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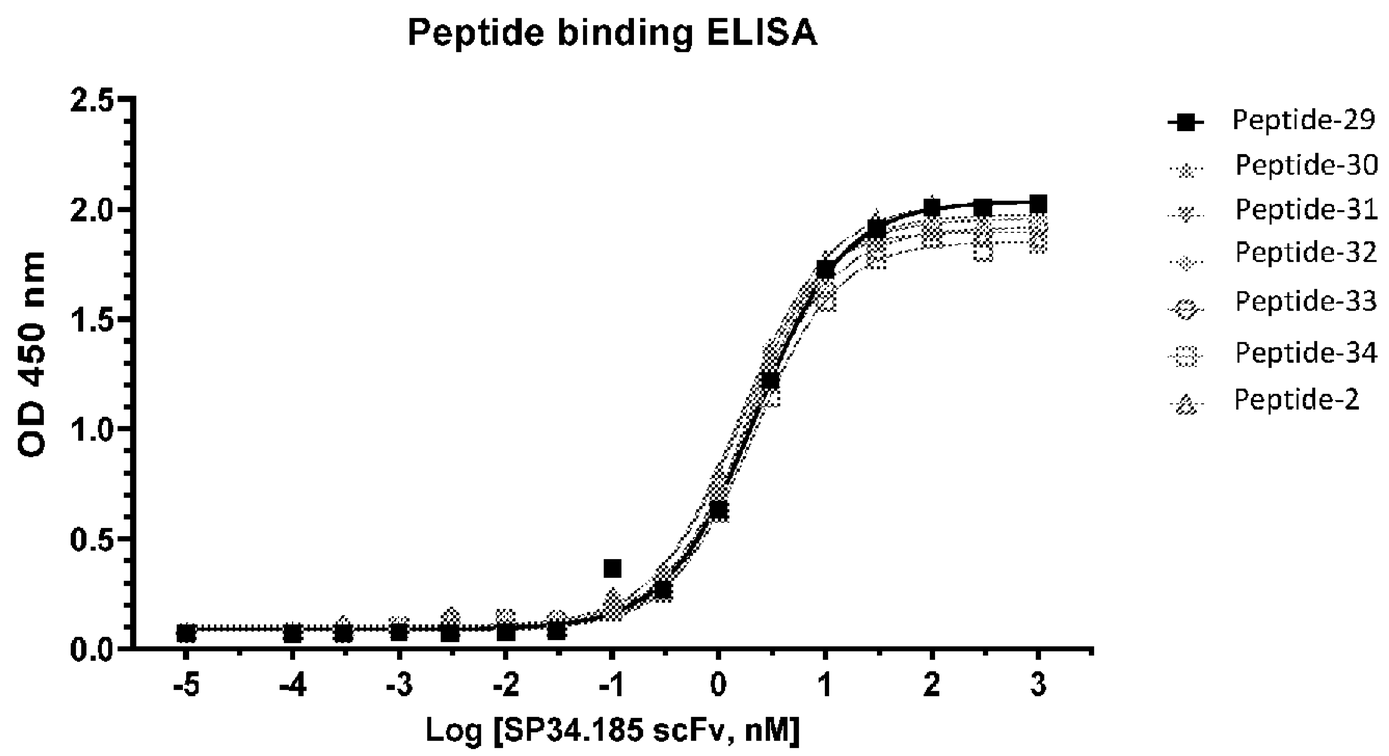


FIG. 5A

(57) Abstract: Disclosed herein are polypeptide and polypeptide complex compositions that comprise a peptide that selectively impairs binding of an anti-CD3 binding domain to CD3 in healthy tissue but not in a disease state.

[Continued on next page]

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PEPTIDE COMPOSITIONS AND METHODS FOR ANTI-CD3 BINDING DOMAINS

CROSS-REFERENCE

[0001] The present application claims the benefit of U.S. Provisional Application No. 63/122,820, filed December 8, 2020, which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on December 2, 2021, is named 52426-732_601_SL.txt and is 280,999 bytes in size.

