding polypeptides (when in inactive form) bind to human CD137 with a K_D of about 500 nM or more. In some embodiments, the activatable binding polypeptides (when in active form) bind to human CD137 with a K_D of about 500 nM or less (*e.g.,* about 500 nM or less, about 400 nM or less, about 300 nM or less, about 200 nM or less, about 150 nM or less, about 100 nM or less, about 90 nM or less, about 80 nM or less, about 75 nM or less, about 70 nM or less, about 60 nM or less, about 50 nM or less, about 40 nM or less, about 30 nM or less, about 25 nM or less, about 20 nM or less, about 10 nM or less, about 1 nM or less, about 0.1 nM or less, *etc.*). In some embodiments, the activatable binding polypeptides bind to human CD137 with a K_D of about 100 nM or less. In some embodiments, the activatable binding polypeptides bind to human CD137 with a K_D of about 50 nM or less. Methods of measuring the K_D of an activatable binding polypeptide may be carried out using any method known in the art, including for example, by surface plasmon resonance, an ELISA, isothermal titration calorimetry, a filter binding assay, an EMSA, *etc.* In some embodiments, the K_D is measured by an ELISA (*see e.g.,* Example 5 below).

[0201] In some embodiments, the activatable binding polypeptides (when in active form) described herein have agonist activity on human CD137. In some embodiments, the activatable binding polypeptides induce one or more (*e.g.,* one or more, two or more, three or more, etc.) activities of human CD137 when a cell (e.g., a human cell) expressing human CD137 is contacted by the (active) activatable binding polypeptide. Various CD137 activities are known in the art and may include, without limitation, induction of NF-κB-dependent transcription, induction of T cell proliferation, prolonging T cell survival, co-stimulation of activated T cells, induction of cytokine secretion (such as IL-2), and induction of monocyte activation . In some embodiments, the one or more CD137 activities is not CD137 binding to its ligand. Methods of measuring CD137 activity (*e.g.,* the induction of NF-κB-dependent transcription and/or T cell proliferation, *etc.*) are known in the art. In some embodiments, the activatable binding

polypeptides increase NF-κB dependent transcription in cells (*e.g.*, human cells) expressing human CD137. In some embodiments, NF-κB dependent transcription is increased by about 10% or more, about 20% or more, about 30% or more, about 40% or more, about 50% or more, about 60% or more, about 70% or more, about 80% or more, about 90% or more, or about 99% or more in cells (e.g., human cells) expressing CD137 contacted with the (active) activatable binding polypeptide, relative to a corresponding cell not contacted with the activatable binding polypeptide (*e.g.*, a corresponding cell contacted with an isotype control antibody), or contacted with the activatable binding polypeptide when in inactive form. In some embodiments, NF-κB dependent transcription is increased by about 2-fold, 3-fold, 4-folr, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 100-fold, 1000-fold or more in cells (*e.g.*, human cells) expressing CD137 contacted with the activatable binding polypeptide (when in active form), relative to a corresponding cell not contacted with the activatable binding polypeptide (*e.g.*, a corresponding cell contacted with an isotype control antibody), or contacted with the activatable binding polypeptide when in inactive form.

[0202] In some embodiments, the activatable binding polypeptides (when in inactive form) are not cross-reactive with monkey (*e.g.*, cynomolgus monkey), mouse, rat, and/or dog CD137. In some embodiments, the activatable binding polypeptides (when in active form) are cross-reactive with monkey (*e.g.*, cynomolgus monkey), mouse, rat, and/or dog CD137. In some embodiments, the activatable binding polypeptides are cross-reactive with monkey CD137. In some embodiments, the activatable binding polypeptides are cross-reactive with mouse CD137. In some embodiments, the activatable binding polypeptides are cross-reactive with rat CD137. In some embodiments, the activatable binding polypeptides are cross-reactive with dog CD137. In some embodiments, the activatable binding polypeptides are cross reactive with monkey and mouse CD137; monkey and rat CD137; monkey and dog CD137; mouse and rat CD137; mouse and dog CD137; rat and dog CD137; monkey, mouse, and rat CD137; monkey, mouse, and dog CD137; monkey, rat, and dog CD137; mouse, rat, and dog CD137; or monkey, mouse, rat, and dog CD137. In some embodiments, the activatable binding polypeptides are cross-reactive at about 100 nM (*e.g.*, at about 1nM, at about 10nM, at about 25nM, at about 50nM, at about 75nM, at about 100nM). Methods of measuring cross-reactivity are known in the art, including,

without limitation, surface plasmon resonance, an ELISA, isothermal titration calorimetry, a filter binding assay, an EMSA, etc.

[0203] In some embodiments, the activatable binding polypeptides do not induce ADCC effects. Methods of measuring ADCC effects are known in the art. In some embodiments, the activatable binding polypeptides (when in active form or inactive form) do not ADCC effects by more than about 10% (do not induce ADCC by more than about 10%, more than about 5%, more than about 1%, more than about 0.1%, more than about 0.01%) relative to a control.

[0204] In some embodiments, the activatable binding polypeptides are capable of inhibiting tumor cell growth and/or proliferation. In some embodiments, the tumor cell growth and/or proliferation is inhibited by at least about 5% (*e.g.*, at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 99%) when contacted with the activatable binding polypeptides relative to corresponding tumor cells not contacted with the activatable binding polypeptides (or relative to corresponding tumor cells contacted with an isotype control antibody). In some embodiments, the activatable binding polypeptides are capable of reducing tumor volume in a subject when the subject is administered the activatable binding polypeptides. In some embodiments, the activatable binding polypeptides are capable of reducing tumor volume in a subject by at least about 5% (*e.g.*, at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 99%) relative to the initial tumor volume in the subject (*e.g.*, prior to administration of the activatable binding polypeptides; as compared to a corresponding tumor in a subject administered an isotype control antibody). Methods of monitoring tumor cell growth/proliferation, tumor volume, and/or tumor inhibition are known in the art.

[0205] In some embodiments, the activatable binding polypeptides have therapeutic effect on a cancer. In some embodiments, the activatable binding polypeptides reduce one or more signs or symptoms of a cancer. In some embodiments, a subject suffering from a cancer goes into partial or complete remission when administered the activatable binding polypeptides.

[0206] In some embodiments, the present disclosure provides isolated activatable binding polypeptides that, when in active form, compete or cross-compete for binding to human CD137 with an antibody comprising: a) an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 65; an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 66; and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 67; and/or b) an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 68; an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 69; and an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 70. In some embodiments, the present disclosure provides isolated activatable binding polypeptides that, when in active form, compete or cross-compete for binding to human CD137 with an antibody comprising: a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 49; and/or b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 50. The ability of an activatable binding polypeptide to compete or cross-compete for binding with an antibody can be determined using standard binding assays known in the art, such as BIAcore analysis, ELISA assays, or flow cytometry. For example, one can allow an antibody (*e.g.,* as described above) to bind to human CD137 under saturating conditions and then measure the ability of the test activatable binding polypeptide (when in active form) to bind to the CD137. If the test activatable binding polypeptide is able to bind to the CD137 at the same time as the antibody, then the test activatable binding polypeptide binds to a different epitope then the antibody. However, if the test activatable binding polypeptide is not able to bind to the CD137 at the same time, then the test activatable binding polypeptide binds to the same epitope, an overlapping epitope, or an epitope that is in close proximity to the epitope bound by the antibody. This experiment can be performed using various methods, such as ELISA, RIA, FACS or surface plasmon resonance.

[0207] In some embodiments, the activatable binding polypeptides (when in inactive form) do not inhibit the binding between CD137 and its ligand (*e.g.,* human CD137 and human CD137L). In some embodiments, the activatable binding polypeptides (when in active form) inhibit the binding between CD137 and its ligand (*e.g.,* human CD137 and human CD137L). In some embodiments, the activatable binding polypeptides inhibit the binding between CD137 and its ligand *in vitro*. In some embodiments, the activatable binding polypeptide (when in active form) has a half maximal inhibitory concentration (IC_{50}) of about 500 nM or less (*e.g.,* about 500

nM or less, about 400nM or less, about 300nM or less, about 200nM or less, about 100nM or less, about 50nM or less, about 25nM or less, about 10nM or less, about 1nM or less, etc.) for inhibiting binding of CD137 to its ligand. In some embodiments, the activatable binding polypeptide has a half maximal inhibitory concentration (IC_{50}) of about 100 nM or less for inhibiting binding of CD137 to its ligand. In some embodiments, the activatable binding polypeptide completely inhibits binding of human CD137 to its ligand when provided at a concentration of about 100 nM or greater (*e.g.,* about 100nM or greater, about 500nM or greater, about 1μM or greater, about 10μM or greater, *etc.*). Methods of measuring the ability of a polypeptide to inhibit binding of a first protein (*e.g.,* CD137) and a second protein (*e.g.,* CD137L) are known in the art, including, without limitation, via BIAcore analysis, ELISA assays, and flow cytometry.

Antibodies

[0208] In some embodiments, the present disclosure relates to an activatable binding polypeptide comprising an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody described above). The antibodies described herein (*e.g.,* a CTLA4 or CD137 antibody) may be in any class, such as IgG, IgM, IgE, IgA, or IgD. In some embodiments, the antibodies described herein (*e.g.,* a CTLA4 or CD137 antibody) are in the IgG class, such as IgG1, IgG2, IgG3, or IgG4 subclass. An antibody described herein (*e.g.,* a CTLA4 or CD137 antibody) antibody can be converted from one class or subclass to another class or subclass using methods known in the art. An exemplary method for producing an antibody in a desired class or subclass comprises the steps of isolating a nucleic acid encoding a heavy chain of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody) and a nucleic acid encoding a light chain of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody), isolating the sequence encoding the V_H region, ligating the V_H sequence to a sequence encoding a heavy chain constant region of the desired class or subclass, expressing the light chain gene and the heavy chain construct in a cell, and collecting the antibody.

Antigen binding fragments

[0209] In some embodiments, the present disclosure relates to an activatable binding polypeptide comprising an antigen-binding fragment (*e.g.*, an antigen binding fragment of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody)).

[0210] The antigen-binding fragment may comprise any sequences of any of the antibodies described herein. In some embodiments, the antigen-binding fragment comprises the amino acid sequence of: (1) a light chain of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody); (2) a heavy chain of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody); (3) a variable region from the light chain of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody); (4) a variable region from the heavy chain of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody); (5) one or more HVRs (*e.g.*, one, two, three, four, five, or six HVRs) of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody); or (6) three HVRs from the light chain and three HVRs from the heavy chain of an antibody described herein (*e.g.*, a CTLA4 or CD137 antibody).

[0211] In some embodiments, the present disclosure provides an antigen-binding fragment of an antibody comprising a heavy chain variable region comprising: an HVR-H1 comprising the amino acid sequence YSISSGYHWSWI (SEQ ID NO: 59), an HVR-H2 comprising the amino acid sequence LARIDWDDDKYYSTSLKSRL (SEQ ID NO: 60), and an HVR-H3 comprising the amino acid sequence ARSYVYFDY (SEQ ID NO: 61); and/or a light chain variable region comprising: an HVR-L1 comprising the amino acid sequence RASQSVRGRFLA (SEQ ID NO: 62), an HVR-L2 comprising the amino acid sequence DASNRATGI (SEQ ID NO: 63), and an HVR-L3 comprising the amino acid sequence YCQQSSSWPPT (SEQ ID NO: 64). In some embodiments, the present disclosure provides an antigen-binding fragment of an antibody comprising: a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 47; and/or b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 48.

[0212] In some embodiments, the present disclosure provides an antigen-binding fragment of an antibody comprising a heavy chain variable region comprising: an HVR-H1 comprising the amino acid sequence FSLSTGGVGVGWI (SEQ ID NO: 65), an HVR-H2 comprising the amino acid sequence LALIDWADDKYYSPSLKSRL (SEQ ID NO: 66), and an HVR-H3 comprising

the amino acid sequence ARGGSDTVIGDWFAY (SEQ ID NO: 67); and/or a light chain variable region comprising: an HVR-L1 comprising the amino acid sequence RASQSIGSYLA (SEQ ID NO: 68), an HVR-L2 comprising the amino acid sequence DASNLETGV (SEQ ID NO: 69), and an HVR-L3 comprising the amino acid sequence YCQQGYYLWT (SEQ ID NO: 70). In some embodiments, the present disclosure provides an antigen-binding fragment of an antibody comprising: a) a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 49; and/or b) a light chain variable region comprising the amino acid sequence of SEQ ID NO: 50.

[0213] In some embodiments, the antigen-binding fragments of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody) include: (i) a Fab fragment, which is a monovalent fragment consisting of the V_L, V_H, C_L and C_H1 domains; (ii) a $F(ab')_2$ fragment, which is a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and C_H1 domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody; (v) a dAb fragment (Ward *et al.*, (1989) Nature 341:544-546), which consists of a V_H domain; (vi) an isolated CDR, and (vii) single chain antibody (scFv), which is a polypeptide comprising a V_L region of an antibody linked to a V_H region of an antibody (*see e.g.,* Bird *et al.* (1988) Science 242:423-426; Huston *et al.* (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883).

Antibody derivatives

[0214] In some embodiments, the present disclosure provides an activatable binding polypeptide comprising a derivative of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody).

[0215] In some embodiments, the antibody derivative is derived from modifications of the amino acid sequences of the parent antibody while conserving the overall molecular structure of the parent antibody amino acid sequence. Amino acid sequences of any regions of the parent antibody chains may be modified, such as framework regions, HVR regions, or constant regions. Types of modifications include substitutions, insertions, deletions, or combinations thereof, of one or more amino acids of the parent antibody.

[0216] In some embodiments, the antibody derivative comprises a V_L or V_H region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence as set forth in any of SEQ ID NOS: 47-50. In some embodiments, the antibody derivative comprises an HVR-H1 amino acid sequence region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOS: 59 or 65. In some embodiments, the antibody derivative comprises an HVR-H2 amino acid sequence region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOS: 60 or 66. In some embodiments, the antibody derivative comprises an HVR-H3 amino acid sequence region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOS: 61 or 67. In some embodiments, the antibody derivative comprises an HVR-L1 amino acid sequence region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOS: 62 or 68. In some embodiments, the antibody derivative comprises an HVR-L2 amino acid sequence region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOS: 63 or 69. In some embodiments, the antibody derivative comprises an HVR-L3 amino acid sequence region that is at least 65%, at least 75%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to an amino acid sequence as set forth in any of SEQ ID NOS: 64 or 70.

[0217] In some particular embodiments, the derivative comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 conservative or non-conservative substitutions, and/or 1, 2, 3, 4, 5, 6, 7, 8, 9,

10, 11, 12, 13, 14, or 15 additions and/or deletions to an amino acid sequence of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody).

[0218] Amino acid substitutions encompass both conservative substitutions and non-conservative substitutions. The term "conservative amino acid substitution" means a replacement of one amino acid with another amino acid where the two amino acids have similarity in certain physico-chemical properties such as polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, substitutions typically may be made within each of the following groups: (a) nonpolar (hydrophobic) amino acids, such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids, such as glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids, such as arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids, such as aspartic acid and glutamic acid.

[0219] The modifications may be made in any positions of the amino acid sequences of the antibody, including the HVRs, framework regions, or constant regions. In one embodiment, the present disclosure provides an antibody derivative that contains the V_H and V_L HVR sequences of an illustrative antibody described herein (*e.g.,* a CTLA4 or CD137 antibody), yet contains framework sequences different from those of the illustrative antibody. Such framework sequences can be obtained from public DNA databases or published references that include germline antibody gene sequences. For example, germline DNA sequences for human heavy and light chain variable region genes can be found in the Genbank database or in the "VBase" human germline sequence database (Kabat *et al.,* Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242 (1991); Tomlinson *et al.*, *J. Mol. Biol.* 227:776-798 (1992); and Cox *et al.*, *Eur. J. Immunol.* 24:827-836 (1994)). Framework sequences that may be used in constructing an antibody derivative include those that are structurally similar to the framework sequences used by illustrative antibodies of the disclosure For example, the HVR-H1, HVR-H2, and HVR-H3 sequences, and the HVR-L1, HVR-L2, and HVR-L3 sequences of an illustrative antibody can be grafted onto framework regions that have the identical sequence as that found in the germline immunoglobulin gene from which the framework sequence derive, or the HVR sequences can be grafted onto framework regions that contain one or more mutations as compared to the germline sequences.

[0220] In some embodiments, the antibody derivative is a chimeric antibody which comprises an amino acid sequence of an illustrative antibody described herein (*e.g.,* a CTLA4 or CD137 antibody). In one example, one or more HVRs from one or more illustrative antibodies are combined with HVRs from an antibody from a non-human animal, such as mouse or rat. In another example, all of the HVRs of the chimeric antibody are derived from one or more illustrative antibodies. In some particular embodiments, the chimeric antibody comprises one, two, or three HVRs from the heavy chain variable region and/or one, two, or three HVRs from the light chain variable region of an illustrative antibody. Chimeric antibodies can be generated using conventional methods known in the art.

[0221] Another type of modification is to mutate amino acid residues within the HVR regions of the V_H and/or V_L chain. Site-directed mutagenesis or PCR-mediated mutagenesis can be performed to introduce the mutation(s) and the effect on antibody binding, or other functional property of interest, can be evaluated in *in vitro* or *in vivo* assays known in the art. Typically, conservative substitutions are introduced. The mutations may be amino acid additions and/or deletions. Moreover, typically no more than one, two, three, four or five residues within an HVR region are altered. In some embodiments, the antibody derivative comprises 1, 2, 3, or 4 amino acid substitutions in the heavy chain HVRs and/or in the light chain HVRs. In another embodiment, the amino acid substitution is to change one or more cysteines in an antibody to another residue, such as, without limitation, alanine or serine. The cysteine may be a canonical or non-canonical cysteine. In one embodiment, the antibody derivative has 1, 2, 3, or 4 conservative amino acid substitutions in the heavy chain HVR regions relative to the amino acid sequences of an illustrative antibody.

[0222] Modifications may also be made to the framework residues within the V_H and/or V_L regions. Typically, such framework variants are made to decrease the immunogenicity of the antibody. One approach is to "back mutate" one or more framework residues to the corresponding germline sequence. An antibody that has undergone somatic mutation may contain framework residues that differ from the germline sequence from which the antibody is derived. Such residues can be identified by comparing the antibody framework sequences to the germline sequences from which the antibody is derived. To return the framework region

sequences to their germline configuration, the somatic mutations can be "back mutated" to the germline sequence by, for example, site-directed mutagenesis or PCR-mediated mutagenesis.

[0223] In addition, modifications may also be made within the Fc region of an illustrative antibody, typically to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding, and/or antigen-dependent cellular cytotoxicity. In one example, the hinge region of CH1 is modified such that the number of cysteine residues in the hinge region is altered, *e.g.,* increased or decreased. This approach is described further in U.S. Pat. No. 5,677,425. The number of cysteine residues in the hinge region of CH1 is altered to, for example, facilitate assembly of the light and heavy chains or to increase or decrease the stability of the antibody. In another case, the Fc hinge region of an antibody is mutated to decrease the biological half-life of the antibody.

[0224] Furthermore, an antibody of the present disclosure may be modified to alter its potential glycosylation site or pattern in accordance with routine experimentation known in the art. In another aspect, the present disclosure provides a derivative of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody) that contains at least one mutation in a variable region of a light chain or heavy chain that changes the pattern of glycosylation in the variable region. Such an antibody derivative may have an increased affinity and/or a modified specificity for binding an antigen. The mutations may add a novel glycosylation site in the V region, change the location of one or more V region glycosylation site(s), or remove a pre-existing V region glycosylation site. In one embodiment, the present disclosure provides a derivative of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody) having a potential N-linked glycosylation site at asparagine in the heavy chain variable region, wherein the potential N-linked glycosylation site in one heavy chain variable region is removed. In another embodiment, the present disclosure provides a derivative of an antibody described herein (*e.g.,* a CTLA4 or CD137 antibody) having a potential N-linked glycosylation site at asparagine in the heavy chain variable region, wherein the potential N-linked glycosylation site in both heavy chain variable regions is removed. Method of altering the glycosylation pattern of an antibody is known in the art, such as those described in U.S. Pat. No. 6,933,368, the disclosure of which incorporated herein by reference.

[0225] Examples of other antibody derivatives provided by the present disclosure include single chain antibodies, diabodies, domain antibodies, nanobodies, and unibodies. A "single-chain antibody" (scFv) consists of a single polypeptide chain comprising a V_L domain linked to a V_H domain wherein V_L domain and V_H domain are paired to form a monovalent molecule. Single chain antibody can be prepared according to method known in the art (*see e.g.,* Bird *et al.*, (1988) Science 242:423-426 and Huston *et al.*, (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). A "diabody" consists of two chains, each chain comprising a heavy chain variable region connected to a light chain variable region on the same polypeptide chain connected by a short peptide linker, wherein the two regions on the same chain do not pair with each other but with complementary domains on the other chain to form a bispecific molecule. Methods of preparing diabodies are known in the art (*see e.g.,* Holliger P. *et al.*, (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448, and Poljak R. J. *et al.*, (1994) Structure 2:1121-1123). Domain antibodies (dAbs) are small functional binding units of antibodies, corresponding to the variable regions of either the heavy or light chains of antibodies. Domain antibodies are well expressed in bacterial, yeast, and mammalian cell systems. Further details of domain antibodies and methods of production thereof are known in the art (*see e.g.,* U.S. Pat. Nos. 6,291,158; 6,582,915; 6,593,081; 6,172,197; 6,696,245; European Patents 0368684 & 0616640; WO05/035572, WO04/101790, WO04/081026, WO04/058821, WO04/003019 and WO03/002609). Nanobodies are derived from the heavy chains of an antibody. A nanobody typically comprises a single variable domain and two constant domains (CH2 and CH3) and retains antigen-binding capacity of the original antibody. Nanobodies can be prepared by methods known in the art (*see e.g.,* U.S. Pat. No. 6,765,087, U.S. Pat. No. 6,838,254, WO 06/079372). Unibodies consist of one light chain and one heavy chain of an IgG4 antibody. Unibodies may be made by the removal of the hinge region of IgG4 antibodies. Further details of unibodies and methods of preparing them may be found in WO2007/059782.