SUMMARY

[0003] Disclosed herein are polypeptides or polypeptide complexes comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2. In some embodiments, the peptide comprises the amino acid sequence of Peptide-1. In some embodiments, the peptide comprises the amino acid sequence of Peptide-2. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration according to: A_1-L_1-P_1 (Formula I) wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, P_1 is connected N-terminal to the cleavable linker and A_1 is connected C-terminal to the cleavable linker. In some embodiments, P_1 is connected C-terminal to the cleavable linker and A_1 is connected N-terminal to the cleavable linker. In some embodiments, P_1 is bound to A_1 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof. In some embodiments, A_1 is further linked to a tumor antigen binding domain (A_2). In some embodiments, the polypeptide or polypeptide complex is according to Formula Ia: P_2-L_2-A_2-A_1-L_1-P_1 wherein P_2 comprises a peptide that impairs binding of A_2 to a tumor antigen; and L_2 comprises a second cleavable linker that connects A_2 to P_2 and is a substrate for a tumor specific protease. In some embodiments, A_1 comprises an antibody or antibody fragment. In some embodiments, A_1 comprises an antibody or antibody fragment that is human or humanized. In some embodiments, L_1 is bound to N-terminus of the antibody or antibody fragment of A_1. In some embodiments, A_2 is bound to N-terminus of the antibody or antibody fragment of A_1. In some embodiments, L_1 is bound to the C-terminus of the antibody or antibody fragment of A_1. In some embodiments, A_2 is bound to the C-terminus of the antibody or antibody fragment of A_1. In some embodiments, the antibody or antibody fragment of A_1 comprises a single chain variable fragment, a single domain antibody, or a Fab fragment. In some embodiments, A_1 is the single chain variable fragment (scFv). In some embodiments, the scFv

comprises a scFv heavy chain polypeptide and a scFv light chain polypeptide. In some embodiments, A_1 is the single domain antibody. In some embodiments, the antibody or antibody fragment thereof comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody. In some embodiments, A_1 comprises an anti-CD3e single chain variable fragment. In some embodiments, A_1 comprises an anti-CD3e single chain variable fragment that has a KD binding of 1 μM or less to CD3 on CD3 expressing cells. In some embodiments, A_1 comprises a variable light chain and variable heavy chain each of which is capable of specifically binding to human CD3. In some embodiments, A_1 comprises the scFv comprising a scFv heavy chain variable domain and an scFv light chain variable domain comprising complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the scFv heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; and HC-CDR3: SEQ ID NO: 5; and the scFv light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the scFv light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8. In some embodiments, the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease. In some embodiments, the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease and A_1 binds to the effector cell. In some embodiments, the effector cell is a T cell. In some embodiments, A_1 binds to a polypeptide that is part of a TCR-CD3 complex on the effector cell. In some embodiments, the polypeptide that is part of the TCR-CD3 complex is human CD3ε. In some embodiments, A_2 comprises an antibody or antibody fragment. In some embodiments, the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment, a single domain antibody, Fab', or a Fab. In some embodiments, the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody. In some embodiments, the antibody or antibody fragment thereof of A_2 is humanized or human. In some embodiments, A_2 is the Fab or Fab'. In some embodiments, the Fab or Fab' comprises (a) a Fab light chain polypeptide and (b) a Fab heavy chain polypeptide. In some embodiments, A_2 comprises an epidermal growth factor receptor (EGFR) binding domain. In some embodiments, A_2 comprises a carcinoembryonic antigen-related cell adhesion molecule CEACAM5 binding domain. In some embodiments, P_1 is further linked to a half-life extending moiety (H_1). In some embodiments, the half-life extending moiety is a single-domain antibody. In some embodiments, H_1 comprises a polymer. In some embodiments, the polymer is polyethylene glycol (PEG). In some embodiments, H_1 comprises albumin. In some embodiments, H_1 comprises an Fc domain. In some embodiments, the albumin is serum albumin. In some embodiments, the albumin is human serum albumin. In some embodiments, H_1 comprises a polypeptide, a ligand, or a small molecule. In some embodiments, the polypeptide, the ligand or the small molecule binds serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or