VII. Compositions

[0226] In other aspects, the present disclosure provides a composition comprising one or more of the polypeptides (*e.g.,* activatable binding polypeptides) described herein. In some embodiments, the composition is a pharmaceutical composition comprising a polypeptide (*e.g.,*

an activatable binding polypeptide) and a pharmaceutically acceptable carrier. The compositions can be prepared by conventional methods known in the art.

[0227] The term "pharmaceutically acceptable carrier" refers to any inactive substance that is suitable for use in a formulation for the delivery of a polypeptide (*e.g.,* an activatable binding polypeptide). A carrier may be an anti-adherent, binder, coating, disintegrant, filler or diluent, preservative (such as antioxidant, antibacterial, or antifungal agent), sweetener, absorption delaying agent, wetting agent, emulsifying agent, buffer, and the like. Examples of suitable pharmaceutically acceptable carriers include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like) dextrose, vegetable oils (such as olive oil), saline, buffer, buffered saline, and isotonic agents such as sugars, polyalcohols, sorbitol, and sodium chloride.

[0228] The compositions may be in any suitable forms, such as liquid, semi-solid, and solid dosage forms. Examples of liquid dosage forms include solution (*e.g.,* injectable and infusible solutions), microemulsion, liposome, dispersion, or suspension. Examples of solid dosage forms include tablet, pill, capsule, microcapsule, and powder. A particular form of the composition suitable for delivering a polypeptide (*e.g.,* an activatable binding polypeptide) is a sterile liquid, such as a solution, suspension, or dispersion, for injection or infusion. Sterile solutions can be prepared by incorporating the polypeptide (*e.g.,* an activatable binding polypeptide) in the required amount in an appropriate carrier, followed by sterilization microfiltration. Dispersions may be prepared by incorporating the polypeptide (*e.g.,* an activatable binding polypeptide) into a sterile vehicle that contains a basic dispersion medium and other carriers. In the case of sterile powders for the preparation of sterile liquid, methods of preparation include vacuum drying and freeze-drying (lyophilization) to yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. The various dosage forms of the compositions can be prepared by conventional techniques known in the art.

[0229] The relative amount of a polypeptide (*e.g.,* an activatable binding polypeptide) included in the composition will vary depending upon a number of factors, such as the specific polypeptide and carriers used, dosage form, and desired release and pharmacodynamic characteristics. The amount of a polypeptide (*e.g.,* an activatable binding polypeptide) in a single

dosage form will generally be that amount which produces a therapeutic effect, but may also be a lesser amount. Generally, this amount will range from about 0.01 percent to about 99 percent, from about 0.1 percent to about 70 percent, or from about 1 percent to about 30 percent relative to the total weight of the dosage form.

[0230] In addition to the polypeptide (*e.g.,* an activatable binding polypeptide), one or more additional therapeutic agents may be included in the composition. Examples of additional therapeutic agents are described herein below. The suitable amount of the additional therapeutic agent to be included in the composition can be readily selected by a person skilled in the art, and will vary depending on a number of factors, such as the particular agent and carriers used, dosage form, and desired release and pharmacodynamic characteristics. The amount of the additional therapeutic agent included in a single dosage form will generally be that amount of the agent which produces a therapeutic effect, but may be a lesser amount as well.

[0231] Any of the polypeptides (*e.g.,* activatable binding polypeptides) and/or compositions (*e.g.,* pharmaceutical compositions) described herein may be used in the preparation of a medicament (*e.g.,* a medicament for use in treating or delaying progression of cancer in a subject in need thereof).

VIII. Use of the activatable binding polypeptides and pharmaceutical compositions

[0232] Polypeptides (*e.g.,* activatable binding polypeptides) and pharmaceutical compositions thereof provided by the present disclosure are useful for therapeutic, diagnostic, or other purposes, such as modulating an immune response, treating cancer, enhancing efficacy of other cancer therapy, enhancing vaccine efficacy, or treating autoimmune diseases. Thus, in other aspects, the present disclosure provides methods of using the polypeptides (*e.g.,* activatable binding polypeptides) or pharmaceutical compositions thereof. In one aspect, the present disclosure provides a method of treating a disorder in a mammal, which comprises administering to the mammal in need of treatment an effective amount of a polypeptide (*e.g.,* an activatable binding polypeptide) or composition thereof provided by the present disclosure. In some embodiments, the polypeptide is an activatable binding polypeptide that binds CTLA4 (*e.g.,* human CTLA4) or CD137 (*e.g.,* human CD137) when in active form. In some embodiments, the mammal is a human.

[0233] In some embodiments, the disorder is a cancer. A variety of cancers may be treated or prevented with a method, use, or medicament provided by the present disclosure. Examples of such cancers include lung cancers such as bronchogenic carcinoma (*e.g.,* squamous cell carcinoma, small cell carcinoma, large cell carcinoma, and adenocarcinoma), alveolar cell carcinoma, bronchial adenoma, chondromatous hamartoma (noncancerous), and sarcoma (cancerous); heart cancer such as myxoma, fibromas, and rhabdomyomas; bone cancers such as osteochondromas, condromas, chondroblastomas, chondromyxoid fibromas, osteoid osteomas, giant cell tumors, chondrosarcoma, multiple myeloma, osteosarcoma, fibrosarcomas, malignant fibrous histiocytomas, Ewing's tumor (Ewing's sarcoma), and reticulum cell sarcoma; brain cancer such as gliomas (*e.g.,* glioblastoma multiforme), anaplastic astrocytomas, astrocytomas, oligodendrogliomas, medulloblastomas, chordoma, Schwannomas, ependymomas, meningiomas, pituitary adenoma, pinealoma, osteomas, hemangioblastomas, craniopharyngiomas, chordomas, germinomas, teratomas, dermoid cysts, and angiomas; cancers in digestive system such as leiomyoma, epidermoid carcinoma, adenocarcinoma, leiomyosarcoma, stomach adenocarcinomas, intestinal lipomas, intestinal neurofibromas, intestinal fibromas, polyps in large intestine, and colorectal cancers; liver cancers such as hepatocellular adenomas, hemangioma, hepatocellular carcinoma, fibrolamellar carcinoma, cholangiocarcinoma, hepatoblastoma, and angiosarcoma; kidney cancers such as kidney adenocarcinoma, renal cell carcinoma, hypernephroma, and transitional cell carcinoma of the renal pelvis; bladder cancers; hematological cancers such as acute lymphocytic (lymphoblastic) leukemia, acute myeloid (myelocytic, myelogenous, myeloblastic, myelomonocytic) leukemia, chronic lymphocytic leukemia (*e.g.,* Sezary syndrome and hairy cell leukemia), chronic myelocytic (myeloid, myelogenous, granulocytic) leukemia, Hodgkin's lymphoma, non-Hodgkin's lymphoma, B cell lymphoma, mycosis fungoides, and myeloproliferative disorders (including myeloproliferative disorders such as polycythemia vera, myelofibrosis, thrombocythemia, and chronic myelocytic leukemia); skin cancers such as basal cell carcinoma, squamous cell carcinoma, melanoma, Kaposi's sarcoma, and Paget's disease; head and neck cancers; eye-related cancers such as retinoblastoma and intraoccular melanocarcinoma; male reproductive system cancers such as benign prostatic hyperplasia, prostate cancer, and testicular cancers (*e.g.,* seminoma, teratoma, embryonal carcinoma, and choriocarcinoma); breast cancer; female reproductive system cancers such as uterine cancer (endometrial carcinoma), cervical cancer (cervical carcinoma), cancer of

the ovaries (ovarian carcinoma), vulvar carcinoma, vaginal carcinoma, fallopian tube cancer, and hydatidiform mole; thyroid cancer (including papillary, follicular, anaplastic, or medullary cancer); pheochromocytomas (adrenal gland); noncancerous growths of the parathyroid glands; pancreatic cancers; and hematological cancers such as leukemias, myelomas, non-Hodgkin's lymphomas, and Hodgkin's lymphomas.

[0234] In another aspect, the present disclosure provides a method of enhancing an immune response in a mammal, which comprises administering to the mammal an effective amount of a polypeptide (*e.g.,* an activatable binding polypeptide) or composition thereof provided by the present disclosure. In some embodiments, the polypeptide is an activatable binding polypeptide that binds CTLA4 (*e.g.,* human CTLA4) or CD137 (*e.g.,* human CD137), and the mammal is a human. The term "enhancing immune response" or its grammatical variations, means stimulating, evoking, increasing, improving, or augmenting any response of a mammal's immune system. The immune response may be a cellular response (*i.e.* cell-mediated, such as cytotoxic T lymphocyte mediated) or a humoral response (*i.e.* antibody mediated), and may be a primary or secondary immune response. Examples of enhancement of immune response include activation of PBMCs and/or T cells (including increasing secretion of one or more cytokines such as IL-2 and/or IFNγ). The enhancement of immune response can be assessed using a number of *in vitro* or *in vivo* measurements known to those skilled in the art, including, but not limited to, cytotoxic T lymphocyte assays, release of cytokines, regression of tumors, survival of tumor bearing animals, antibody production, immune cell proliferation, expression of cell surface markers, and cytotoxicity. Typically, methods of the present disclosure enhance the immune response by a mammal when compared to the immune response by an untreated mammal or a mammal not treated using the recited methods.

[0235] In practicing the therapeutic methods, the polypeptides (*e.g.,* activatable binding polypeptides) may be administered alone as monotherapy, or administered in combination with one or more additional therapeutic agents or therapies. Thus, in another aspect, the present disclosure provides a combination therapy, which comprises a polypeptide (*e.g.,* an activatable binding polypeptide) in combination with one or more additional therapies or therapeutic agents for separate, sequential or simultaneous administration. The term "additional therapeutic agent" may refer to any therapeutic agent other than a polypeptide (*e.g.,* an activatable binding

polypeptide) provided by the disclosure. In one particular aspect, the present disclosure provides a combination therapy for treating cancer in a mammal, which comprises administering to the mammal an effective amount of a polypeptide (*e.g.,* an activatable binding polypeptide) provided herein in combination with one or more additional therapeutic agents. In a further embodiment, the mammal is a human.

[0236] A wide variety of cancer therapeutic agents may be used in combination with a polypeptide (*e.g.,* an activatable binding polypeptide) provided by the present disclosure. One of ordinary skill in the art will recognize the presence and development of other cancer therapies which can be used in combination with the methods and polypeptides of the present disclosure, and will not be restricted to those forms of therapy set forth herein. Examples of categories of additional therapeutic agents that may be used in the combination therapy for treating cancer include (1) chemotherapeutic agents, (2) immunotherapeutic agents, and (3) hormone therapeutic agents. In some embodiments, the additional therapeutic is a viral gene therapy, an immune checkpoint inhibitor, a target therapy, a radiation therapies, and/or a chemotherapeutic.

[0237] The term "chemotherapeutic agent" refers to a chemical or biological substance that can cause death of cancer cells, or interfere with growth, division, repair, and/or function of cancer cells. Examples of chemotherapeutic agents include those that are disclosed in WO 2006/129163, and US 20060153808, the disclosures of which are incorporated herein by reference. Examples of particular chemotherapeutic agents include: (1) alkylating agents, such as chlorambucil (LEUKERAN), mcyclophosphamide (CYTOXAN), ifosfamide (IFEX), mechlorethamine hydrochloride (MUSTARGEN), thiotepa (THIOPLEX), streptozotocin (ZANOSAR), carmustine (BICNU, GLIADEL WAFER), lomustine (CEENU), and dacarbazine (DTIC-DOME); (2) alkaloids or plant vinca alkaloids, including cytotoxic antibiotics, such as doxorubicin (ADRIAMYCIN), epirubicin (ELLENCE, PHARMORUBICIN), daunorubicin (CERUBIDINE, DAUNOXOME), nemorubicin, idarubicin (IDAMYCIN PFS, ZAVEDOS), mitoxantrone (DHAD, NOVANTRONE). dactinomycin (actinomycin D, COSMEGEN), plicamycin (MITHRACIN), mitomycin (MUTAMYCIN), and bleomycin (BLENOXANE), vinorelbine tartrate (NAVELBINE)), vinblastine (VELBAN), vincristine (ONCOVIN), and vindesine (ELDISINE); (3) antimetabolites, such as capecitabine (XELODA), cytarabine (CYTOSAR-U), fludarabine (FLUDARA), gemcitabine (GEMZAR), hydroxyurea (HYDRA),

methotrexate (FOLEX, MEXATE, TREXALL), nelarabine (ARRANON), trimetrexate (NEUTREXIN), and pemetrexed (ALIMTA); (4) Pyrimidine antagonists, such as 5-fluorouracil (5-FU); capecitabine (XELODA), raltitrexed (TOMUDEX), tegafur-uracil (UFTORAL), and gemcitabine (GEMZAR); (5) taxanes, such as docetaxel (TAXOTERE), paclitaxel (TAXOL); (6) platinum drugs, such as cisplatin (PLATINOL) and carboplatin (PARAPLATIN), and oxaliplatin (ELOXATIN); (7) topoisomerase inhibitors, such as irinotecan (CAMPTOSAR), topotecan (HYCAMTIN), etoposide (ETOPOPHOS, VEPESSID, TOPOSAR), and teniposide (VUMON); (8) epipodophyllotoxins (podophyllotoxin derivatives), such as etoposide (ETOPOPHOS, VEPESSID, TOPOSAR); (9) folic acid derivatives, such as leucovorin (WELLCOVORIN); (10) nitrosoureas, such as carmustine (BiCNU), lomustine (CeeNU); (11) inhibitors of receptor tyrosine kinase, including epidermal growth factor receptor (EGFR), vascular endothelial growth factor (VEGF), insulin receptor, insulin-like growth factor receptor (IGFR), hepatocyte growth factor receptor (HGFR), and platelet-derived growth factor receptor (PDGFR), such as gefitinib (IRESSA), erlotinib (TARCEVA), bortezomib (VELCADE), imatinib mesylate (GLEEVEC), genefitinib, lapatinib, sorafenib, thalidomide, sunitinib (SUTENT), axitinib, rituximab (RITUXAN, MABTHERA), trastuzumab (HERCEPTIN), cetuximab (ERBITUX), bevacizumab (AVASTIN), and ranibizumab (LUCENTIS), lym-1 (ONCOLYM), antibodies to insulin-like growth factor-1 receptor (IGF-1R) that are disclosed in WO2002/053596); (12) angiogenesis inhibitors, such as bevacizumab (AVASTIN), suramin (GERMANIN), angiostatin, SU5416, thalidomide, and matrix metalloproteinase inhibitors (such as batimastat and marimastat), and those that are disclosed in WO2002055106; and (13) proteasome inhibitors, such as bortezomib (VELCADE).

[0238] The term "immunotherapeutic agents" refers to a chemical or biological substance that can enhance an immune response of a mammal. Examples of immunotherapeutic agents include: *bacillus* Calmette-Guerin (BCG); cytokines such as interferons; vaccines such as MyVax personalized immunotherapy, Onyvax-P, Oncophage, GRNVAC1, Favld, Provenge, GVAX, Lovaxin C, BiovaxID, GMXX, and NeuVax; and antibodies such as alemtuzumab (CAMPATH), bevacizumab (AVASTIN), cetuximab (ERBITUX), gemtuzunab ozogamicin (MYLOTARG), ibritumomab tiuxetan (ZEVALIN), panitumumab (VECTIBIX), rituximab (RITUXAN, MABTHERA), trastuzumab (HERCEPTIN), tositumomab (BEXXAR), ipilimumab

(YERVOY) tremelimumab, CAT-3888, agonist antibodies to OX40 receptor (such as those disclosed in WO2009/079335), agonist antibodies to CD40 receptor (such as those disclosed in WO2003/040170, and TLR-9 agonists (such as those disclosed in WO2003/015711, WO2004/016805, and WO2009/022215).

[0239] The term "hormone therapeutic agent" refers to a chemical or biological substance that inhibits or eliminates the production of a hormone, or inhibits or counteracts the effect of a hormone on the growth and/or survival of cancerous cells. Examples of such agents suitable for the methods herein include those that are disclosed in US20070117809. Examples of particular hormone therapeutic agents include tamoxifen (NOLVADEX), toremifene (Fareston), fulvestrant (FASLODEX), anastrozole (ARIMIDEX), exemestane (AROMASIN), letrozole (FEMARA), megestrol acetate (MEGACE), goserelin (ZOLADEX), and leuprolide (LUPRON). The binding molecules of this disclosure may also be used in combination with non-drug hormone therapies such as (1) surgical methods that remove all or part of the organs or glands which participate in the production of the hormone, such as the ovaries, the testicles, the adrenal gland, and the pituitary gland, and (2) radiation treatment, in which the organs or glands of the patient are subjected to radiation in an amount sufficient to inhibit or eliminate the production of the targeted hormone.

[0240] In some embodiments, the additional therapeutic agent is one or more of pomalyst, revlimid, lenalidomide, pomalidomide, thalidomide, a DNA-alkylating platinum-containing derivative, cisplatin, 5-fluorouracil, cyclophosphamide, an anti-CD137 antibody, an anti-CTLA4 antibody, an anti-PD-1 antibody, an anti-PD-L1 antibody, an anti-CD20 antibody, an anti-CD40 antibody, an anti-DR5 antibody, an anti-CD1d antibody, an anti-TIM3 antibody, an anti-SLAMF7 antibody, an anti-KIR receptor antibody, an anti-OX40 antibody, an anti-HER2 antibody, an anti-ErbB-2 antibody, an anti-EGFR antibody, cetuximab, rituximab, trastuzumab, pembrolizumab, radiotherapy, single dose radiation, fractionated radiation, focal radiation, whole organ radiation, IL-12, IFNα, GM-CSF, a chimeric antigen receptor, adoptively transferred T cells, an anti-cancer vaccine, and an oncolytic virus.

[0241] The combination therapy for treating cancer also encompasses the combination of a binding molecule with surgery to remove a tumor. The binding molecule may be administered to the mammal before, during, or after the surgery.

[0242] The combination therapy for treating cancer also encompasses combinations of a polypeptide (*e.g.,* an activatable binding polypeptide) with radiation therapy, such as ionizing (electromagnetic) radiotherapy (*e.g.,* X-rays or gamma rays) and particle beam radiation therapy (*e.g.,* high linear energy radiation). The source of radiation can be external or internal to the mammal. The polypeptide may be administered to the mammal before, during, or after the radiation therapy.

[0243] The polypeptides (*e.g.,* activatable binding polypeptides) and compositions thereof provided by the present disclosure can be administered via any suitable enteral route or parenteral route of administration. The term "enteral route" of administration refers to the administration via any part of the gastrointestinal tract. Examples of enteral routes include oral, mucosal, buccal, and rectal route, or intragastric route. "Parenteral route" of administration refers to a route of administration other than enteral route. Examples of parenteral routes of administration include intravenous, intramuscular, intradermal, intraperitoneal, intratumor, intravesical, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, transtracheal, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal, subcutaneous, or topical administration. The polypeptides (*e.g.,* activatable binding polypeptides) and compositions of the present disclosure can be administered using any suitable method, such as by oral ingestion, nasogastric tube, gastrostomy tube, injection, infusion, implantable infusion pump, and osmotic pump. The suitable route and method of administration may vary depending on a number of factors such as the specific polypeptide being used, the rate of absorption desired, specific formulation or dosage form used, type or severity of the disorder being treated, the specific site of action, and conditions of the patient, and can be readily selected by a person skilled in the art.

[0244] The term "effective amount" of a binding molecule may refer to an amount that is effective for an intended therapeutic purpose. For example, in the context of enhancing an immune response, an "effective amount" may be any amount that is effective in stimulating,

evoking, increasing, improving, or augmenting any response of a mammal's immune system. In the context of treating a disease, an "effective amount" may be any amount that is sufficient to cause any desirable or beneficial effect in the mammal being treated. Specifically, in the treatment of cancer, examples of desirable or beneficial effects include inhibition of further growth or spread of cancer cells, death of cancer cells, inhibition of reoccurrence of cancer, reduction of pain associated with the cancer, or improved survival of the mammal. The effective amount of a polypeptide (*e.g.,* an activatable binding polypeptide) described herein may range from about 0.001 to about 500 mg/kg, or about 0.01 to about 100 mg/kg, of the body weight of the mammal. For example, the amount can be about 0.3 mg/kg, 1 mg/kg, 3 mg/kg, 5 mg/kg, 10 mg/kg, 50 mg/kg, or 100 mg/kg of body weight of the mammal. In some embodiments, the effective amount of a polypeptide (*e.g.,* an activatable binding polypeptide) of the present disclosure is in the range of about 0.01-30 mg/kg of body weight of the mammal. In some other embodiments, the effective amount of a polypeptide (*e.g.,* an activatable binding polypeptide) of the present disclosure is in the range of about 0.05-15 mg/kg of body weight of the mammal. The precise dosage level to be administered can be readily determined by a person skilled in the art and will depend on a number of factors, such as the type, and severity of the disorder to be treated, the particular polypeptide employed, the route of administration, the time of administration, the duration of the treatment, the particular additional therapy employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0245] A polypeptide (*e.g.,* an activatable binding polypeptide) or composition thereof may be administered on multiple occasions. Intervals between single doses can be, for example, daily, weekly, monthly, every three months or yearly. An exemplary treatment regimen entails administration once per week, once every two weeks, once every three weeks, once every four weeks, once a month, once every three months or once every three to six months. Dosage regimens for a polypeptide (*e.g.,* an activatable binding polypeptide) of the present disclosure may include 1 mg/kg body weight or 3 mg/kg body weight via intravenous administration, using one of the following dosing schedules: (i) every four weeks for six dosages, then every three months; (ii) every three weeks; (iii) 3 mg/kg body weight once followed by 1 mg/kg body weight every three weeks.

IX. Kits

[0246] In another aspect, provided herein is a kit comprising a library of polynucleotides of the present disclosure. In some embodiments, the kit further comprises a package insert comprising instructions for expressing, modifying, screening, or otherwise using the library, *e.g.*, to identify an activatable binding polypeptide of interest. In some embodiments, the kit further comprises one or more buffers, *e.g.*, for storing, transferring, transfecting, or otherwise using one or more of the polynucleotides (*e.g.*, synthetic polynucleotides). In some embodiments, the kit further comprises one or more containers for storing one or more of the polynucleotides. In some embodiments, the kit further comprises one or more vectors, *e.g.*, for transfection of a host cell with one or more of the polynucleotides.

[0247] In another aspect, provided herein is a kit comprising activatable binding polypeptides and/or compositions described herein. In some embodiments, the kit further comprises a package insert comprising instructions for use of the activatable binding polypeptides and/or compositions. In some embodiments, the kit further comprises one or more buffers, *e.g.*, for storing, transferring, administering, or otherwise using the activatable binding polypeptides and/or compositions. In some embodiments, the kit further comprises one or more containers for storing or administering (*e.g.*, syringes, *etc.*) the activatable binding polypeptides and/or compositions.

[0248] The foregoing written description is considered to be sufficient to enable one skilled in the art to practice the present disclosure. The following Examples are offered for illustrative purposes only, and are not intended to limit the scope of the present disclosure in any way. Indeed, various modifications of the present disclosure in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

EXAMPLES

Example 1: Methods of identifying self-blocking peptides for activatable binding polypeptides

[0249] As described above, there exists a need for improved methods and products useful for identifying self-blocking peptides for activatable binding polypeptides. Accordingly, described herein is a new system that has been designed and executed for efficient discovery of masking moieties with good developability. In this system, the target antibody fragments, either Fab (**FIG. 1**) or scFv (**FIG. 2**), were first displayed on the yeast surface, and were confirmed to be functional in binding to its antigen. Then the improved peptide libraries were directly fused to the N-terminus of the light chain, and a yeast library was constructed that displays the fusion protein on the yeast surface. The yeast library then underwent several rounds of FACS-based screening: first the yeast clones that have low binding to antigen were enriched, then the enriched yeast clones were treated with a protease to remove the N-terminal peptide, and the clones with high binding to antigen were selected (**FIGS. 1 and 2**). After 4-5 rounds of sorting, the plasmids were extracted from these clones and the masking peptide sequences were confirmed through DNA sequencing.

[0250] There are several unique features built into this new system that make it powerful in identifying masking peptides for target antibodies with good developability:

1) The peptide libraries were directly fused to the N-terminus of the target antibody fragments instead of any foreign scaffold proteins, and the masking peptides were discovered in the same context as the final product. This eliminated the contamination with false positive peptide sequences, and dramatically reduced the amount of work for their downstream characterizations.

2) A protease cleavage-mediated activation mechanism was integrated into the screening processes. This was to ensure that the discovered peptides not only masked antigen binding before activation, but no longer blocked antigen binding after protease cleavage. These were the prerequisites considered for qualifying as a good masking peptide for any activatable antibody.

3) Improved designs of peptide libraries were employed. In contrast to the random peptide libraries commonly used, a pair of cysteine residues was introduced into fixed positions in the peptide libraries, to ensure that the display peptides had constrained conformations. It was observed that constrained peptides tend to exhibit increased binding affinity and specificity (Uchiyama *et al.* (2005) 99(5):448-56). In contrast to the widely used NNK (or NNS) codons that encode all 20 residues, including the chemically labile residues such as M and W, NHC

codons were employed in part or all of the peptide libraries. The NHC codon encodes 12 amino acid residues (D, A, Y, S, T, N, I, L, F, V, H, and P), and does not include unfavorable residues for manufacturing processes, such as methionine, tryptophan, or cysteine. In addition, use of the NHC codon also dramatically reduced the theoretical peptide library size relative to an NNK (or NNS) codon, and therefore, enabled the construction of libraries with much better coverage. These libraries performed well when tested against different target antibodies.

Example 2: Design of constrained peptide libraries (CPLs)

[0251] Four exemplary constrained peptide libraries (CPLs) were designed (**Table 1**).

Table 1: Designed CPLs

CPL name:	**Amino Acid Sequence:**	**Nucleic Acid sequence:**
CPL010	EVGSY(Z6)C(Z6)C(Z2)SGRSA (SEQ ID NO: 4)	gaggttggatcctac(NHC)6tgt(NHC)6tgc(NHC)2tca ggtcgttccgct (SEQ ID NO: 8)
CPL011	EVGSY(Z6)C(X6)C(Z2)SGRSA (SEQ ID NO: 5)	gaggttggatcctac(NHC)6tgt(NNK)6tgc(NHC)2tca ggtcgttccgct (SEQ ID NO: 9)
CPL012	EVGSY(Z6)C(Z8)C(Z2)SGRSA (SEQ ID NO: 6)	gaggttggatcctac(NHC)6tgt(NHC)8tgc(NHC)2tca ggtcgttccgct (SEQ ID NO: 10)
CPL013	EVGSY(Z6)C(X8)C(Z2)SGRSA (SEQ ID NO: 7)	gaggttggatcctac(NHC)6tgt(NNK)8tgc(NHC)2tca ggtcgttccgct (SEQ ID NO: 11)

Each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y; each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P

[0252] At their cores were the sequences Z6CX6CZ2 (SEQ ID NO: 55) or Z6CX8CZ2 (SEQ ID NO: 56), and the two fixed cysteine residues formed a disulfide bond to constrain the peptide conformations. In the synthesized oligonucleotides, the degenerate codon NHC was adopted in all places except inside the loop, where an NNK codon was also employed in CPL011 and CPL013. In constrast to the NNK or NNS codon, NHC codon encodes 12 residues (Table 2), encompassing significant diversity, but lacking the chemically labile residues methionine, tryptophan, and cysteine. In addition, the reduced theoretical diversity compared with the NNK or NNS codon enabled the construction of libraries with better coverage.

Table 2: NHC codons

NHC:	AAC	ACC	ATC	TAC	TCC	TTC	GAC	GCC	GTC	CAC	CCC	CTC
Amino acid:	N	T	I	Y	S	F	D	A	V	H	P	L

[0253] Following these masking peptide sequences was an invariant cleavage peptide sequence (SGRSAGGGGSPLGLAGSGGS, SEQ ID NO: 12) containing two protease recognition sites: SGRSA (SEQ ID NO: 13) for the protease urokinase-type plasminogen activator (uPA), and PLGLAG (SEQ ID NO: 14) for the proteases matrix metalloproteinase-2 (MMP-2) and matrix metalloproteinase-9 (MMP-9). These recognition sites have been used by many group in *in vivo* tumor cell-specific activation of targeting agents (*see e.g.,* Ke *et al.* (1997) J Biol Chem 272(33):20456-62; Gerspach *et al.* (2006) Cancer Immunol Immunother 55(12):1590-600; and Jiang *et al.* (2004) Proc Natl Acad Sci USA 101(51):17867-72). During yeast-based screening, the MMP-9 recognition sequence was replaced with the Tobacco Etch Virus (TEV) protease recognition sequence (ENLYFQG, SEQ ID NO: 15) due to the availability and specificity of the TEV protease.

[0254] The CPLs and the invariant cleavage peptide were fused to the N-terminus of light chain of the target antibody, in the form of either scFv or Fab, that is connected to the yeast surface displayed Aga2 protein. The inclusion of the surrogate TEV protease recognition site was important in identifying the right type of masking peptide sequences, *i.e,* the antigen binding is blocked before protease cleavage, and antigen binding is enabled after protease cleavage. The exmples described below demonstrated that the cleavage-activation mechanism of activatable antibodies initially shown in yeast was replicated in full IgG molecules expressed in mamalian cells.

Example 3: Construction and validation of activatable antibodies targeting CTLA4

Display of the functional target antibody on the yeast surface

[0255] A low copy number, CEN/ARS-based vector was used to express the target antibody (antibody TY21580, targeting human CTLA4) under the control of the inducible GAL1-10 promoter in the yeast *S. cerevisiae*. The surface display of scFvs was achieved through the Aga2

protein fused at its C-terminus under the control of the GAL1 promoter, similar to previously published arrangements (Boder and Wittrup (1997) Nat Biotechnol 15(6):553-7). For Fabs, their surface display was achieved through the Aga2 protein fused to the N-terminus of the heavy chain (fusion of VH and CH1), under the control of the GAL1 promoter, while the light chain (fusion of VL and CL) was under the control of the GAL10 promoter. The Fabs were displayed on the yeast surface through its association with the membrane anchored heavy chain.

[0256] The surface display of the Fab or scFv was verified by staining with antibodies recognizing the fused affinity tag, and the functionality of the Fabs or scFvs displayed on yeast was examined using biotinylated human CTLA4. Briefly, 48 hours after induction in galactose medium, yeast cells (1x10^6) were harvested, washed once with PBSA buffer, and then incubated with 10 nM of biotinylated antigen for 1 hour at room temperature. The yeast cells were then washed twice with PBSA buffer, and incubated with PE conjugated streptavidin (1:500 dilution) (eBioscience #2-4317-87) for 30 minutes at 4°C. The yeast cells were then analyzed by flow cytometry. As shown in **FIGS. 3A-B**, both Fabs (**FIG. 3A**) and scFvs (**FIG. 3B**) targeting CTLA4 were successfully displayed on the yeast surface, and were both capable of binding strongly to their antigens.

Construction of yeast libraries containing CPLs

[0257] Synthesized oligonucleotides encoding the CPLs were fused with the oligonucleotides encoding the cleavage peptides through 5 cycles of PCR. The primers used (F-primer and R-primer) are listed in **Table 3**. The compositions of PCR reactions were: 1X PrimeSTAR buffer, 2.5 mM dNTP, 100 μM of F-primer and R-primer each, and 100 μM each of template 1 (CPL oligonucleotide) and template 2 (oligonucleotide encoding the cleavage peptide), and 2.5 U of PrimeSTAR HS DNA Polymerase. The PCR program used was: a) 1 cycle of 96°C for 5 minutes; 2) 5 cycles of 96°C (15 sec), 60°C (15 sec), 72°C (6 sec); and 3) 1 cycle of 72 °C for 3 minutes. Exonuclease I was used to digest the single- stranded DNA before purification of the PCR product through gel electrophoresis. The purified PCR product was then digested with BamHI and KpnI, and cloned into a bacterial filter vector digested with the same two restriction enzymes. In the filter vector, the CPL and the cleavage peptides were placed downstream of a bacterial secretion signal peptide, and upstream of a beta-lactamase lacking

signal sequence. The functional beta-lactamase, selected on ampicillin plates, indicated in-frame fusions of CPLs and the cleavage peptides, thereby eliminating any out-of-frame errors (N-1 or N-2) introduced into the synthesized degenerate oligonucleotides. In addition, some poorly folded sequences were also reduced from the pool. The ligation product was transformed into electro-competent bacterial cells, and the diversity of CPL libraries was generally between 5x10^9 and 1x10^10. Sequencing of individual clones indicated that very high in-frame rate (in many cases, almost 100%) were achieved through this approach.

Table 3: PCR primers

Primer name:	**Sequence:**	**SEQ ID NO:**
F-primer	Tcgggtgaggttggatcctac	51
R-primer	gtacaggttctcggtaccacc	52
PL0009_F	tggagacacagacaggatcactggagactgggtcagcaggatatcggatcctgaaccgcctgaac	53
BL1024_R	cttcgctgtttttcaatattttctgttattgcttcagttttagcaggatccgaggttggatcctac	54

[0258] To make yeast libraries containing CPLs, the plasmids were extracted from the bacterial libraries, and used as templates for PCR amplification of the DNA fragments encoding the CPLs and cleavage peptide. The primers used (PL0009_F and BL1024_R) are listed in T**able 3**. The amplified PCR fragments were purified through gel-electrophoresis, and together with a linearized plasmid that expressed the target antibody fused to Aga2, were transformed into electro-competent yeast cells. The homologous sequences on both ends of the PCR fragments and the plasmids ensured efficient homologous recombination inside yeast cells. The diversity of the constructed yeast libraries was generally between 1x10^9 to 2x10^9.

FACS-based screening of masking peptides against a CTLA4 antibody

[0259] A total of 1x10^8 yeast cells from a CPL yeast library were used to screen for masking peptides against the target antibody. For each round of sorting through MoFlo XDP, yeast cells induced in galactose medium were harvested, washed once with PBSA buffer, and then incubated with 10 nM (decreased to 1 nM in the later rounds) of biotinylated antigen for 1 hour at room temperature. The yeast cells were then washed twice with PBSA buffer, and incubated with PE conjugated streptavidin (1:500 dilution) (eBioscience #2-4317-87) for 30 minutes at 4°C. After two more washes with PBSA buffer, the yeast cells were adjusted to 2-3

OD/mL, and subject to sorting. As shown in **FIG. 4**, in round 1, 10 nM of biotinylated CTLA4-Fc was used, and the weak binders were enriched. The yeast cells from round 1, after growth in glucose medium, were induced in galactose medium and treated with AcTEV protease (6U/OD cell) (Thermo Fisher Scientific #12575015) for 2 hours at 30°C, and the strong binders were purified. Starting from the 3rd round of sorting, the concentration of the biotinylated CTLA4-Fc was reduced to 1 nM, and the weak binders were collected. At the 4th round, fractions of the yeast cells were also treated with AcTEV in parallel, to verify the protease cleavage mediated activation of the target antibody. As shown in **FIG. 4**, it was apparent that AcTEV cleavage resulted in a dramatic increase of the population of cells that bound strongly to antigen, suggesting that the screening strategy was effective. The single clones from the 5th round of sorting were plated on selective media, and grown individually for further confirmation of cleavage mediated activated antigen binding.

[0260] As shown in **FIGS. 5A-B**, the selected CTLA4 activatable antibody clones, either in scFv (**FIG. 5A**) or Fab (**FIG.5B**) format, exhibited little binding to antigen in the presence of masking peptide. However, binding to antigen was dramatically increased when the yeast cells were treated with TEV protease to remove the masking peptide. The incorporation of the TEV recognition site in the cleavage peptide, combined with the application of TEV protease to verify the selected clones, significantly increased the success rate of masking peptide selection.

[0261] To identify the masking peptide sequences, the shuttle plasmids were extracted from the selected yeast clones (Generay #GK2002-200), and transformed into competent *E.coli* cells. The plasmids were prepared, and the regions encoding the masking peptides were sequenced and aligned. As anticipated, these sequences could be separated into several groups, indicating clear enrichment through rounds of sorting. Four groups of masking peptide sequences, together with the invariant cleavage peptide sequences, are listed in **Table 4**.

Table 4: Masking peptide sequences

Sample ID:	**Peptide name:**	**Masking + cleavage peptide sequences:**
TY22401	B13189	EVGSYNFVADSCPDHPYPCSASGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 28)
TY22402	B13180	EVGSYIVHHSDCDAFYPYCDSSGRSAGGGGSPLGLAGSGGS

		(SEQ ID NO: 30)
TY22403	B13192	EVGSYYSAYPACDSHYPYCNSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 32)
TY22404	B13197	EVGSYPNPSSDCVPYYYACAYSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 34)

IgG conversion and expression

[0262] The four groups of masking peptides listed in **Table 4**, as well as additional four masking peptide sequences (**Table 5**) derived from two of them (B13192 and B13197) to eliminate a potential glycosylation site, were converted into IgG1s.

Table 5: additional masking peptide sequences

Sample ID:	**Masking + cleavage peptide sequences:**
TY22563	EVGSYYSAYPACDSHYPYCQSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 36)
TY22564	EVGSYYSAYPACDSHYPYCNSAGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 37)
TY22565	EVGSYPQPSSDCVPYYYACAYSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 38)
TY22566	EVGSYPNPASDCVPYYYACAYSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 39)

[0263] The heavy and light chains were cloned into the mammalian expression vector pCDNA3.3 (Thermo Fisher Scientific, cat# K830001) separately, and the masking peptides and the invariant cleavage peptide were fused to the N-terminus of the light chain in the same manner as displayed on yeast surface. The VH and VL sequences for the parental CTLA4 antibody (TY21580) are listed below (*See also* PCT International Application titled "Compositions Comprising Cross-reactive Anti-CTLA4 Antibodies, and Methods of Making and Using the Same" filed concurrently herewith under Attorney Docket No. 69540-2000540, incorporated herein by reference in its entirety):

Anti-CTLA4 heavy chain variable region (SEQ ID NO: 47):

EVQLVESGGGLVQPGGSLRLSCAASGYSISSGYHWSWIRQAPGKGLEWLARIDWDDDK
YYSTSLKSRLTISRDNSKNTLYLQLNSLRAEDTAVYYCARSYVYFDYWGQGTLVTVSS

Anti-CTLA4 light chain variable region (SEQ ID NO: 48):

DIQLTQSPSSLSASVGDRVTITCRASQSVRGRFLAWYQQKPGKAPKLLIYDASNRATGIPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQSSSWPPTFGQGTKVEIKR.

[0264] Pairs of plasmids were transiently transfected into HEK293F cells. After six days, the supernatants were harvested, cleared by centrifugation and filtration, and IgGs were purified with standard protein A affinity chromatography (MabSelect SuRe, GE Healthcare). The IgGs were eluted and neutralized, and buffer exchanged into PB buffer (20 mM sodium phosphate, 150 mM NaCl, pH 7.0). Protein concentrations were determined by UV-spectrophotometry, and IgG purity was analyzed under denaturing, reducing and non-reducing conditions by SDS-PAGE or SEC-HPLC. Importantly, the expression levels of the activatable antibodies in HEK293 cells were similar to their parental antibody, and their purification yields after protein A resin were also similar, suggesting that the presence of the masking and cleavage peptides do not have a negative impact on antibody expression in mammalian cells.

Measurement of masking efficiency

[0265] The ForteBio Octet RED96 system (Pall, USA) was used to quickly assess the efficiency of the masking peptides. Briefly, activatable antibodies (and their parent antibody, TY21580) were diluted to 30 μg/mL in KB buffer (PBS buffer supplemented with 0.02% Tween 20 and 0.1% BSA), and captured by anti-Human IgG Capture (AHC) Biosensors (Pall, USA) in parallel. The sensors were then allowed to associate with His-tagged CTLA4 protein (25 nM) for 300 seconds, and then dissociate in KB buffer for another 300 seconds. The association and dissociation curves were fitted to a 1:1 Langmuir binding model using ForteBio Data Analysis 7.1 (Pall, USA) according to the manufacturer's guidelines. As shown in **FIGS. 6A-B**, the responses achieved with the activatable antibodies were significantly lower than that for the parent antibody, suggesting that masking peptides effectively blocked the binding of the antibody to its antigen. Among the four activatable antibodies, however, TY22401 was less effective, consistent with the results from the ELISA assay discussed below.

[0266] Recombinant human CTLA4-Fc was diluted to 1 μg/mL in PBS and coated on a Maxisorp plate at 4°C overnight. Plates were blocked with PBS supplemented with 3% non-fat

milk at 37°C for 1 hour. After washing, 100 µL of 3-fold serial dilutions of antibodies were added to each well. After incubation at 37°C for 1 hour, plates were washed four times, and 100 µL HRP conjugated anti-human IgG (Fab specific) (1:6000 dilution) was added to each well. Plates were incubated at 37°C for 1 hour, washed four times, and then 50 µL TMB substrate solution was added to each well, and the plate was incubated at room temperature. Absorbance at 450 nm was measured after the reactions were stopped with 50 µL H_2SO_4 per well. The EC_{50} was evaluated by fitting the ELISA data using the asymmetrical sigmoidal (five-parameter logistic equation) model of GraphPad Prism 6 software. Experiments for activatable antibodies TY22401, TY22402, and TY22404 were performed twice, leading to two calculated masking efficiencies being obtained for each of these activatable antibodies. Masking efficiencies for each activatable antibody were calculated by dividing the EC_{50} for binding of the activatable antibody by the EC_{50} of the parental antibody (TY21580). As shown in **FIGS. 7A-C** and **Table 6**, compared with the parental antibody, all of the activatable antibodies showed dramatically reduced binding to its antigen, and the calculated masking efficiency ranged from 48 to 2213. Differences in masking efficiency likely resulted from variation in measurement and data fitting for the EC_{50} values, and the masking efficiency for each activatable antibody likely falls within the calculated ranges (*e.g.*, the masking efficiency for activatable antibody TY22402 is between 377 and 2213). These results indicated that multiple masking peptides identified from the CPLs maintained their masking efficiency when expressed in mammalian cells, and as part of a full IgG molecule.