CD35/CR1. In some embodiments, the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin. In some embodiments, the circulating immunoglobulin comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD. In some embodiments, the serum protein is albumin. In some embodiments, the polypeptide is an antibody. In some embodiments, the antibody comprises a single domain antibody, a single chain variable fragment, or a Fab. In some embodiments, the single domain antibody comprises a single domain antibody that binds to albumin. In some embodiments, the single domain antibody is a human antibody or humanized antibody. In some embodiments, the single domain antibody is 645gH1gL1. In some embodiments, the single domain antibody is 645dsgH5gL4. In some embodiments, the single domain antibody is 23-13-A01 -sc02. In some embodiments, the single domain antibody is A10m3 or a fragment thereof. In some embodiments, the single domain antibody is DOM7r-31. In some embodiments, the single domain antibody is Alb-1, Alb-8, or Alb-23. In some embodiments, the single domain antibody is 10G or 10GE. In some embodiments, the single domain antibody is SA21. In some embodiments, the polypeptide or polypeptide complex comprises a modified amino acid, a non-natural amino acid, a modified non-natural amino acid, or a combination thereof. In some embodiments, the modified amino acid or modified non-natural amino acid comprises a post-translational modification. In some embodiments, H_1 comprises a linking moiety (L_3) that connects H_1 to P_1. In some embodiments, L_3 is a peptide sequence having at least 5 to no more than 50 amino acids. In some embodiments, L_3 is a peptide sequence having at least 10 to no more than 30 amino acids. In some embodiments, L_3 is a peptide sequence having at least 10 amino acids. In some embodiments, L_3 is a peptide sequence having at least 18 amino acids. In some embodiments, L_3 is a peptide sequence having at least 26 amino acids. In some embodiments, L_3 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1. In some embodiments, L_3 comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)). In some embodiments, the Fab light chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) A_1. In some embodiments, the Fab light chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1. In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1. In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2.In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2. In some embodiments, the Fab

heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2. In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2. In some embodiments, P_2 impairs binding of A_2 to the tumor antigen. In some embodiments, P_2 is bound to A_2 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof. In some embodiments, P_2 is bound to A_2 at or near an antigen binding site.In some embodiments, P_2 has less than 70% sequence homology to the tumor antigen. In some embodiments, P_2 comprises a peptide sequence of at least 10 amino acids in length. In some embodiments, P_2 comprises a peptide sequence of at least 10 amino acids in length and no more than 20 amino acids in length. In some embodiments, P_2 comprises a peptide sequence of at least 16 amino acids in length. In some embodiments, P_2 comprises a peptide sequence of no more than 40 amino acids in length. In some embodiments, P_2 comprises at least two cysteine amino acid residues. In some embodiments, P_2 comprises a cyclic peptide or a linear peptide.In some embodiments, P_2 comprises a cyclic peptide. In some embodiments, P_2 comprises a linear peptide. In some embodiments, L_1 is bound to N-terminus of A_1. In some embodiments, L_1 is bound to C-terminus of A_1. In some embodiments, L_2 is bound to N-terminus of A_2. In some embodiments, L_2 is bound to C-terminus of A_2. In some embodiments, L_1 or L_2 is a peptide sequence having at least 5 to no more than 50 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 10 to no more than 30 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 10 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 18 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 26 amino acids. In some embodiments, L_1 or L_2 has a formula comprising $(G_2S)_n$ (SEQ ID NO: 922), wherein n is an integer from 1 to 3. In some embodiments, L_1 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1. In some embodiments, P_1 becomes unbound from A_1 when L_1 is cleaved by the tumor specific protease thereby exposing A_1 to CD3. In some embodiments, P_2 becomes unbound from A_2 when L_2 is cleaved by the tumor specific protease thereby exposing A_2 to the tumor antigen. In some embodiments, the tumor specific protease is selected from the group consisting of metalloprotease, serine protease, cysteine protease, threonine protease, and aspartic protease. In some embodiments, L_1 or L_2 comprises a urokinase cleavable amino acid sequence, a matriptase cleavable amino acid sequence, a matrix metalloprotease cleavable amino acid sequence, or a legumain cleavable amino acid sequence. In some embodiments, L_1 or L_2 comprises an amino acid sequence selected from the group consisting of GGGGSLSGRSDNHGSSGT (SEQ ID NO: 923), GGGGSSGGSGGSGLSGRSDNHGSSGT (SEQ ID NO: 924), ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), ISSGLLAGRSDNH (SEQ ID NO: 928), LSGRSDNH (SEQ ID NO: 929), ISSGLLSGRSDNP (SEQ ID NO: 930), ISSGLLSGRSDNH (SEQ ID NO: 931), LSGRSDNHSPLGLAGS (SEQ ID NO: 932), SPLGLAGSLSGRSDNH (SEQ ID NO: 933), SPLGLSGRSDNH (SEQ ID NO: 934), LAGRSDNHSPLGLAGS (SEQ ID NO: 935),