Table 6: Activatable antibody ELISAs prior to protease cleavage

Sample ID:	LogEC$_{50}$:	EC$_{50}$			
		M:	nM:	R^2:	Masking efficiency:
Data Batch 1					
TY21580	-9.665	2.161E-10	0.216	0.999	1.0
TY22401	-7.623	2.382E-08	23.82	0.997	110
TY22402	-6.321	4.779E-07	477.9	0.997	2213
TY22404	-6.749	178.4E-07	178.4	0.998	826
Data Batch 2					
TY21580	-9.478	3.324E-10	0.3324	0.998	1.0
TY22401	-7.800	1.586E-08	15.86	0.994	48
TY22402	-6.902	1.254E-07	125.4	0.998	377
TY22404	-6.892	1.281E-07	128.1	0.998	385

TY21580	-9.48	3.3E-10	0.33		1.0
TY22563	-7.32	4.771E-08	47.71		143.5
TY22564	-7.41	3.898E-08	38.98		117.3
TY22565	-6.68	2.099E-07	209.9		631.5
TY22566	-6.79	1.6264E-07	162.6		489.2

Removal of the masking peptide restores antibody activity

[0267] The purified activatable antibodies were treated with the proteases which recognize the cleavage sequences, and were then tested to determine whether removal of the masking peptide restored their activity. As an example, 20 μg of TY22404 (0.5 mg/mL) was treated with 1 μg of recombinant human uPA (Acrobiosystems, # PLU-H5229) in reaction buffer (50 mM Tris-HCl, 0.01% Tween 20, pH 8.5); or TY22404 was treated with 5 or 10 units of recombinant human MMP-9 (BioVision, # 7867-500) in reaction buffer (50 mM Tris, 150 mM NaCl, 5 mM $CaCl_2$, 20 μM $ZnCl_2$, pH 7.5). The reactions were carried out at 37°C for 21 hours. The masking peptides were confirmed to be removed from the light chain by SDS-PAGE analysis **FIG. 8A**. The masking efficiency was then measured by ELISA as described above. As shown in **FIG. 8B and Table 7**, after removal of masking peptide, the activatable antibody became indistinguishable from the parent antibody in its binding to the antigen.

Table 7: Activatable antibody ELISAs after protease cleavage

Sample ID:	**LogEC_{50}:**	**EC_{50}**	
		nM:	**Masking efficiency:**
TY21580	-9.35	0.447	1.0
TY22404	-7.01	96.8	216
TY22404-uPA	-9.40	0.402	0.9
TY22404-MMP-9	-9.39	0.412	0.9

Activatable antibody developability profiles

[0268] For manufacturing purpose, it is critical that the discovered activatable antibodies have a good developability profile. Several different tests were performed with purified activatable antibodies that were expressed in mammalian cells. The activatable antibodies were adjusted to 1 mg/mL in 20 mM Histidine, pH 5.5, and antibody quality analysis was performed

using analytical size-exclusion chromatography using a Waters 2695 with a Waters 2996 UV detector and aTSKgel g3000 SWXL column (300 mm × 7.8 mm) (Tosoh Bioscience). For each assay, 10 μg of antibody was injected, and fractionation was performed at a flow rate of 0.5 mL/min in buffer (200 mM sodium phosphate at pH 7.0).

[0269] Three accelerated stress tests were conducted: incubation of the activatable antibodies at 50°C for 7 days, incubation of the activatable antibodies at 40°C for 28 days, and six cycles of freeze-thaw. The freeze-thaw tests were conducted by freezing 100 μL sample (1 mg/mL in 20 mM histidine, pH 5.5) at -80°C for 30 minutes, followed by thawing at room temperature for 60 min. As shown in **FIGS. 9A-C**, all activatable antibodies remained stable, and exhibited little aggregation after storage at 50°C for 7 days or 40°C for 28 days. After six cycles of freeze-thaw, they showed slight deterioration; however, the main monomer peak remained around 95%, indicating that these activatable antibodies were very stable under these accelerated stress tests. Without wishing to be bound by theory, it is worth noting that the activatable antibodies had not yet gone through an extensive buffer optimization process, and therefore, the stability of the activatable antibodies may be further improved with optimized buffer and excipient.

[0270] Next, activatable antibodies were concentrated to more than 150 mg/mL in 20 mM histidine, pH 5.5 (**Table 8**). No activatable antibody precipitation was observed, and viscosity of the samples was quite manageable. The concentrated activatable antibodies were then diluted to either 20 mg/mL or 1 mg/mL for analysis of high molecular weight (HMW) species. As shown in **FIG. 10 and Table 8**, no apparent increase of the HMW species was observed, suggesting that these activatable antibodies were very soluble and stable in the buffer tested, up to high concentrations.

Table 8: Concentration of activatable antibodies >150 mg/mL

Sample ID:	Starting conc. (mg/mL):	High conc. (mg/mL):
TY22401	10.9	187.2
TY22402	8.4	160.0

[0271] To study the stability of the activatable antibodies at low pH, the purified activatable antibodies (at 10 mg/mL in 20 mM histidine, pH 5.5) were titrated to 1 mg/mL with citric acid, and the pH was adjusted to 3.7 and held at room temperature for 30 and 60 minutes. Afterwards,

the samples were neutralized to pH 7.0 with 1 M Tris-base. The masking efficiency of the activatable antibodies was measured with ForteBio, as described above. As shown in **FIG. 11**, masking efficiency remained unchanged after low pH incubation for 30 or 60 minutes, suggesting that the masking peptides retained their blocking efficacy after low pH incubation.

[0272] Taken together, the data indicates that the discovered activatable antibodies remained stable under various stress conditions,and therefore, they have good developability profile.

Example 4: *In vitro* and *in vivo* characterization of activatable antibodies targeting CTLA4

[0273] It was previously shown that the parental antibody TY21580 alone does not stimulate human T cell activation or the activation of human PBMC cells (*See* PCT International Application titled "Compositions Comprising Cross-reactive Anti-CTLA4 Antibodies, and Methods of Making and Using the Same" filed concurrently herewith under Attorney Docket No. 69540-2000540, incorporated herein by reference in its entirety). It is known that CTLA-4 activity on T cells is related to the first (TCR/CD3) and second signals involving B7-CD28/CTLA-4. Consistently, it was shown that, with low concentrations of anti-CD3, the parental antibody TY21580 significantly enhanced human PBMC cell activation.

In vitro functional characterization

[0274] Here the activities of the activatable antibodies targeting CTLA4 were evaluated in the presence of a low concentration of anti-CD3 antibody on human PMBC activation. Human PBMCs were freshly isolated from the blood of a healthy donor (#44) by density gradient centrifugation using Histopaque-1077 (Sigma). Anti-CD3 (OKT-3) antibody was coated on a 96 well plate overnight at 4°C. After washing, 1x10^5 freshly isolated human PBMCs were added to each well, followed by the addition of the test articles at different concentrations. Induction of IL-2 was measured 48 hours after stimulation using a Human IL-2 ELISA Ready-SET-Go (Invitrogen) kit. IFN-γ in the supernatant was measured using a Human IFN-γ ELISA Ready-SET-Go (Invitrogen) kit. As demonstrated in **FIGS. 12A-B**, at high concentrations, TY22404 induced IL-2 production, and TY22401 induced IFN-γ production. Nevertheless, the activities of the activatable antibodies were significantly lower than that of the parental TY21580 antibody.

[0275] Next, the antibody-dependent cell cytotoxicity activities of the activatable antibodies were tested and compared with that of the parental antibody TY21580. An ADCC reporter gene assay was used to evaluate the ADCC activities of the activatable antibodies. HEK293F cells overexpressing human CTLA4 (HEK293F/hCTLA-4 cells) were used as target cells; a Jurkat cell line overexpressing CD16a and NFAT-Luc (Jurkat/CD16a cells) was used as effector cells. 1x10^5 Jurkat/CD16a cells and 1x10^4 HEK293F/hCTLA-4 cells (E:T ratio 10:1) were mixed with different concentrations of antibody. After incubation for 6 hours, 100 µL of One-Glo reagent was added to the cells, and the cells were lysed for 10 min. Supernatants were removed for luminescence measurements using a SpectraMax i3x plate reader. As shown in **FIG. 13**, the activatable antibodies showed several log lower ADCC activities than the parental antibody TY21580. The ADCC activity of TY22401 was higher than that of TY22402 and TY22404. Taken together, the *in vitro* data indicates that the better masked activatable antibodies had less ADCC activity.

[0276] The anti-tumor activities of the activatable antibodies were next evaluated and compared with the anti-tumor activity of the parental antibody TY21580 in multiple syngeneic mouse tumor models, including an MC38 colorectal tumor model, a CT26 colorectal tumor models, an H22 liver tumor model, and a 3LL lung tumor model.

Anti-tumor efficacy in an MC38 colorectal tumor model

[0277] C57BL/6 mice (n=8 per group, female, 6-8 weeks old) were inoculated subcutaneously with MC38 (NTCC-MC38) murine colon cancer cells. When tumors were established (70 mm3), treatment began with isotype control antibody, parental antibody TY21580, or one of three activatable antibodies by intraperitoneal injection, twice a week. Tumor growth was monitored twice a week, the mean tumor volume ± s.e.m. over time (**FIG. 14A**) and individual tumor growth curves (**FIG. 14B**) were assessed. As shown in **FIGS. 14A-B**, all three activatable antibodies showed potent anti-tumor activities, comparable to the parental antibody TY21580 in the MC38 syngeneic mouse tumor model.

Anti-tumor efficacy in a CT26 colorectal tumor model

[0278] BALB/c mice (n=8 per group, female, 7-8 weeks old) were inoculated subcutaneously with CT26 (Shanghai Institutes for Biological Sciences) murine colon cancer cells. When tumors were established (100 mm3), treatment began with isotype control antibody, parental antibody TY21580, or one of three activatable antibodies at 5mg/kg by intraperitoneal injection, twice a week. Tumor growth was monitored twice a week and reported as the mean tumor volume ± s.e.m. over time. As shown in **FIG. 15**, all three activatable antibodies showed potent anti-tumor activities, comparable to the parental antibody TY21580 in CT26 syngeneic mouse tumor model.

Anti-tumor efficacy in an H22 liver tumor model

[0279] BALB/c mice (n=8 per group, female, 7-8 weeks old) were inoculated subcutaneously with H22 (China Center for Type Culture Collection) murine liver cancer cells. When tumors were established (100 mm3), treatment began with isotype control antibody, parental antibody TY21580, or one of three activatable antibodies at 5mg/kg by intraperitoneal injection, twice a week. Tumor growth was monitored twice a week and reported as the mean tumor volume ± s.e.m. over time. As shown in **FIG. 16**, all three activatable antibodies showed potent anti-tumor activities, comparable to the parental antibody TY21580 in H22 syngeneic mouse tumor model.

Anti-tumor efficacy in a 3LL lung cancer model

[0280] C57BL/6 mice (n=10 per group, female, 6-8 weeks old) were inoculated subcutaneously with 3LL (JCRB) murine lung cancer cells. When tumors were established (75 mm3), treatment began with isotype control antibody, parental antibody TY21580, or one of three activatable antibodies by intraperitoneal injection, twice a week. Tumor growth was monitored twice a week, the mean tumor volume ± s.e.m. over time (**FIG. 17A**) and individual tumor growth curves (**FIG. 17B**) were assessed. As shown in **FIGS. 17A-B**, all three activatable antibodies showed potent anti-tumor activities, comparable to the parental antibody TY21580 in 3LL syngeneic mouse tumor model.

Pharmacokinetic analysis

[0281] A pharmacokinetics study was conducted in BALB/c female mice at about eight weeks of age. Three mice per group were intraperitoneally injected with the test article at 10 mg/kg. Blood samples (~50ul per sample) were collected at 3, 6, 24, 48, 96, and 168 hours post-dosing. Blank control blood was collected from three naïve female mice without antibody administration. Serum concentrations of each test antibody were determined by ELISA, in which anti-human IgG Fc was used for capture, and HRP-labeled anti-human IgG (Fab specific) antibody (Sigma) was used for detection (**FIGS. 18A-C**). As compared to the previous data collected for parental antibody TY21580, activatable antibodies TY22401 (**FIG. 18A**), TY22402 (**FIG. 18B**), and TY22404 (**FIG. 18C**) had a much slower clearance time and longer half-life. TY22401 has a half-life of 196 hours, and the drug concentration at 168 hours was about 55 μg/mL. TY22402 had a half-life of 134 hours, and the drug concentration at 168 hours was about 40 μg/mL. TY22404 had a half-life of 254 hours, and the drug concentration at 168 hours was about 45 μg/mL. In comparison, the parental antibody TY21580 had a half-life of 107 hours, and the drug concentration at 168 hours was about 17 μg/mL.

Repeated dosing toxicity studies

[0282] While evaluating the effect of TY21580 on diabetes onset age in NOD mice, it was found that high dosages of TY21580 could lead to animal death of NOD but not normal BALB/c mice. Here the NOD mouse model was used to evaluate the safety of the activatable antibodies, as compared to that of TY21580. NOD mice (n=5 per group, female, 6 weeks old) were treated with isotype control antibody, parental antibody TY21580, or one of three activatable antibodies by intraperitoneal injection at 50 mg/kg on days 0, 3, 7, and 12. In the TY21580 treatment group, 1 animal died after the third dosing, and 3 animals died after the fourth dosing. As shown in **FIG. 19**, all animals treated with the isotype control or any of the three activatable antibodies were alive and in good health at the termination of the study. These data indicated that the activatable antibodies have acceptable safety/toxicity profiles in mice, and, in NOD mice, the activatable antibodies are much safer than the parental antibody TY21580.

Example 5: Construction and validation of activatable antibodies targeting CD137

[0283] Activatable antibodies targeting human CD137 were developed similarly to the scheme used for the development of the anti-CTLA4 activatable antibodies described in Example

3 above. Fab fragments (**FIG. 20A**) or scFvs (**FIG. 20B**) of a parental CD137 antibody were displayed on the surface of yeast through fusion to the Aga2 protein, and their ability to bind to CD137 was confirmed by flow cytometry. The VH and VL sequences for the parental CD137 antibody (TY21242) are listed below (*See also* PCT International Application No. PCT/CN2017/098332, incorporated herein by reference in its entirety):

Anti-CD137 heavy chain variable region (SEQ ID NO: 49):

EVQLVESGGGLVQPGGSLRLSCAASGFSLSTGGVGVGWIRQAPGKGLEWLALIDWADD KYYSPSLKSRLTISRDNSKNTLYLQLNSLRAEDTAVYYCARGGSDTVIGDWFAYWGQG TLVTVSS

Anti-CD137 light chain variable region (SEQ ID NO: 50):

DIQLTQSPSSLSASVGDRVTITCRASQSIGSYLAWYQQKPGKAPKLLIYDASNLETGVPSR FSGSGSGTDFTLTISSLQPEDFATYYCQQGYYLWTFGQGTKVEIK.

[0284] The yeast libraries were constructed with CPLs fused to the N-terminus of the light chain, and were subjected to a FACS-based screening processes. The single clones from the 4th or 5th round of sorting (**FIG. 21**) were plated on selective media, and grown individually for confirmation of cleavage-mediated activated antigen binding. As shown in **FIGS. 22A-B**, the selected CD137 activatable antibody clones exhibited little binding to antigen in the presence of masking peptide; however, the binding to antigen was dramatically increased when the yeast cells were treated with TEV protease to remove the masking peptide.

[0285] As observed with CTLA4 activatable antibodies, the identified masking sequences could be separated into several groups, indicating clear enrichment through rounds of sorting. Seven groups of masking peptide sequences, together with the invariant cleavage peptide sequence, are listed in **Table 9**. Several of these sequence groups (TY22594, TY22595, TY22596, TY22598, TY22599) were derived from the CPL011 library, which contains NNK codons in the loop between the two fixed Cys residues. Interestingly, there are two or more Arg residues in the loop for all these sequence groups, suggesting that charge-charge interactions may

be involved between the masking peptides and the CDRs of the parental antibody. Indeed, there are negatively charged Asp residues in the VH CDR2 and VH CDR3.

Table 9: Masking peptide sequences

Sample ID:	Masking + cleavage peptide sequences:
TY22586	EVGSYPTDLDACADAPNHCHFSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 40)
TY22591	EVGSYSSTHAHCHHSPANCISSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 41)
TY22594	EVGSYDTDYDFCPILRHRCDSSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 42)
TY22595	EVGSYNDYNYHCKWRPSRCHNSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 43)
TY22596	EVGSYYHDYDDCRVLPRRCFNSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 44)
TY22598	EVGSYSNNFASCLWRHRSCADSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 45)
TY22599	EVGSYTDNYDYCPRLRRKCYHSGRSAGGGGSPLGLAGSGGS (SEQ ID NO: 46)

[0286] The masking sequences and the invariant cleavage sequences were then tested in full IgG4 molecules expressed in mammalian cells. Their expression levels were similar to their parental antibody, and their purification yields after protein A resin were also similar, suggesting that the presence of masking peptide and cleavage peptide did not have any negative impacts on antibody expression in mammalian cells.

[0287] The masking efficiency was then measured through flow cytometry. Briefly, yeast cells displaying human CD137 on their surface washed twice with PBSA buffer, and 50 µL (1x10^6) cells were dispensed into each well of a 96 well plate. Cells were then incubated with 3-fold serial dilutions of antibodies for 1 hour on ice, washed once with PBSA buffer, and then incubated with 100 µL of PE conjugated mouse anti-human Fc (1µg/ml) for 30 minutes on ice. The cells were then washed once prior to analysis by flow cytometry (Beckman® CytoFlex). As shown in **FIG. 23 and Table 10**, compared with the parental antibody TY21242, all activatable antibodies showed dramatically reduced binding to human CD137 on the cell surface, and the calculated masking efficiency ranged from 20 fold for TY22596 to more than 300 fold for TY22586, TY22595 and TY22599. These results indicated that the masking peptides identified

from the CPL libraries displayed on yeast maintained their masking efficiency when expressed in mammalian cells.

Table 10: Masking efficiency of CD137 activatable antibodies

Sample ID:	**EC_{50}**	
	K_D (nM):	**Masking efficiency:**
TY21242	0.28	1.0
TY22586	Too low*	Very high
TY22591	10.8	38.3
TY22594	23.6	83.7
TY22595	106.8	378.7
TY22596	5.86	20.8
TY22598	8.61	30.5
TY22599	98.1	347.9

Tow low = binding was so weak it was not detectable in this assay.

[0288] Taken together, the data indicated that multiple potent masking peptides were successfully discovered against each target antibody using the methods described herein.

CLAIMS

What is claimed is:

1. A library comprising polynucleotides, wherein at least one of the polynucleotides encodes a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

2. The library of claim 1, wherein the polynucleotides in the library encode at least two, at least three, at least four, at least five, or at least ten unique polypeptides and each unique polypeptide comprise, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

3. The library of claim 1 or claim 2, wherein each of the polynucleotides in the library encodes a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

4. The library of any one of claims 1-3, wherein the FP is encoded by a polynucleotide sequence comprising a nucleic acid sequence according to Formula (XIV): $(NNK)_mTGY(NNK)_nTGY(NNK)_o$ (SEQ ID NO: 87), wherein each N is independently A, G, T, or C, wherein each K is independently T or G, and wherein each Y is independently T or C.

5. The library of any one of claims 1-4, wherein each X is not M, W, or C.

6. The library of any one of claims 1-5, wherein each X in X_m of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

7. The library of any one of claims 1-6, wherein each X in X_n of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

8. The library of any one of claims 1-7, wherein each X in X_o of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

9. The library of any one of claims 1-8, wherein m is 6.

10. The library of any one of claims 1-9, wherein n is from 6-8.

11. The library of any one of claims 1-9, wherein n is 6.

12. The library of any one of claims 1-11, wherein o is from 1-2.

13. The library of any one of claims 1-11, wherein o is 2

14. The library of any one of claims 1-13 wherein the FP further comprises, at its N-terminus, an additional amino acid sequence.

15. The library of claim 14, wherein the additional amino acid sequence comprises the amino acid sequence of SEQ ID NO: 16.

16. The library of any one of claims 1-15, wherein the first cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

17. The library of any one of claims 1-16, wherein the CM further comprises a first linker (L_1) C-terminal to the first cleavage site.

18. The library of claim 17, wherein the L_1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 17-24.

19. The library of any one of claims 1-18, wherein the CM further comprises a second cleavage site.

20. The library of claim 19, wherein the second cleavage site is C-terminal to the L_1.

21. The library of claim 19 or claim 20, wherein the second cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9,

MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

22. The library of any one of claims 19-21, wherein the first and second cleavage sites are different.

23. The library of any one of claims 19-22, wherein the CM further comprises a second linker (L_2) C-terminal to the second cleavage site.