LSGRSDNHVPLSLKMG (SEQ ID NO: 936), and LSGRSDNHVPLSLSMG (SEQ ID NO: 937). In some embodiments, L_1 or L_2 comprises an amino acid sequence selected from the group consisting of ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), and ISSGLLAGRSDNH (SEQ ID NO: 928).

[0004] Disclosed herein are pharmaceutical compositions comprising (i) the polypeptides or polypeptide complexes of any one of the previous embodiments; and (ii) a pharmaceutically acceptable excipient.

[0005] Disclosed herein are isolated recombinant nucleic acid molecules encoding the polypeptides or polypeptide complexes of any one of the previous embodiments.

[0006] Disclosed herein are isolated polypeptides or polypeptide complexes according to Formula II: L_{1a}-P_{1a}-H_{1a} wherein: L_{1a} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1a} to an anti-CD3 binding domain that binds to CD3 and; P_{1a} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1a} is uncleaved wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2; and H_{1a} comprises a half-life extending molecule. In some embodiments, the peptide comprises the amino acid sequence of Peptide-1. In some embodiments, the peptide comprises the amino acid sequence of Peptide-2. In some embodiments, H_{1a} comprises a polymer. In some embodiments, the polymer is polyethylene glycol (PEG). In some embodiments, H_{1a} comprises albumin. In some embodiments, H_{1a} comprises an Fc domain. In some embodiments, the albumin is serum albumin. In some embodiments, the albumin is human serum albumin. In some embodiments, H_{1a} comprises a polypeptide, a ligand, or a small molecule. In some embodiments, the polypeptide, the ligand or the small molecule binds a serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1. In some embodiments, the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin. In some embodiments, the circulating immunoglobulin molecule comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD. In some embodiments, the serum protein is albumin. In some embodiments, the polypeptide is an antibody. In some embodiments, the antibody comprises a single domain antibody, a single chain variable fragment or a Fab. In some embodiments, the antibody comprises a single domain antibody that binds to albumin. In some embodiments, the antibody is a human or humanized antibody. In some embodiments, the single domain antibody is 645gH1gL1. In some embodiments, the single domain antibody is 645dsgH5gL4. In some embodiments, the single domain antibody is 23-13-A01 -sc02. In some embodiments, the single domain antibody is A10m3 or a fragment thereof. In some embodiments, the single domain antibody is DOM7r-31. In some embodiments, the single domain antibody is DOM7h-11-15. In some embodiments, the single domain antibody is Alb-1, Alb-8, or Alb-23. In some embodiments, the single domain antibody is 10G or 10GE. In some embodiments, the single domain antibody is SA21. In some embodiments, H_{1a} comprises a

linking moiety (L_{3a}) that connects H_{1a} to P_{1a}. In some embodiments, L_{3a} is a peptide sequence having at least 5 to no more than 50 amino acids.

In some embodiments, L_{3a} is a peptide sequence having at least 10 to no more than 30 amino acids. In some embodiments, L_{3a} is a peptide sequence having at least 10 amino acids. In some embodiments, L_{3a} is a peptide sequence having at least 18 amino acids. In some embodiments, L_{3a} is a peptide sequence having at least 26 amino acids. In some embodiments, L_{3a} has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1. In some embodiments, L_{3a} comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)).

BRIEF DESCRIPTION OF THE DRAWINGS

[0007] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0008] Fig. 1A illustrates Peptide-1 peptide binding data to SP34.185 scFv by ELISA.

[0009] Fig. 1B illustrates Peptide-1 alanine scanning peptides binding data to SP34.185 scFv by ELISA.

[0010] Fig. 1C illustrates Peptide-1 alanine scanning peptides binding data to SP34.185 scFv by ELISA.

[0011] Fig. 1D illustrates Peptide-2 peptide binding data to SP34.185 scFv by ELISA.

[0012] Fig. 1E illustrates Peptide-2 alanine scanning peptides binding data to SP34.185 scFv by ELISA.

[0013] Fig. 1F illustrates Peptide-2 alanine scanning peptides binding data to SP34.185 scFv by ELISA.

[0014] Fig. 2A illustrates Peptide-1 inhibitory data of SP34.185 binding to CD3e.

[0015] Fig. 2B illustrates Peptide-1 alanine scanning peptides inhibitory data of SP34.185 binding to CD3e.

[0016] Fig. 2C illustrates Peptide-1 alanine scanning peptides inhibitory data of SP34.185 binding to CD3e.

[0017] Fig. 2D illustrates Peptide-2 inhibitory data of SP34.185 binding to CD3e.

[0018] Fig. 2E illustrates Peptide-2 alanine scanning peptides inhibitory data of SP34.185 binding to CD3e.

[0019] Fig. 2F illustrates Peptide-2 alanine scanning peptides inhibitory data of SP34.185 binding to CD3e.

[0020] Fig. 3 illustrates titration data for CD3ε binding for several polypeptide complexes of this disclosure.

[0021] Fig. 4 illustrates functional tumor cell killing of PC-1, PC-2, and PC-3.

[0022] Fig. 5A illustrates peptides (Peptide-29 – Peptide-34) peptide binding data to SP34.185 scFv by ELISA. Peptide-2 is used as a positive control.

[0023] Fig. 5B illustrates peptides (Peptide-35 – Peptide-40) peptide binding data to SP34.185 scFv by ELISA. Peptide-2 is used as a positive control.

[0024] Fig. 6A illustrates peptides (Peptide-29 – Peptide-34) inhibiting binding of SP34.185 scFv to CD3 by ELISA. Peptide-2 is used as a positive control.

[0025] **Fig. 6B** illustrates peptides (Peptide-35 – Peptide-40) inhibiting binding of SP34.185 scFv to CD3 by ELISA. Peptide-2 is used as a positive control.

[0026] **Fig. 7** illustrates the core sequence motif of Peptide-2 generated by WebLogo 3.

DETAILED DESCRIPTION

[0027] Protein-based therapies such as antibodies and bispecific or multispecific antibodies, such as T cell engagers, have proven effective for a variety diseases and disorders. As with any therapy, there is a need to minimize off-target effects of the protein-based therapy in healthy tissue while maintaining activity of the protein-based therapy in disease tissue. One such strategy is to create an inactive form of the protein-based therapy in which a necessary binding site on the protein-based therapy is blocked with a peptide linked to the protein-based therapy, thereby preventing the protein-based therapy from binding or interacting with its cognate receptor or target antigen when in healthy tissue. For activating the protein-based therapy in the desired disease-state microenvironment, the peptide is linked to the protein-based therapy with a linker that is cleavable by a protease that is specific to the disease-state microenvironment. The peptide is then released from the protein-based therapy when in the disease-state microenvironment.

[0028] Accordingly, disclosed herein, are peptides that impair binding of anti-CD3 binding domains to cluster of differentiation 3 (CD3). The peptides as disclosed herein can be applied to a variety of antibody formats that bind to anti-CD3 to reduce the off-target effects of the antibodies in healthy tissue, while maintaining activity of the anti-CD3 antibody in a disease tissue. The peptides are attached to the anti-CD3 binding domains via protease cleavable linkers. In some embodiments, the antibodies described herein are used in a method of treating cancer. In some instances, the cancer is a solid tumor cancer. In some embodiments, the cancer is lung, breast (e.g. HER2+; ER/PR+; TNBC), cervical, ovarian, colorectal, pancreatic or gastric.

[0029] Disclosed herein are isolated polypeptides or polypeptide complexes comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2.