24. The library of claim 23, wherein the L_2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 17-24.

25. The library of any one of claims 1-24, wherein the polypeptide comprises an amino acid sequence according to Formula (III): $EVGSYX_1X_2X_3X_4X_5X_6CX_7X_8X_9X_{10}X_{11}X_{12}CX_{13}X_{14}$SGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 3), wherein X1 is A, D, I, N, P, or Y, x2 is A, F, N, S, or V, X3 is A, H, L, P, S, V, or Y, X4 is A, H, S, or Y, X5 is A, D, P, S, V, or Y, X6 is A, D, L, S, or Y, X7 is D, P, or V, X8 is A, D, H, P, S, or T, X9 is A, D, F, H, P, or Y, X10 is L, P, or Y, X11 is F, P, or Y, X12 is A, P, S, or Y, X13 is A, D, N, S, T, or Y, and X14 is A, S, or Y.

26. The library of claim 25, wherein each of the polynucleotides in the library encodes a polypeptide comprising an amino acid sequence according to Formula (III).

27. The library of any one of claims 1-26, wherein the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 25-46.

28. The library of any one of claims 1-27, wherein the TBM comprises an antibody light chain variable region.

29. The library of claim 28, wherein the polypeptide further comprises a heavy chain variable region C-terminal to the light chain variable region.

30. The library of claim 28, further comprising polynucleotides that encode one or more antibody heavy chain variable regions.

31. The library of any one of claims 1-27, wherein the TBM comprises an antibody heavy chain variable region.

32. The library of claim 31, wherein the polypeptide further comprises a light chain variable region C-terminal to the heavy chain variable region.

33. The library of claim 31, further comprising polynucleotides that encode one or more antibody light chain variable regions.

34. The library of any one of claims 1-33, wherein at least one of the polynucleotides encoding the polypeptide is in a vector.

35. The library of claim 34, wherein the vector is an expression vector or a display vector.

36. The library of any one of claims 1-35, wherein at least one of the polynucleotides encoding the polypeptide is in a cell.

37. The library of claim 36, wherein the cell is a bacterial cell, a yeast cell, an insect cell, or a mammalian cell.

38. A method of producing an activatable antibody comprising culturing the cell of claim 36 or claim 37 under conditions suitable for producing the activatable antibody.

39. The method of claim 38, further comprising recovering the activatable antibody produced by the cell.

40. The method of claim 39, further comprising testing the activatable antibody for the ability to maintain an activatable phenotype while soluble.

41. A method of using the library of any one of claims 1-37 to screen for a activatable antibody that binds to a target, the method comprising:

a) contacting the expression products of the library with the target before the CM is cleaved;

b) contacting the expression products of the library with the target after the CM is cleaved; and

c) isolating one or more of the expression products that binds to the target after the CM is cleaved, but does not bind to the target before the CM is cleaved.

42. The method of claim 41, wherein the CM comprises at least a first protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

43. The method of claim 41 or claim 42, wherein the target is CTLA4 or CD137.

44. A polypeptide encoded by one or more polynucleotides from the library of any one of claims 1-37.

45. A kit comprising the library of any one of claims 1-37.

46. A library comprising antigen binding domains, wherein at least one of the antigen binding domains comprises a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

47. The library of claim 46, wherein at least two, at least three, at least four, at least five, or at least ten of the antigen binding domains comprise a unique polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

48. The library of claim 46 or claim 47, wherein each of the antigen binding domains comprises a unique polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (XIII): $X_mCX_nCX_o$ (SEQ ID NO: 86), wherein m is from 3-10, n is from 3-10, and o is from 1-10, and wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

49. The library of any one of claims 46-48, wherein the TBM comprises an antibody light chain variable region and the antigen binding domain further comprises an antibody heavy chain variable region.

50. The library of any one of claims 46-48, wherein the TBM comprises an antibody heavy chain variable region and the antigen binding domain further comprises an antibody light chain variable region.

51. The library of any one of claims 46-50, wherein each X is not M, W, or C.

52. The library of any one of claims 46-51, wherein each X in X_m in formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

53. The library of any one of claims 46-52, wherein each X in X_n of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

54. The library of any one of claims 46-53, wherein each X in X_o of Formula (XIII) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

55. An antibody light chain comprising a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region.

56. An antibody comprising a heavy chain and a light chain, wherein the light chain is a light chain of claim 55.

57. An antibody heavy chain comprising a polypeptide comprising, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody heavy chain variable region.

58. An antibody comprising a heavy chain and a light chain, wherein the heavy chain is a heavy chain of claim 57.

59. A cell comprising at least one polypeptide displayed on its surface, wherein the at least polypeptide comprises, from N-terminus to C-terminus, a first peptide (FP), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the FP comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region and/or an antibody heavy chain variable region.

60. The cell of claim 59, wherein the cell is a bacterial cell, a yeast cell, an insect cell, or a mammalian cell.

61. The cell of claim 59 or claim 60, wherein each X is not M, W, or C.

62. The cell of any one of claims 59-61, wherein each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

63. The cell of any one of claims 59-62, wherein each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

64. An activatable antibody comprising:

a) a polypeptide comprising, from N-terminus to C-terminus, a masking moiety (MM), a cleavable moiety (CM), and a target binding moiety (TBM),

wherein the MM comprises an amino acid sequence according to Formula (I): $X_mCX_nCZ_o$ (SEQ ID NO: 1), wherein m is from 3-10, n is from 3-10, and o is from 1-10, wherein each X is independently an amino acid selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, and Y, and wherein each Z is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P; wherein the MM inhibits the binding of the activatable antibody to human CD137 when the CM is not cleaved;

wherein the CM comprises at least a first cleavage site; and

wherein the TBM comprises an antibody light chain variable region (VL); and

b) an antibody heavy chain variable region (VH); and

wherein the activatable antibody binds to human CD137 when the CM is cleaved.

65. The activatable antibody of claim 64, wherein m is 6.

66. The activatable antibody of claim 64 or claim 65, wherein n is from 6-8.

67. The activatable antibody of claim 64 or claim 65, wherein n is 6.

68. The activatable antibody of any one of claims 64-67, wherein o is from 1-2.

69. The activatable antibody of any one of claims 64-67, wherein o is 2.

70. The activatable antibody of any one of claims 64-69, wherein each X is not M, W, or C.

71. The activatable antibody of any one of claims 64-70, wherein each X in X_m of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

72. The activatable antibody of any one of claims 64-71, wherein each X in X_n of formula (I) is independently an amino acid selected from the group consisting of D, A, Y, S, T, N, I, L, F, V, H, and P.

73. The activatable antibody of any one of claims 64-72, wherein the MM further comprises, at its N-terminus, an additional amino acid sequence.

74. The activatable antibody of claim 73, wherein the additional amino acid sequence comprises the amino acid sequence of SEQ ID NO: 16.

75. The activatable antibody of any one of claims 64-74, wherein the first cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

76. The activatable antibody of any one of claims 64-75, wherein the CM further comprises a first linker (L_1) C-terminal to the first cleavage site.

77. The activatable antibody of claim 76, wherein the L_1 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 17-24.

78. The activatable antibody of any one of claims 64-77, wherein the CM further comprises a second cleavage site.

79. The activatable antibody of claim 78, wherein the second cleavage site is C-terminal to the L_1.

80. The activatable antibody of claim 78 or claim 79, wherein the second cleavage site is a protease cleavage site for a protease selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

81. The activatable antibody of any one of claims 78-80, wherein the first and second cleavage sites are different.

82. The activatable antibody of any one of claims 78-81, wherein the CM further comprises a second linker (L_2) C-terminal to the second cleavage site.

83. The activatable antibody of claim 82, wherein the L_2 comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 17-24.

84. The activatable antibody of any one of claims 64-83, wherein the CM comprises at least a first protease cleavage site and is cleaved with one or more proteases selected from the group consisting of urokinase-type plasminogen activator (uPA), matrix metalloproteinase-1 (MMP-1), MMP-2, MMP-3, MMP-8, MMP-9, MMP-14, Tobacco Etch Virus (TEV) protease, plasmin, Thrombin, Factor X, PSA, PSMA, Cathepsin D, Cathepsin K, Cathepsin S, ADAM10, ADAM12, ADAMTS, Caspase-1, Caspase-2, Caspase-3, Caspase-4, Caspase-5, Caspase-6, Caspase-7, Caspase-8, Caspase-9, Caspase-10, Caspase-11, Caspase-12, Caspase-13, Caspase-14, and TACE.

85. The activatable antibody of any one of claims 64-84, wherein the activatable antibody comprises an amino acid sequence according to Formula (III): $EVGSYX_1X_2X_3X_4X_5X_6CX_7X_8X_9X_{10}X_{11}X_{12}CX_{13}X_{14}$SGRSAGGGGTENLYFQGSGGS (SEQ ID NO: 3), wherein X1 is A, D, I, N, P, or Y, x2 is A, F, N, S, or V, X3 is A, H, L, P, S, V, or Y, X4

is A, H, S, or Y, X5 is A, D, P, S, V, or Y, X6 is A, D, L, S, or Y, X7 is D, P, or V, X8 is A, D, H, P, S, or T, X9 is A, D, F, H, P, or Y, X10 is L, P, or Y, X11 is F, P, or Y, X12 is A, P, S, or Y, X13 is A, D, N, S, T, or Y, and X14 is A, S, or Y.

86. The activatable antibody of any one of claims 64-85, wherein the activatable antibody comprises an amino acid sequence selected from the group consisting of SEQ ID NOS: 40-46.

87. The activatable antibody of any one of claims 64-86, wherein the VL comprises an HVR-L1 comprising the amino acid sequence of SEQ ID NO: 68, an HVR-L2 comprising the amino acid sequence of SEQ ID NO: 69, and an HVR-L3 comprising the amino acid sequence of SEQ ID NO: 70.

88. The activatable antibody of any one of claims 64-87, wherein the VL comprises the amino acid sequence of SEQ ID NO: 50.

89. The activatable antibody of any one of claims 64-88, wherein the VH comprises an HVR-H1 comprising the amino acid sequence of SEQ ID NO: 65, an HVR-H2 comprising the amino acid sequence of SEQ ID NO: 66, and an HVR-H3 comprising the amino acid sequence of SEQ ID NO: 67.

90. The activatable antibody of any one of claims 64-89, wherein the VH comprises the amino acid sequence of SEQ ID NO: 49.

91. A method of treating or delaying progression of cancer in a subject in need thereof, the method comprising administering to the subject an effective amount of a polypeptide encoded by one or more polynucleotides from the library of any one of claims 1-37, or an activatable antibody of any one of claims 64-90.

92. The method of claim 91, further comprising administering to the subject an effective amount of at least one additional therapeutic agent.

93. The method of claim 92, wherein the at least one additional therapeutic agent is selected from the group consisting of viral gene therapy, immune checkpoint inhibitors, target therapies, radiation therapies, and chemotherapies.

94. The method of claim 92 or claim 93, wherein the at least one additional therapeutic agent is selected from the group consisting of pomalyst, revlimid, lenalidomide, pomalidomide, thalidomide, a DNA-alkylating platinum-containing derivative, cisplatin, 5-fluorouracil, cyclophosphamide, an anti-CD137 antibody, an anti-CTLA4 antibody, an anti-PD-1 antibody, an anti-PD-L1 antibody, an anti-CD20 antibody, an anti-CD40 antibody, an anti-DR5 antibody, an anti-CD1d antibody, an anti-TIM3 antibody, an anti-SLAMF7 antibody, an anti-KIR receptor antibody, an anti-OX40 antibody, an anti-HER2 antibody, an anti-ErbB-2 antibody, an anti-EGFR antibody, cetuximab, rituximab, trastuzumab, pembrolizumab, radiotherapy, single dose radiation, fractionated radiation, focal radiation, whole organ radiation, IL-12, IFNα, GM-CSF, a chimeric antigen receptor, adoptively transferred T cells, an anti-cancer vaccine, and an oncolytic virus.

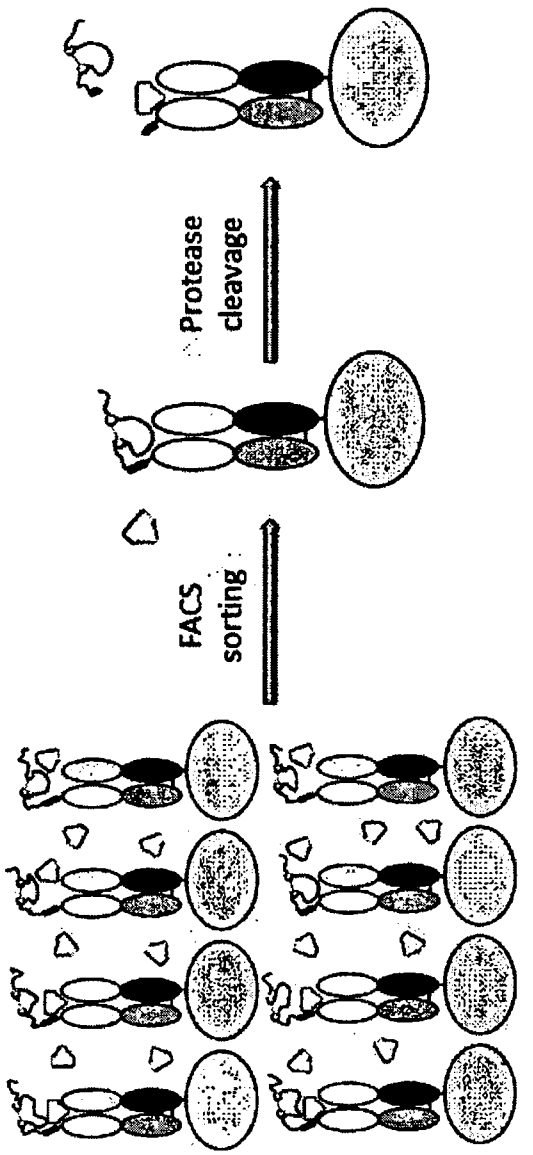

FIG. 1

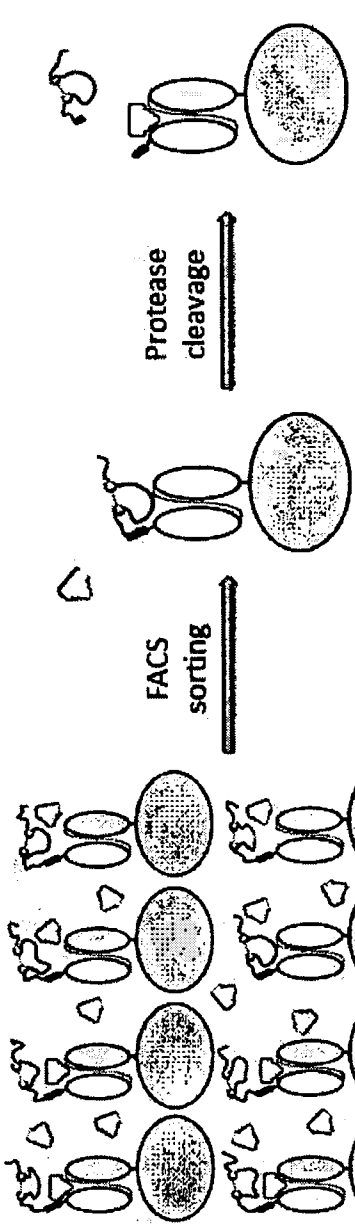

FIG. 2

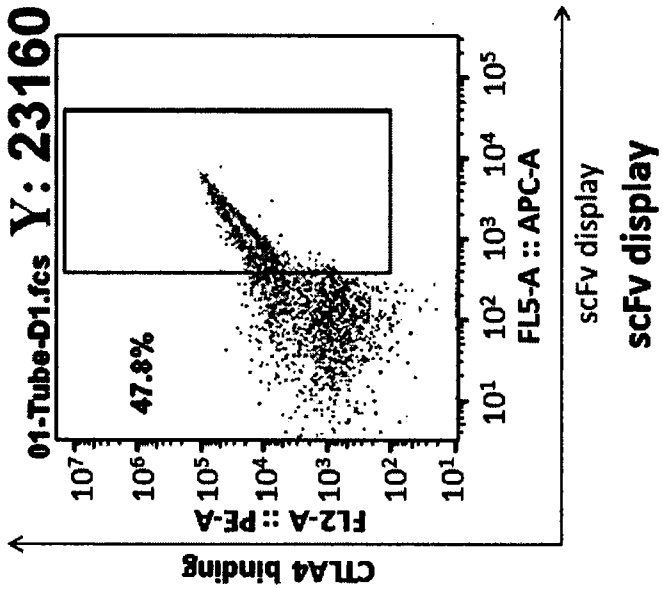
01-Tube-D1.fcs Y: 23160
47.8%
CTLA4 binding
FL2-A :: PE-A
FL5-A :: APC-A
scFv display
scFv display

FIG. 3B

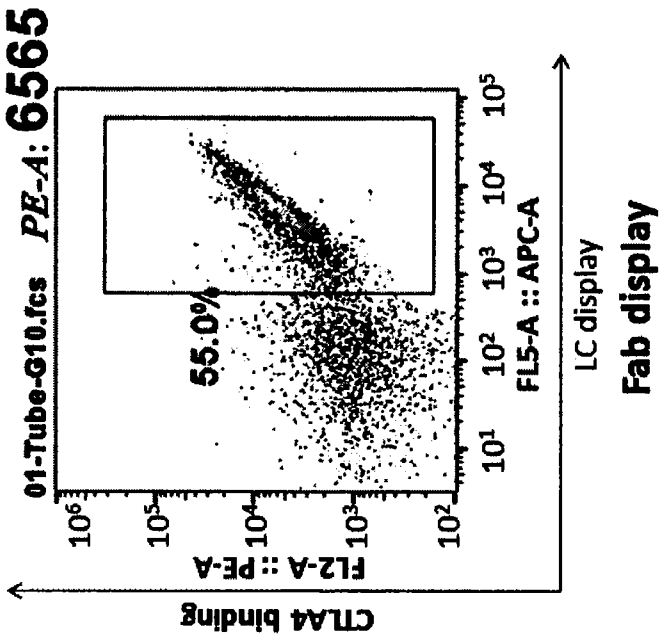
01-Tube-G10.fcs PE-A: 6565
55.0%
CTLA4 binding
FL2-A :: PE-A
FL5-A :: APC-A
LC display
Fab display

FIG. 3A

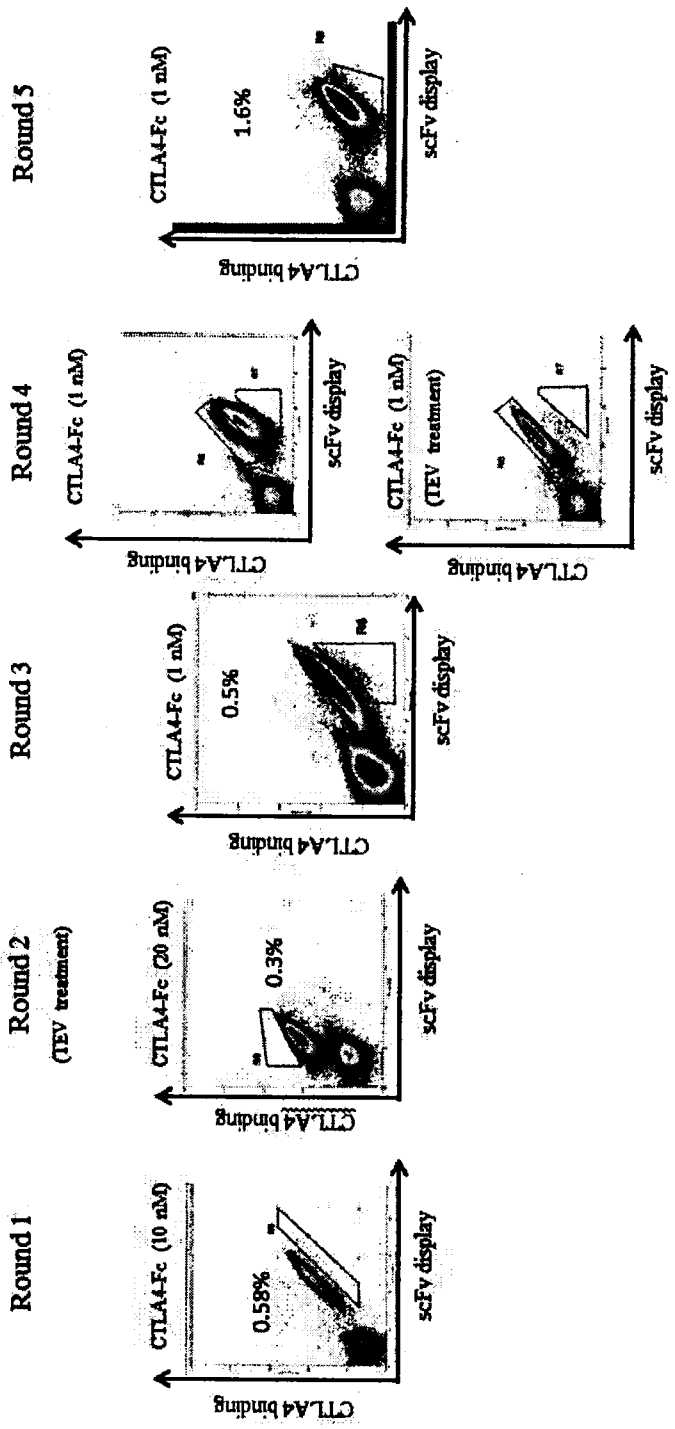
Round 1
CTLA4-Fc (10 nM)
0.58%
CTLA4 binding
scFv display
Round 2
(TEV treatment)
CTLA4-Fc (20 nM)
0.3%
CTLA4 binding
scFv display
Round 3
CTLA4-Fc (1 nM)
0.5%
CTLA4 binding
scFv display
Round 4
CTLA4-Fc (1 nM)
CTLA4 binding
scFv display
CTLA4-Fc (1 nM)
(TEV treatment)
CTLA4 binding
scFv display
Round 5
CTLA4-Fc (1 nM)
1.6%
CTLA4 binding
scFv display