[0030] Disclosed herein are isolated polypeptides or polypeptide complexes comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2 and 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to an amino acid sequence selected from SEQ ID NOs: 1-2 and 19-55. In some embodiments, the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0031] Disclosed herein are isolated polypeptides or polypeptide complexes comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}- Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L and S. In some embodiments, Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P. In some embodiments, Z_1 is selected from D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; and Z_{14} is selected from D, Y, and N. In some embodiments, the peptide comprises an amino acid sequence of **Table 17**. In some embodiments, the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0032] Disclosed herein are isolated polypeptides or polypeptide complexes comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}-U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; and U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S. In some embodiments, U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E, D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; and U_{14} is selected from D, Y, N, F, I, M, and P. In some embodiments, U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; and U_{14} is selected from D, Y, M, and N. In some embodiments, the peptide comprises an amino acid sequence of

Table 17. In some embodiments, the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0033] Disclosed herein, are methods of treating cancer comprising administering to a subject in need thereof an isolated polypeptide or polypeptide complex comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2.

[0034] Disclosed herein, are methods of treating cancer comprising administering to a subject in need thereof an isolated polypeptide or polypeptide complex comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to amino acid sequences of SEQ ID NOs: 1-2, and 19-55. In some embodiments, the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0035] Disclosed herein, are methods of treating cancer comprising administering to a subject in need thereof an isolated polypeptide or polypeptide complex comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}- Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L and S. In some embodiments, Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P. In some embodiments, Z_1 is selected from D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; and Z_{14} is selected from D, Y, and N. In some embodiments, the peptide comprises an amino acid sequence of **Table 17**. In some embodiments, the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55. In some embodiments, the peptide comprises the amino acid

sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0036] Disclosed herein, are methods of treating cancer comprising administering to a subject in need thereof an isolated polypeptide or polypeptide complex comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}- U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; and U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S. In some embodiments, U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E, D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; and U_{14} is selected from D, Y, N, F, I, M, and P. In some embodiments, U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; and U_{14} is selected from D, Y, M, and N. In some embodiments, the peptide comprises an amino acid sequence of **Table 17**. In some embodiments, the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0037] In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration according to: **A_1-L_1-P_1 (Formula I)** wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration according to: A_1-L_1-P_1 (Formula I) wherein A_1 is the anti-CD3 binding domain; L_1 is a cleavable linker that is a substrate for a tumor specific protease; P_1 is the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration comprising Formula I: A_1-L_1-P_1 (Formula I) wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration comprising Formula I: A_1-L_1-P_1 (Formula I) wherein A_1 is the anti-CD3 binding domain; L_1 is a cleavable linker that is a substrate for a tumor specific protease; $P_1$is the peptide that impairs binding of the anti-CD3 binding domain to CD3.

In some embodiments, A_1 is further linked to a tumor antigen binding domain (A_2). In some embodiments, the polypeptide or polypeptide complex is according to **Formula Ia: P_2-L_2-A_2-A_1-L_1-P_1 (Formula Ia)** wherein P_2 comprises a peptide that impairs binding of A_2 to a tumor antigen; and L_2 comprises a second cleavable linker that connects A_2 to P_2 and is a substrate for a tumor specific protease.

[0038] In some embodiments, P_1 is connected N-terminal to the cleavable linker and A_1 is connected C-terminal to the cleavable linker. In some embodiments, P_1 is connected C-terminal to the cleavable linker and A_1 is connected N-terminal to the cleavable linker. In some embodiments, P_1 is bound to A_1 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof.

[0039] Disclosed herein are isolated polypeptides or polypeptide complexes according to **Formula II: L_{1a}-P_{1a}-H_{1a} (Formula II)** wherein: L_{1a} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1a} to an anti-CD3 binding domain that binds to CD3 and; P_{1a} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1a} is uncleaved wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to amino acid sequences of SEQ ID NOs: 1-2, 19-55; and H_{1a} comprises a half-life extending molecule. In some embodiments, P_{1a} comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55. In some embodiments, P_{1a} comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, P_{1a} comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, P_{1a} comprises the amino acid sequence of SEQ ID NO: 54.

[0040] Disclosed herein are isolated polypeptides or polypeptide complexes according to **Formula III**: L_{1b}-P_{1b}-H_{1b} wherein: L_{1b} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1b} to an anti-CD3 binding domain that binds to CD3 and; P_{1b} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1b} is uncleaved wherein the peptide comprises the amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}- Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L and S; and H_{1b} comprises a half-life extending molecule. In some embodiments, Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P. In some embodiments, Z_1 is selected D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; Z_{14} is selected from D, Y, and N. In some embodiments, P_{1b}

comprises an amino acid sequence of **Table 17.** In some embodiments, P_{1b} comprises an amino acid sequences according to any one of SEQ ID NOs: 44-55. In some embodiments, P_{1b} comprises the amino acid sequences according to SEQ ID NO: 2. In some embodiments, P_{1b} comprises the amino acid sequences according to SEQ ID NO: 54.