FIG. 4

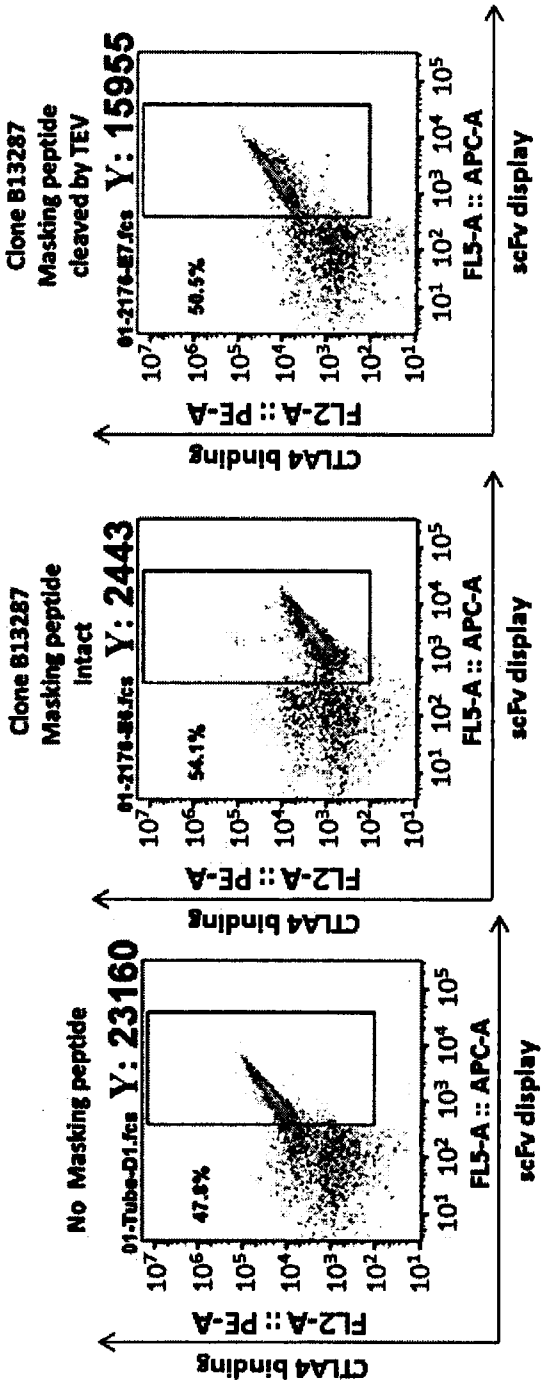
No Masking peptide
01-Tube-D1.fcs
Y: 23160
47.8%
Clone B13287
Masking peptide
Intact
01-2170-B5.fcs
Y: 2443
54.1%
Clone B13287
Masking peptide
cleaved by TEV
01-2170-E7.fcs
Y: 15955
50.5%
CTLA4 binding
FL2-A :: PE-A
FL5-A :: APC-A
scFv display

FIG. 5A

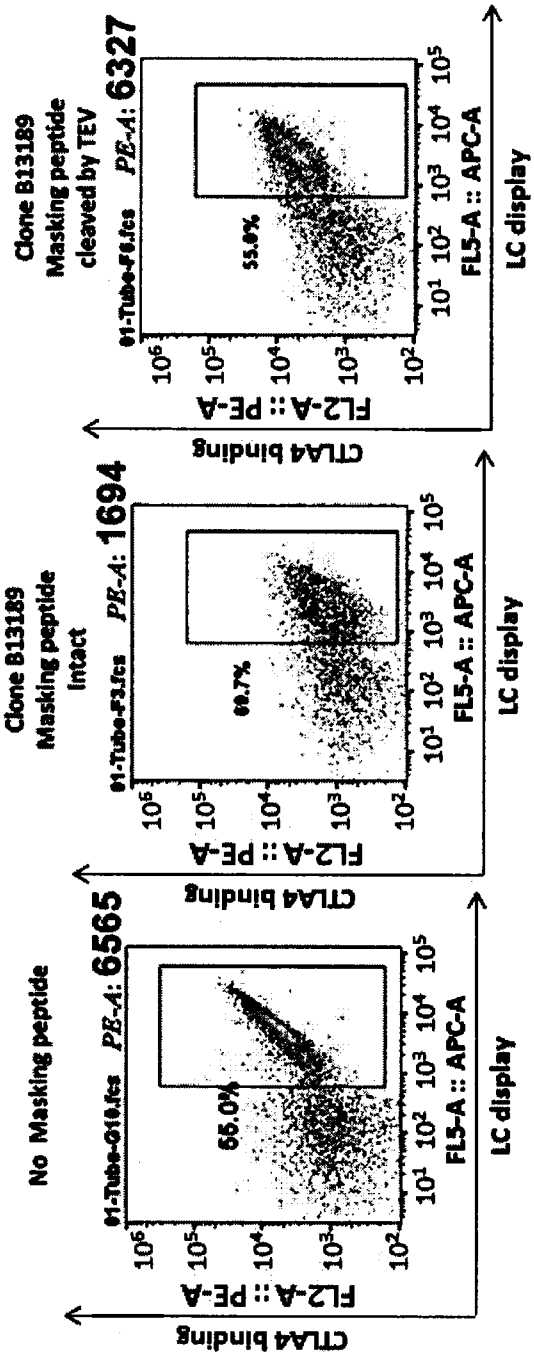
No Masking peptide
01-Tube-D10.fcs
PE-A: 6565
66.0%
Clone B13189
Masking peptide
Intact
01-Tube-F3.fcs
PE-A: 1694
69.7%
Clone B13189
Masking peptide
cleaved by TEV
01-Tube-F6.fcs
PE-A: 6327
55.9%
CTLA4 binding
FL2-A :: PE-A
FL5-A :: APC-A
LC display

FIG. 5B

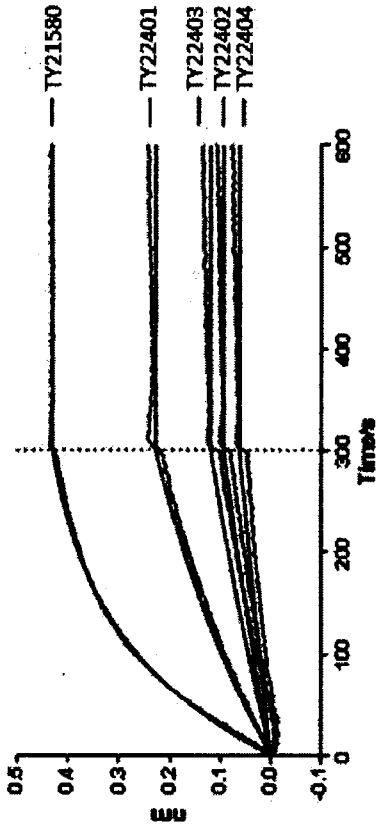
TY21580
TY22401
TY22403
TY22402
TY22404
RU
Time/s
0.5
0.4
0.3
0.2
0.1
0.0
-0.1
0
100
200
300
400
500
600

FIG. 6A

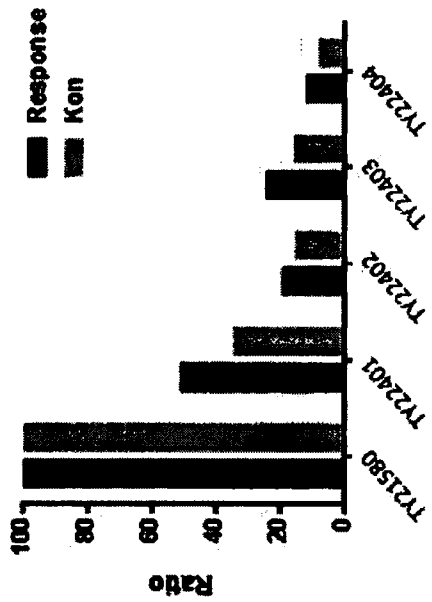
Response
Kon
Ratio
100
80
60
40
20
0
TY21580
TY22401
TY22402
TY22403
TY22404

FIG. 6B

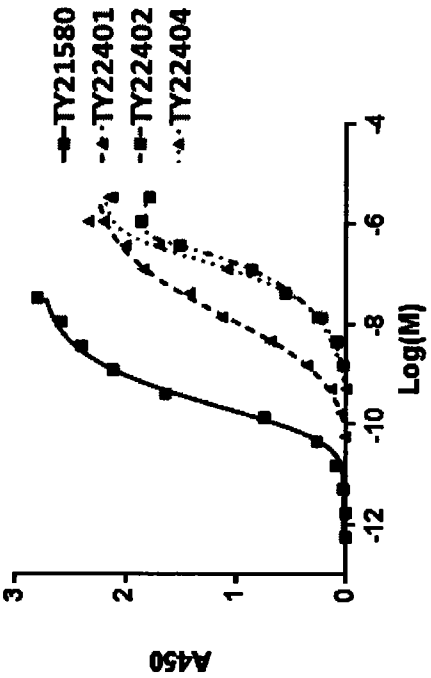

FIG. 7B

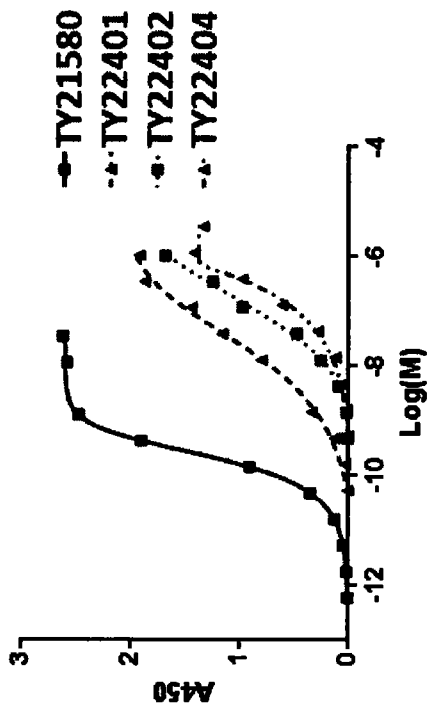

FIG. 7A

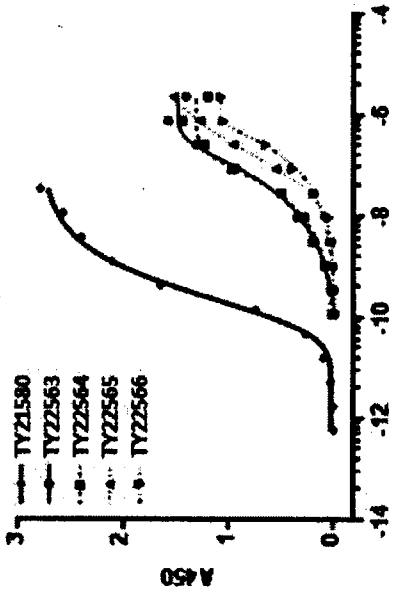

FIG. 7C

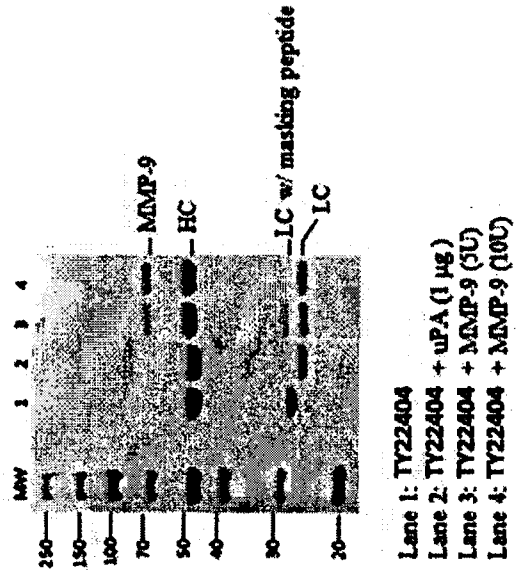
MW
1
2
3
4
250
150
100
70
50
40
30
20
MMP-9
HC
LC w/ masting peptide
LC
Lane 1: TY22404
Lane 2: TY22404 + uPA (1 μg)
Lane 3: TY22404 + MMP-9 (5U)
Lane 4: TY22404 + MMP-9 (10U)

FIG. 8A

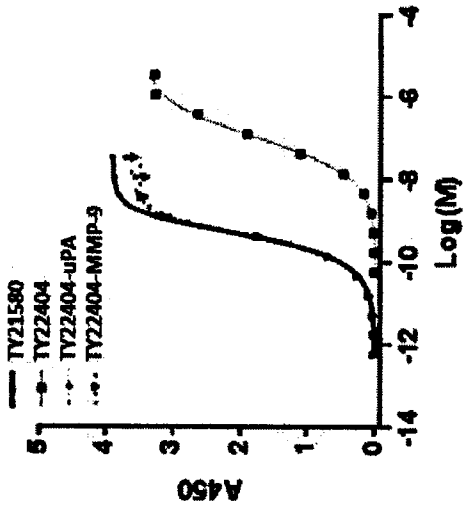
TY21580
TY22404
TY22404-uPA
TY22404-MMP-9
A450
Log(M)
5
4
3
2
1
0
-4
-6
-8
-10
-12
-14

FIG. 8B

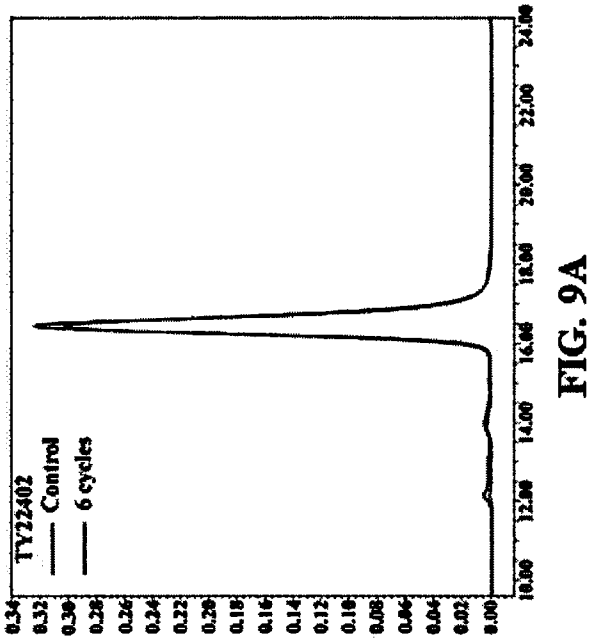

FIG. 9A

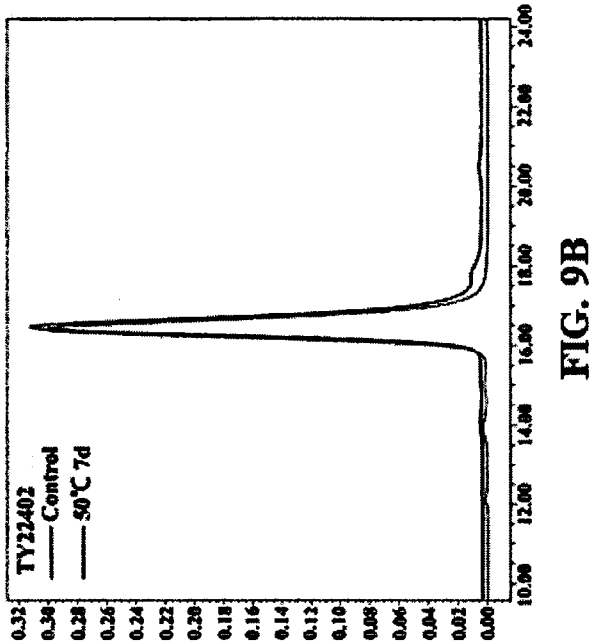

FIG. 9B

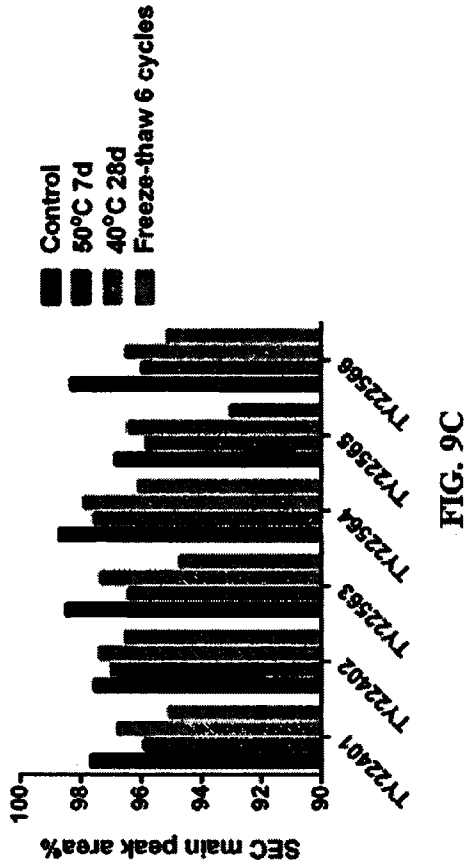

FIG. 9C

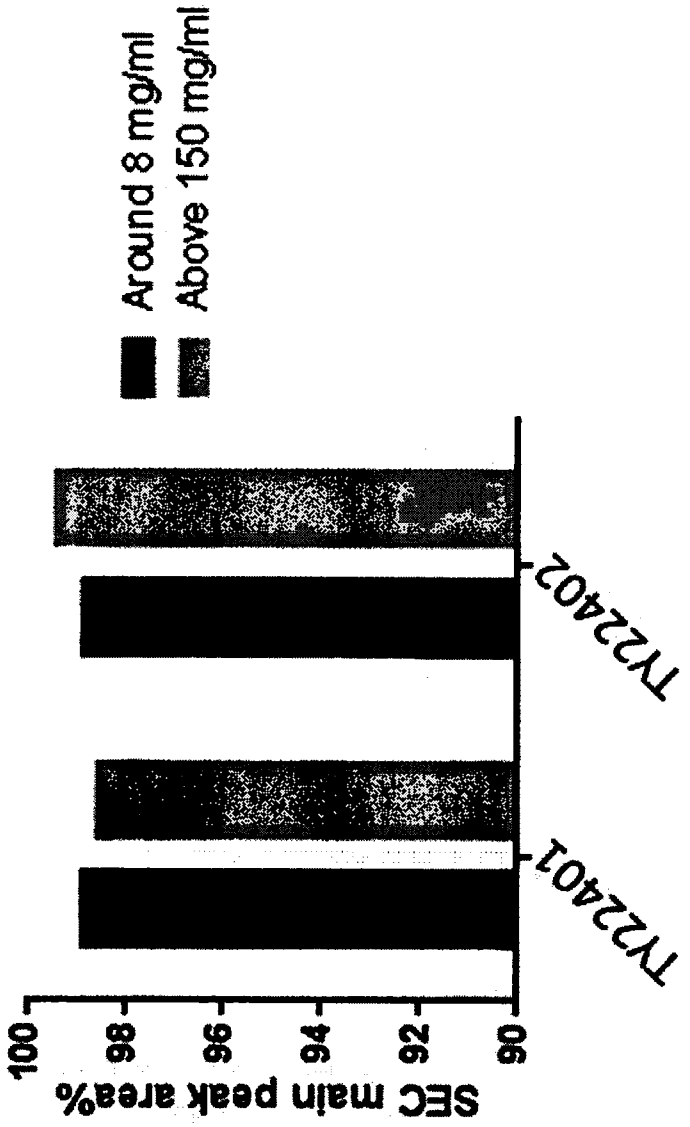
Around 8 mg/ml
Above 150 mg/ml
SEC main peak area%
100
98
96
94
92
90
TY22402
TY22401

FIG. 10

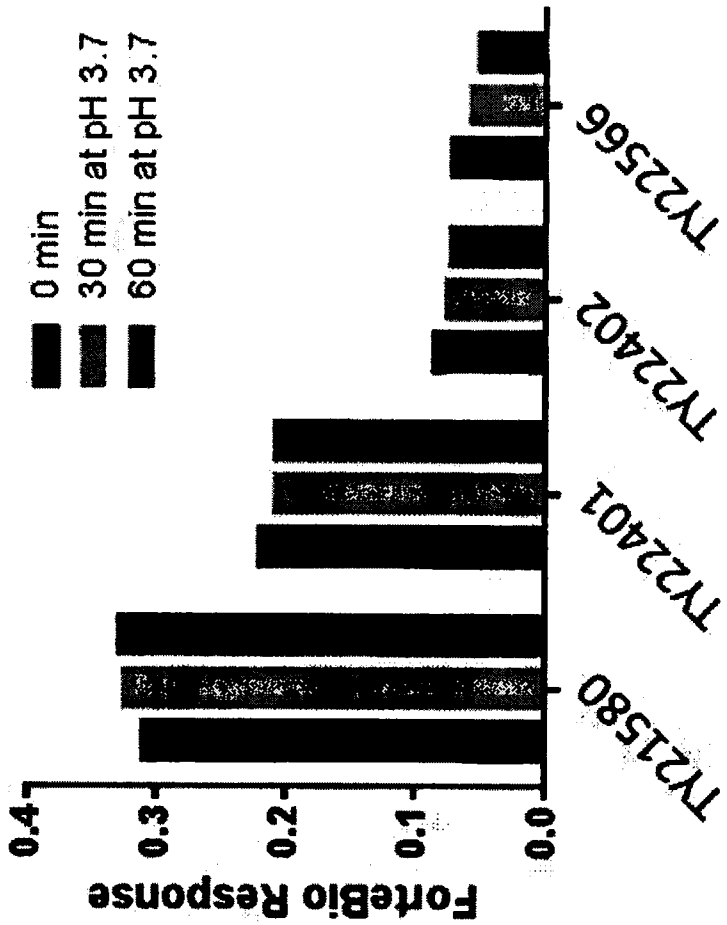
0 min
30 min at pH 3.7
60 min at pH 3.7
ForteBio Response
0.0
0.1
0.2
0.3
0.4
TY2580
TY2401
TY2402
TY2566

FIG. 11

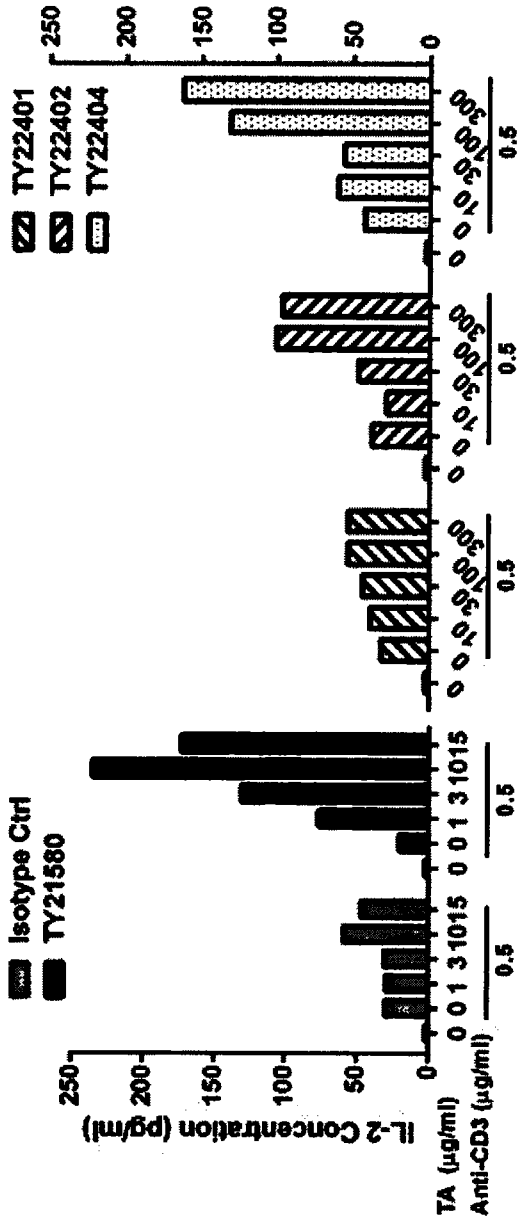

FIG. 12A

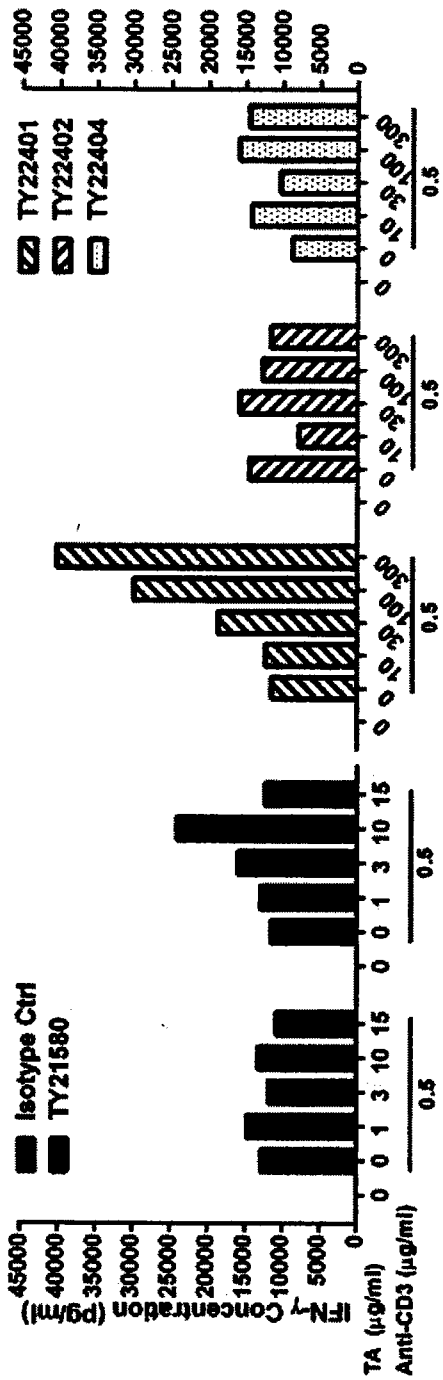

FIG. 12B

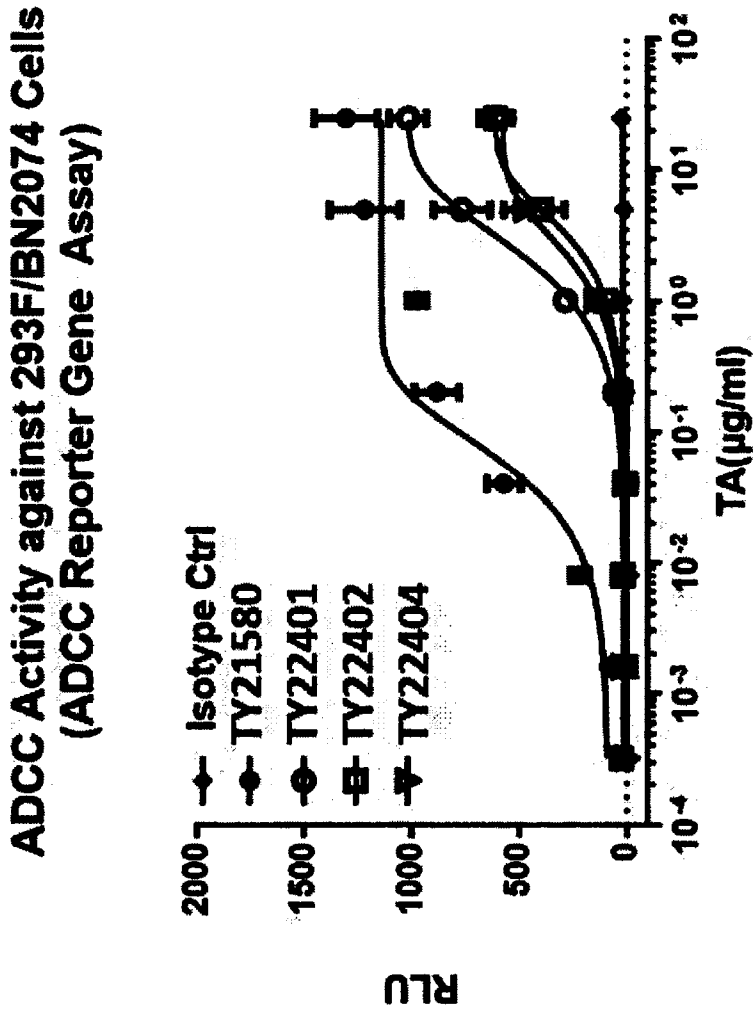
ADCC Activity against 293F/BN2074 Cells
(ADCC Reporter Gene Assay)
Isotype Ctrl
TY21580
TY22401
TY22402
TY22404
RLU
2000
1500
1000
500
0
10⁻⁴
10⁻³
10⁻²
10⁻¹
10⁰
10¹
10²
TA(μg/ml)

FIG. 13

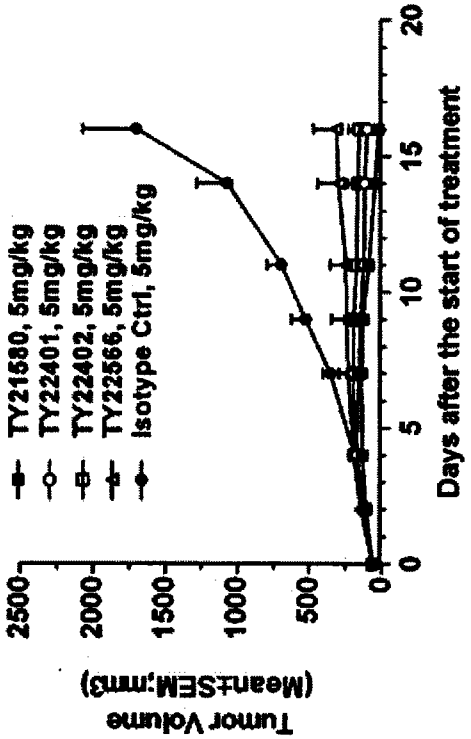

FIG. 14A

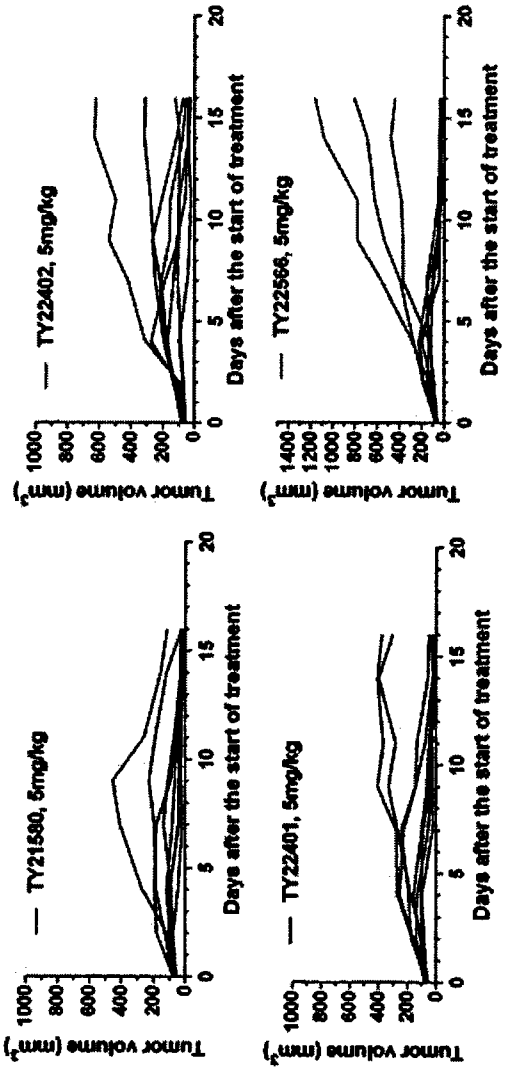

FIG. 14B

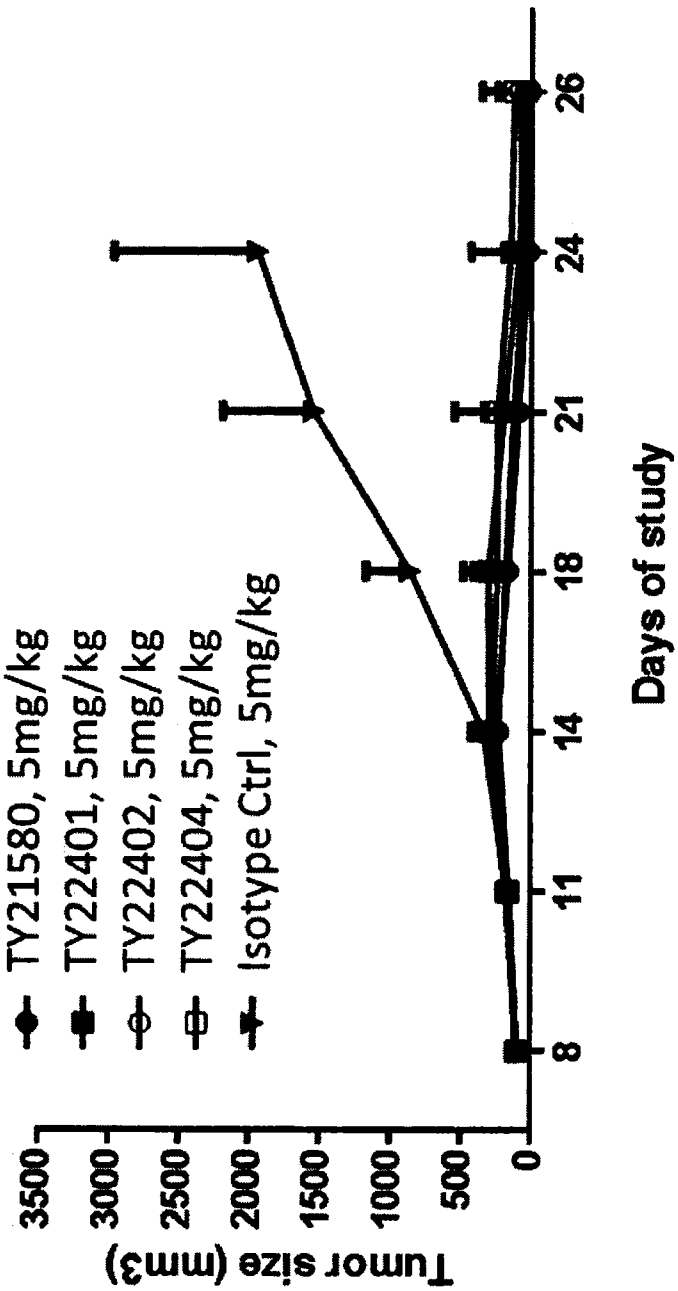
Tumor size (mm3)
3500
3000
2500
2000
1500
1000
500
0
8
11
14
18
21
24
26
Days of study
TY21580, 5mg/kg
TY22401, 5mg/kg
TY22402, 5mg/kg
TY22404, 5mg/kg
Isotype Ctrl, 5mg/kg

FIG. 15

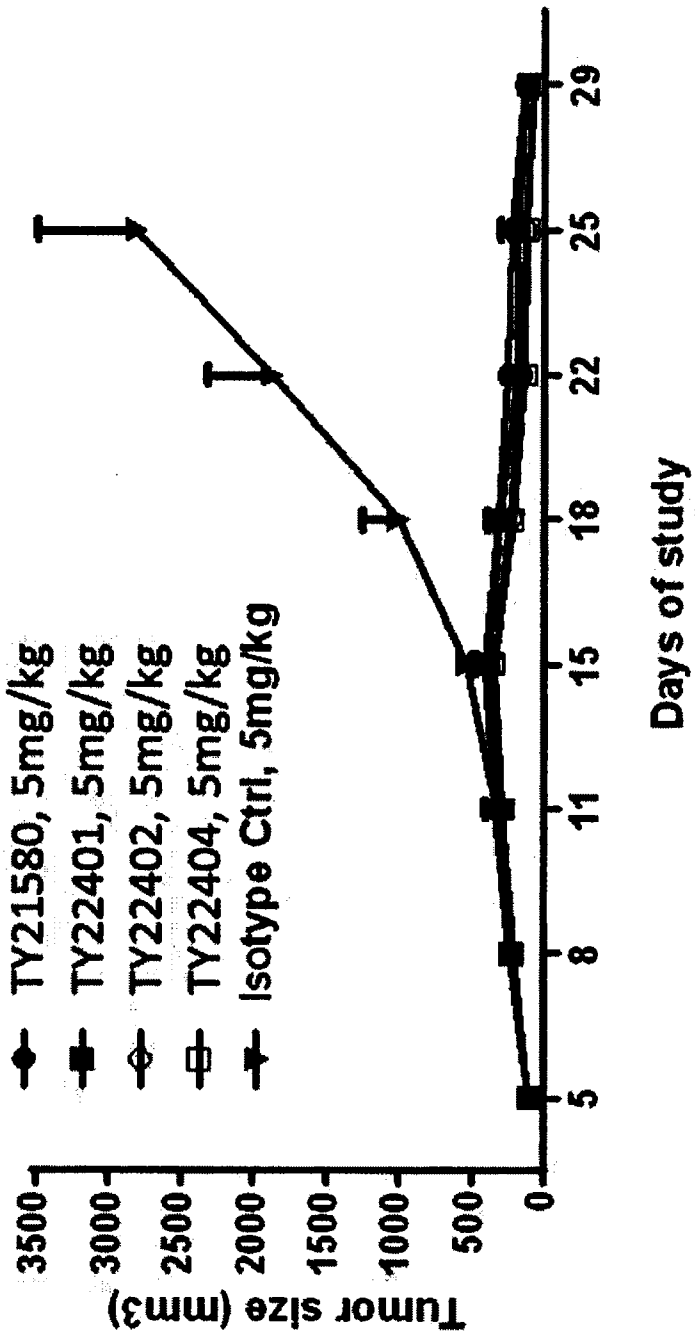
Tumor size (mm3)
3500
3000
2500
2000
1500
1000
500
0
5
8
11
15
18
22
25
29
Days of study
TY21580, 5mg/kg
TY22401, 5mg/kg
TY22402, 5mg/kg
TY22404, 5mg/kg
Isotype Ctrl, 5mg/kg