[0041] Disclosed herein are isolated polypeptide or polypeptide complex according to **Formula IV**: L_{1c}-P_{1c}-H_{1c} wherein: L_{1c} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1c} to an anti-CD3 binding domain that binds to CD3 and; P_{1c} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1b} is uncleaved wherein the peptide comprises the amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}- U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S; and H_{1c} comprises a half-life extending molecule. In some embodiments, U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E, D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; U_{14} is selected from D, Y, N, F, I, M, and P. In some embodiments, U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; U_{14} is selected from D, Y, M, and N. In some embodiments, P_{1c} comprises comprises an amino acid sequence of **Table 17.** In some embodiments, P_{1c} comprises an amino acid sequences according to any one of SEQ ID NOs: 44-55. In some embodiments, P_{1c} comprises the amino acid sequences according to SEQ ID NO: 2. In some embodiments, P_{1c} comprises the amino acid sequences according to SEQ ID NO: 54.

[0042] In some embodiments, the peptide (P_1, P_{1a}, P_{1b}, or P_{1c}) comprises the amino acid sequence of Peptide-1.

[0043] In some embodiments, the peptide (P_1, P_{1a}, P_{1b}, or P_{1c}) comprises the amino acid sequence of Peptide-2.

[0044] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid substitution relative to Peptide-1. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 2 amino acid substitution relative to Peptide-1. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid substitution relative to Peptide-1.

[0045] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid substitution relative to Peptide-2. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c})

comprises an amino acid sequence that has 2 amino acid substitutions relative to Peptide-2. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid substitutions relative to Peptide-2.

[0046] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid deletion relative to Peptide-1. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 2 amino acid deletions relative to Peptide-1. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid deletions relative to Peptide-1.

[0047] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid deletions relative to Peptide-2. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 2 amino acid deletions relative to Peptide-2. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid deletions relative to Peptide-2.

[0048] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid additions relative to Peptide-1. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 2 amino acid additions relative to Peptide-1. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid additions relative to Peptide-1.

[0049] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid addition relative to Peptide-2. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 2 amino acid additions relative to Peptide-2. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid additions relative to Peptide-2.

[0050] In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 1 amino acid addition relative to Peptide-39. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 2 amino acid additions relative to Peptide-39. In some embodiments, the peptide (P_1, P_{1a}, P_{1b} or P_{1c}) comprises an amino acid sequence that has 3 amino acid additions relative to Peptide-39.

[0051] In some embodiments, P_1 is bound to A_1 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof.

[0052] In some embodiments, P_{1a} is bound to the anti-CD3 binding domain through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof when L_{1a} is uncleaved.

[0053] In some embodiments, P_1, P_{1a}, P_{1b} or P_{1c} comprise a modified amino acid or non-natural amino acid, or a modified non-natural amino acid, or a combination thereof. In some embodiments, the modified amino acid or a modified non-natural amino acid comprises a post-translational modification. In some embodiments P_1, P_{1a}, P_{1b} or P_{1c} comprises a modification including, but not limited to acetylation, acylation,

ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. Modifications are made anywhere to P_1, P_{1a}, P_{1b} or P_{1c} including the peptide backbone, the amino acid side chains, and the terminus.