FIG. 16

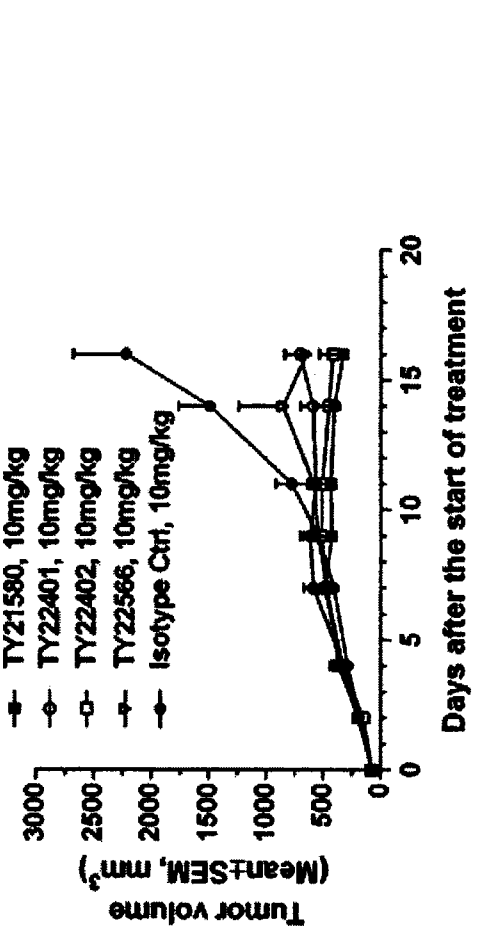

FIG. 17A

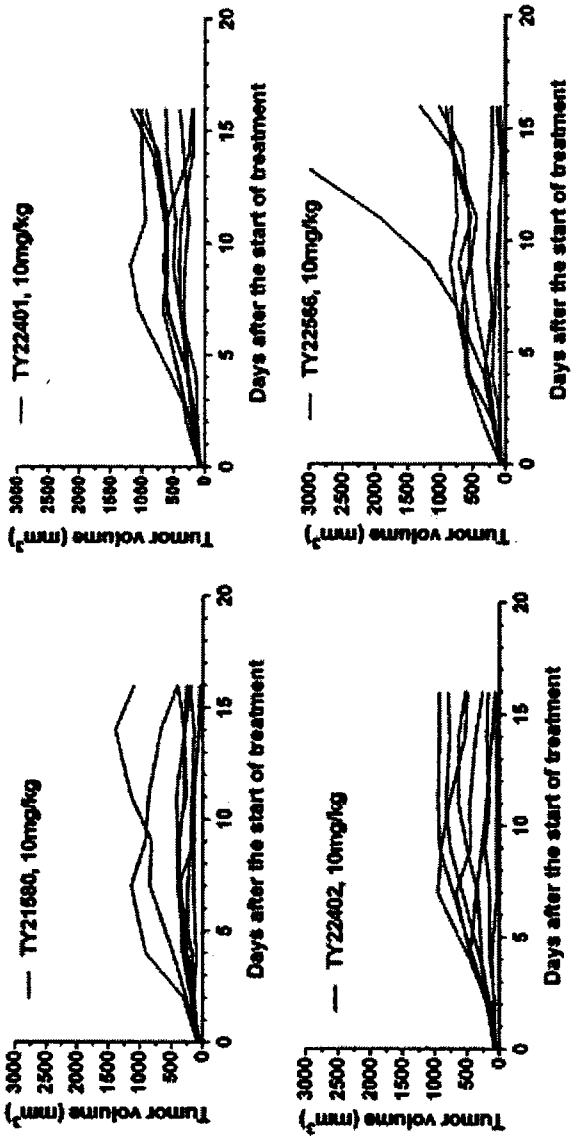

FIG. 17B

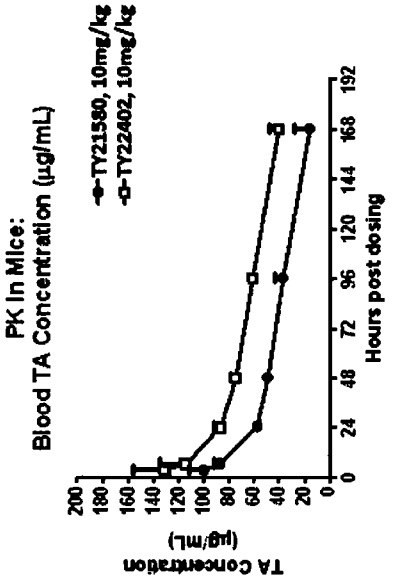

FIG. 18A

FIG. 18B

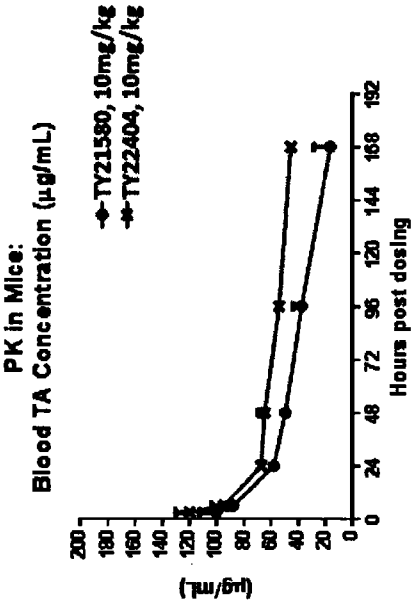

FIG. 18C

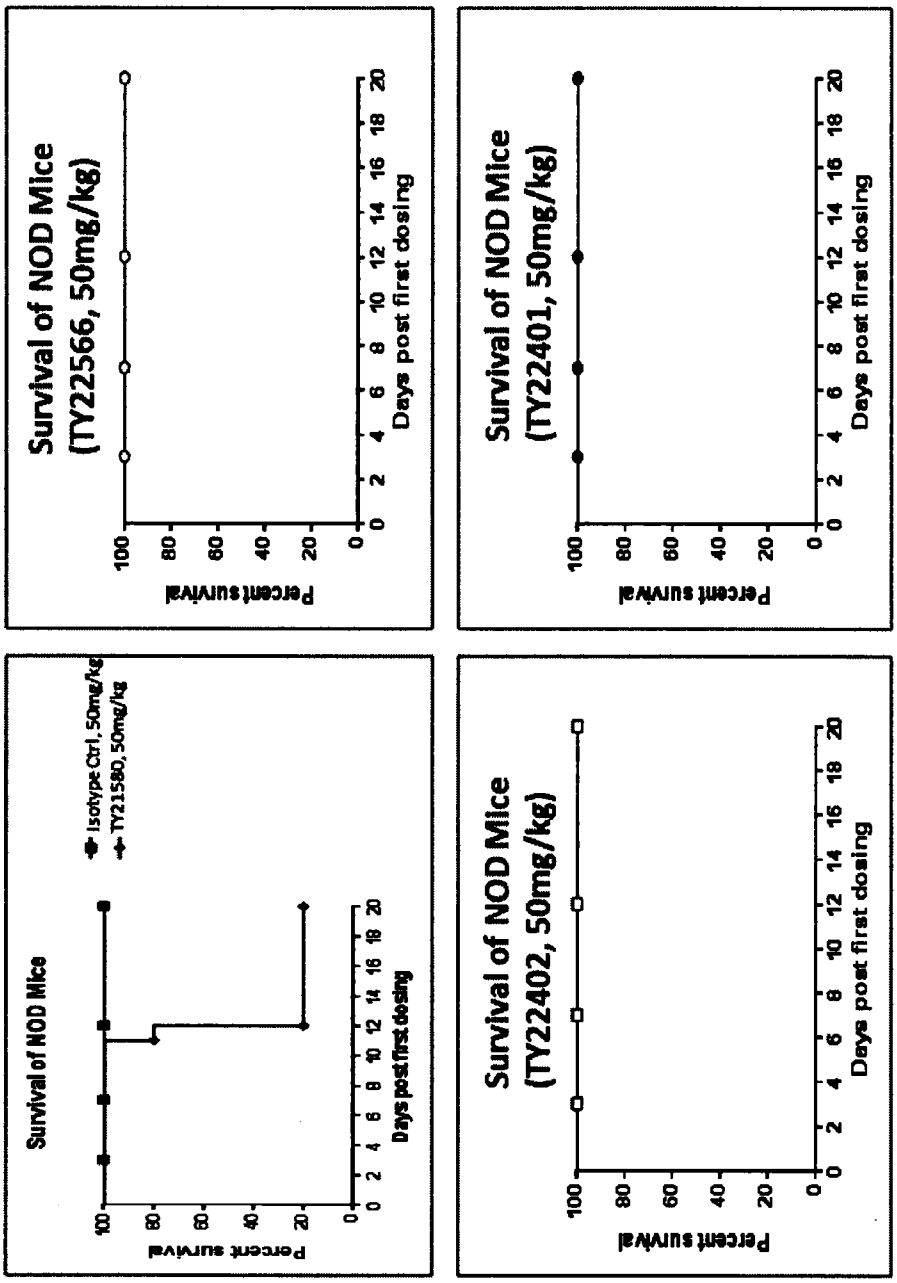
Survival of NOD Mice
Isotype Ctrl, 50mg/kg
TY21580, 50mg/kg
Percent survival
Days post first dosing
Survival of NOD Mice (TY22566, 50mg/kg)
Survival of NOD Mice (TY22401, 50mg/kg)
Survival of NOD Mice (TY22402, 50mg/kg)

FIG. 19

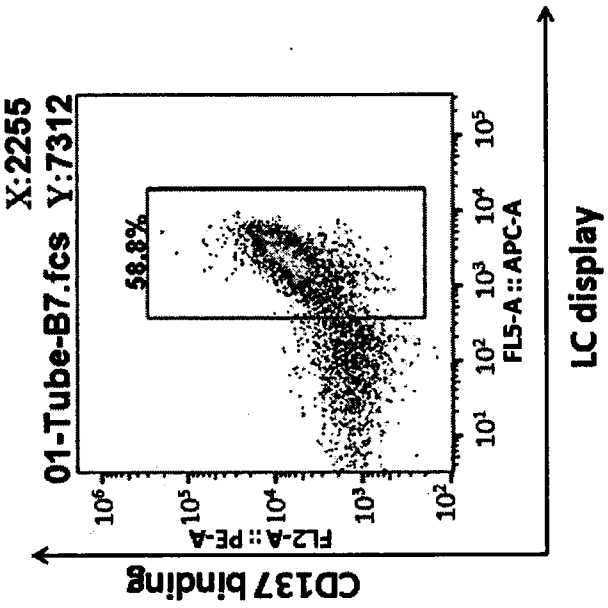

FIG. 20B

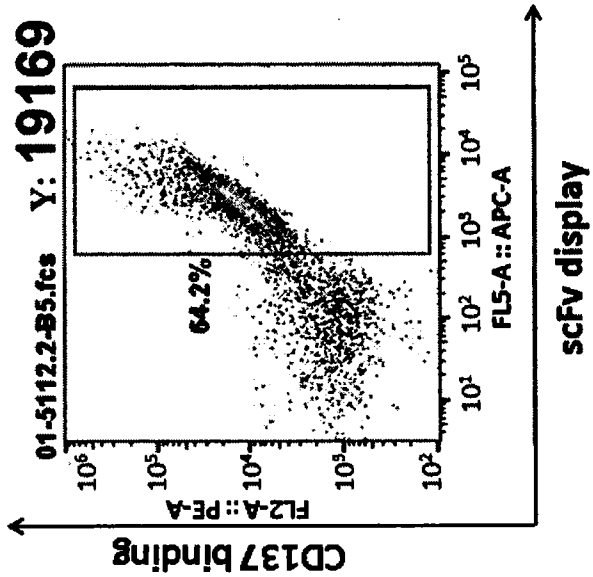

FIG. 20A

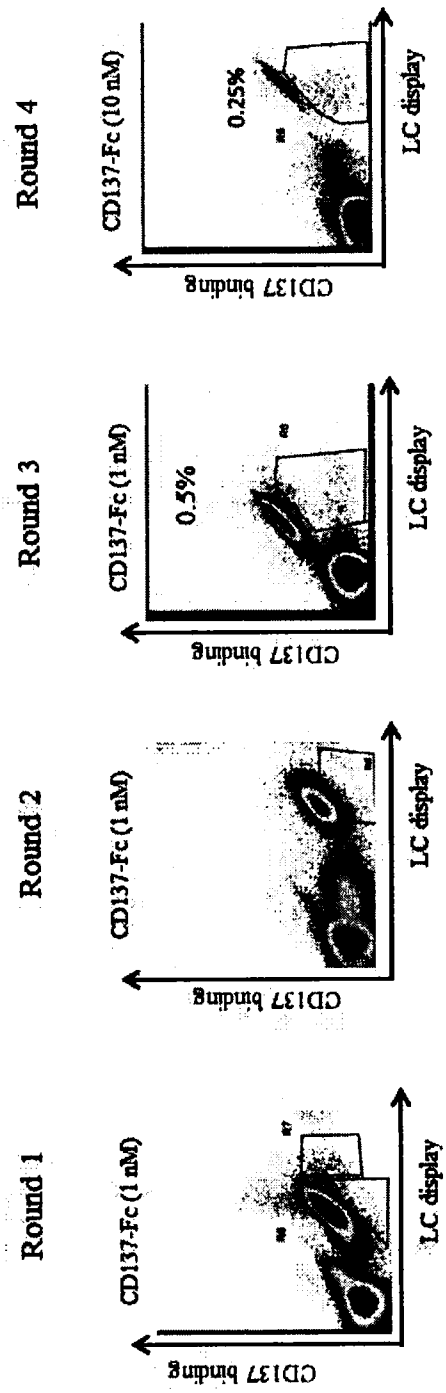
Round 1
CD137-Fc (1 nM)
CD137 binding
LC display
Round 2
CD137-Fc (1 nM)
CD137 binding
LC display
Round 3
CD137-Fc (1 nM)
0.5%
CD137 binding
LC display
Round 4
CD137-Fc (10 nM)
0.25%
CD137 binding
LC display

FIG. 21

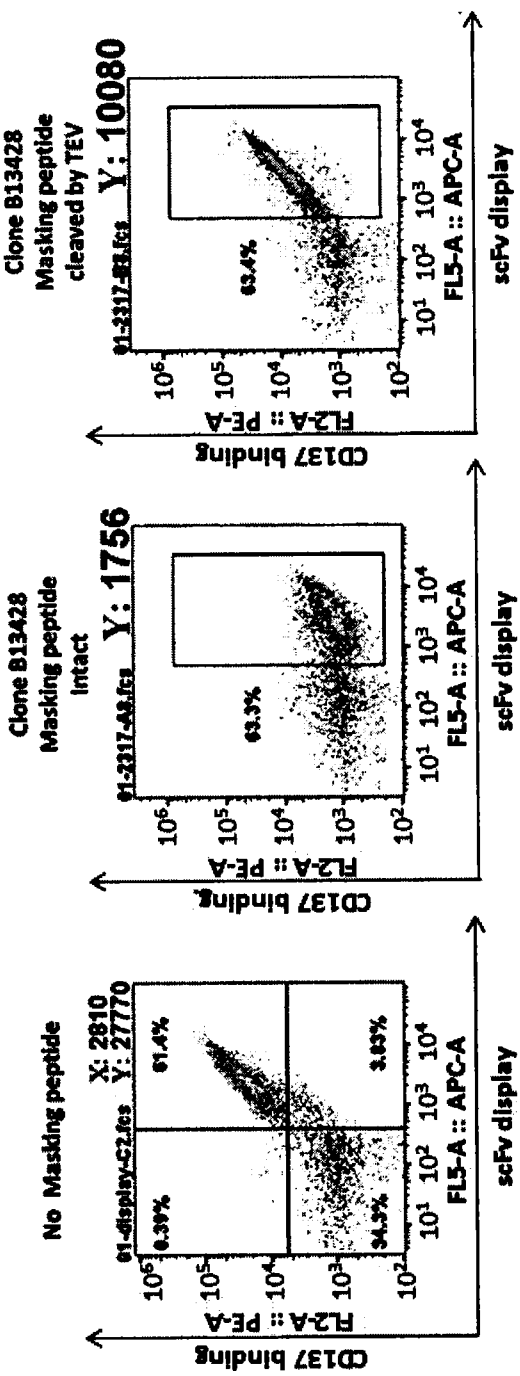

FIG. 22A

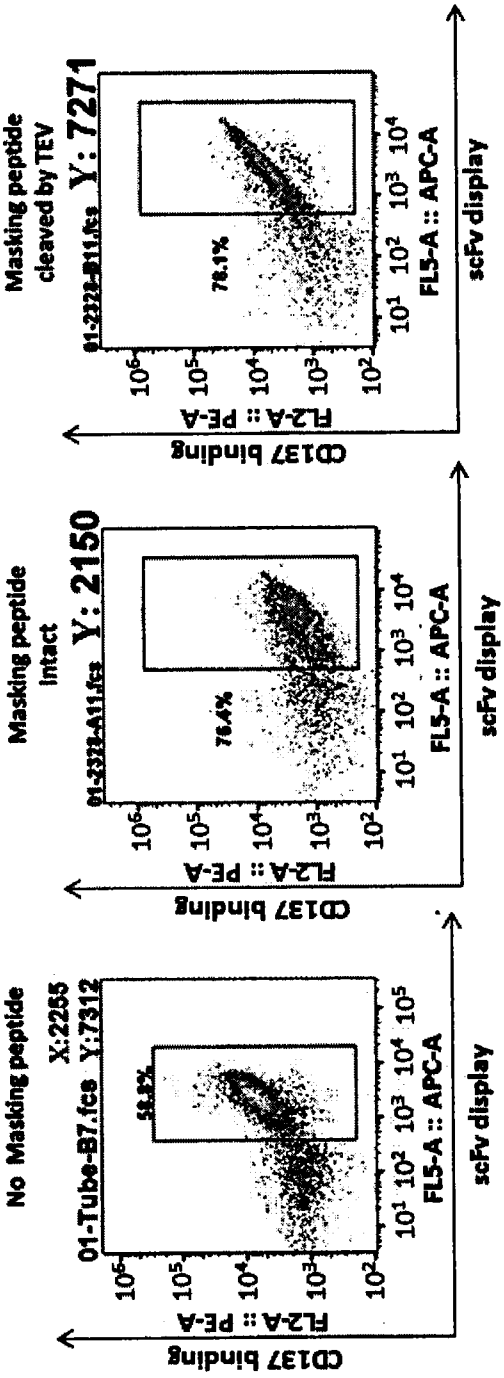

FIG. 22B

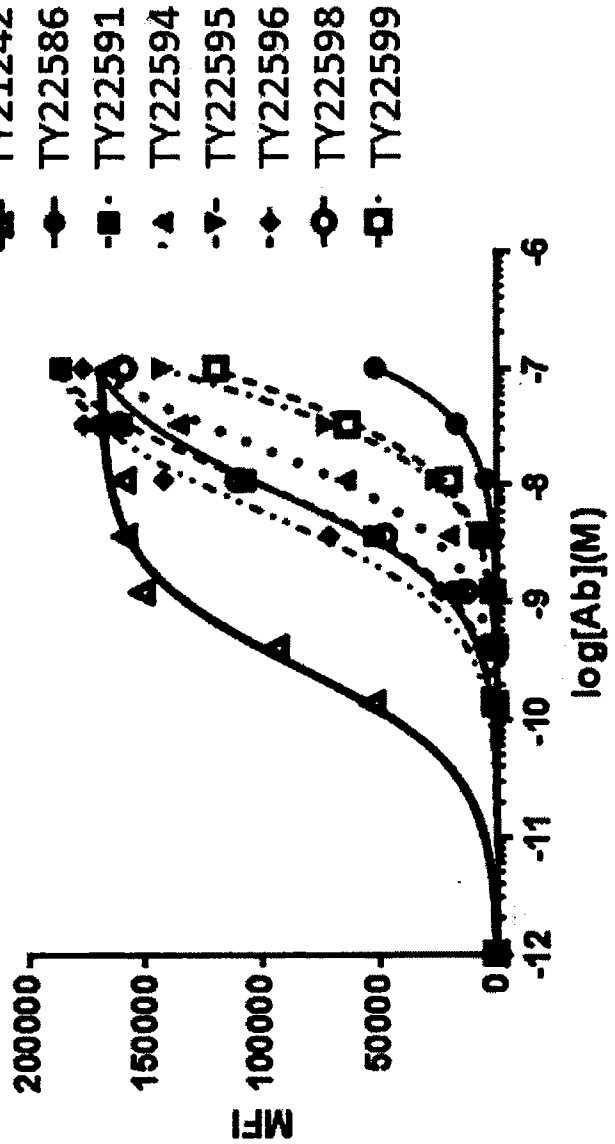
TY21242
TY22586
TY22591
TY22594
TY22595
TY22596
TY22598
TY22599
MFI
200000
150000
100000
50000
0
-12
-11
-10
-9
-8
-7
-6
log[Ab](M)

FIG. 23

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2018/075065

A. CLASSIFICATION OF SUBJECT MATTER

C40B 40/08(2006.01)i; C40B 40/10(2006.01)i; C40B 30/06(2006.01)i; C07K 19/00(2006.01)i; C12N 1/15(2006.01)i; C12N 1/21(2006.01)i; C12N 5/16(2006.01)i; A61P 35/00(2006.01)i

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C40B; C12N; C07K; A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

CNKI, CNABS, CNTXT, DWPI, CPEA, SIPOABS, EPTXT, WOTXT, USTXT, JPTXT, ELSEVIER, EMBASE, ISI web of science and searched terms: antibody, masking, cleavable, activatable, protease, library, peptide, antigen, binding, etc.; GENBANK, EMBL, Retrieving System for Biological Sequence of Chinese Patent and searched sequences: SEQ ID NOs: 1-87.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2010081173 A2 (CYTOMX THERAPEUTICS LLC ET. AL.) 15 July 2010 (2010-07-15) claims 1-234, description, paragraph [0098], examples 5-17, and tables 9, 15 and 42	1-94
X	CN 106163556 A (CYTOMX THERAPEUTICS INC) 23 November 2016 (2016-11-23) claims 1-44, description, paragraphs [0120], [0170]-[175] and [0202]-[204], and tables 1	1-94

☐ Further documents are listed in the continuation of Box C. ☑ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18 October 2018	**06 November 2018**

Name and mailing address of the ISA/CN	Authorized officer
STATE INTELLECTUAL PROPERTY OFFICE OF THE P.R.CHINA **6, Xitucheng Rd., Jimen Bridge, Haidian District, Beijing 100088** **China**	**LI,Chen**
Facsimile No. **(86-10)62019451**	Telephone No. **86-10-62411100**

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2018/075065

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☑ Claims Nos.: **91-94**
because they relate to subject matter not required to be searched by this Authority, namely:

[1] PCT Rule 39.1(iv)----methods for treatment of the human or animal body by surgery or therapy.

[2] The international search report of claims 91-94 is based on the following subject-matter that could reasonably be expected: use of a polypeptide encoded by the library of any one of claims 1-37, or an activatable antibody of any one of claims 64-90 in manufacturing a medicament for treating or delaying progression of cancer.

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/CN2018/075065

Patent document cited in search report	Publication date (day/month/year)	Patent family member(s)	Publication date (day/month/year)
WO 2010081173 A2	15 July 2010	US 10059762 B2	28 August 2018
		AU 2018214147 A1	30 August 2018
		JP 2017200955 A	09 November 2017
		US 2012207756 A1	16 August 2012
		CA 2749339 A1	15 July 2010
		WO 2010081173 A3	04 November 2010
		US 8563269 B2	22 October 2013
		US 8513390 B2	20 August 2013
		CN 102482347 A	30 May 2012
		CN 102482347 B	26 April 2017
		AU 2016225810 B2	24 May 2018
		JP 2012514982 A	05 July 2012
		AU 2010203353 B2	16 June 2016
		US 2013309230 A1	21 November 2013
		EP 2385955 A2	16 November 2011
		JP 5851842 B2	03 February 2016
		CN 106995495 A	01 August 2017
		US 2012149061 A1	14 June 2012
		EP 2385955 A4	13 February 2013
		RU 2011133819 A	20 February 2013
		US 2010189651 A1	29 July 2010
		US 2016228546 A1	11 August 2016
		US 2014024810 A1	23 January 2014
		RU 2636046 C2	17 November 2017
		JP 6271476 B2	31 January 2018
		JP 2015193654 A	05 November 2015
		AU 2010203353 A1	11 August 2011
		BR PI1006141 A2	23 February 2016
		US 2017081397 A1	23 March 2017
		AU 2010203353 A2	11 August 2011
		US 9453078 B2	27 September 2016
		AU 2016225810 A1	22 September 2016
CN 106163556 A	23 November 2016	US 2015087810 A1	26 March 2015
		JP 2016538240 A	08 December 2016
		EP 3049111 A2	03 August 2016
		KR 20160074510 A	28 June 2016
		BR 112016006665 A8	30 January 2018
		IL 244744 D0	21 April 2016
		AU 2014324884 A1	21 April 2016
		MX 2016003957 A	02 February 2017
		CA 2925106 A1	02 April 2015
		WO 2015048329 A3	04 June 2015
		WO 2015048329 A2	02 April 2015
		BR 112016006665 A2	12 September 2017
		RU 2016115542 A	30 October 2017