Table 1. Amino acid sequence of Peptide-1 and Peptide-2

Construct Description	Amino Acid Sequence (N to C)	SEQ ID NO:
Peptide-1	GSQCLGPEWEVCPY	1
Peptide-2	VYCGPEFDESVGCM	2

Anti-CD3 binding domain (A_1)

[0054] In some embodiments, A_1 comprises an antibody or antibody fragment. In some embodiments, A_1 comprises an antibody or antibody fragment that is human or humanized. In some embodiments, L_1 is bound to N-terminus of the antibody or antibody fragment of A_1. In some embodiments, A_2 is bound to N-terminus of the antibody or antibody fragment of A_1. In some embodiments, L_1 is bound to the C-terminus of the antibody or antibody fragment of A_1. In some embodiments, A_2 is bound to the C-terminus of the antibody or antibody fragment of A_1. In some embodiments, the antibody or antibody fragment comprises a single chain variable fragment, a single domain antibody, or a Fab fragment. In some embodiments, A_1 is the single chain variable fragment (scFv). In some embodiments, the scFv comprises a scFv heavy chain polypeptide and a scFv light chain polypeptide. In some embodiments, A_1 is the single domain antibody. In some embodiments, the antibody or antibody fragment thereof comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody.

[0055] In some embodiments, the first target antigen is CD3. In some embodiments, A_1 comprises an anti-CD3e single chain variable fragment. In some embodiments, A_1 comprises an anti-CD3e single chain variable fragment that has a KD binding of 1 μM or less to CD3 on CD3 expressing cells. In some embodiments, A_1 comprises a variable light chain and variable heavy chain each of which is capable of specifically binding to human CD3. In some embodiments, A_1 comprises complementary determining regions (CDRs) from sp34 scFv. In some embodiments, the scFv comprises a scFv heavy chain variable domain and an scFv light chain variable domain. In some embodiments, the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease. In some embodiments, the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease and A_1 binds to the effector cell. In some embodiments, the effector

cell is a T cell. In some embodiments, A_1 binds to a polypeptide that is part of a TCR-CD3 complex on the effector cell. In some embodiments, the polypeptide that is part of the TCR-CD3 complex is human CD3ε.

[0056] In some embodiments, the scFv heavy chain variable domain comprises complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the scFv heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5, and wherein the CDRs comprise from 0-2 amino acid modifications in at least one of the HC-CDR1, HC-CDR2, or HC-CDR3.

[0057] In some embodiments, the scFv light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the scFv light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8, and wherein the CDRs comprise from 0-2 amino acid modifications in at least one of the LC-CDR1, LC-CDR2, or LC-CDR3.

[0058] In some embodiments, the scFv heavy chain variable domain comprises complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the scFv heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5; and the scFv light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the scFv light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8.

[0059] In some embodiments, A_1 comprises complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of A_1 comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5, and wherein the CDRs comprise from 0-2 amino acid modifications in at least one of the HC-CDR1, HC-CDR2, or HC-CDR3.

[0060] In some embodiments, A_1 comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of A_1 comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8, and wherein the CDRs comprise from 0-2 amino acid modifications in at least one of the LC-CDR1, LC-CDR2, or LC-CDR3.

[0061] In some embodiments, A_1 comprises complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of A_1 comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5; and A_1 comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of A_1 comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8.

[0062] In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 70% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 80% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv

heavy chain variable domain comprises an amino acid sequence that has at least 85% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 90% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 91% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 92% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 93% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 94% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 95% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence that has at least 99% sequence identity to the amino acid sequence according to SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence according to SEQ ID NO: 9.

[0063] In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 50 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 50 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 60 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 60 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 70 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 70 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 80 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 80 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 90 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 90 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 100 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 100 consecutive amino acid residues of SEQ ID NO: v. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 105 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 105 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 110 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 110 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid

sequence of at least 115 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 115 consecutive amino acid residues of SEQ ID NO: 9. In some embodiments, the scFv heavy chain variable domain comprises an amino acid sequence of at least 120 consecutive amino acid residues of SEQ ID NO: 9, and has at least 95% sequence identity to the at least 120 consecutive amino acid residues of SEQ ID NO: 9.

Table 2. Exemplary amino acid sequence of Anti-CD3 binding domain (A_1) (CDRs determined by IMGT definition)

Construct Description	Amino Acid Sequence (N to C)	SEQ ID NO:
CD3: HC: CDR1	GFTFNKYA	3
CD3: HC: CDR2	IRSKYNNYAT	4
CD3: HC: CDR3	VRHGNFGNSYISYWAY	5
CD3: LC: CDR1	TGAVTSGNY	6
CD3: LC: CDR2	GTK	7
CD3: LC: CDR3	VLWYSNRWV	8
Anti-CD3 SP34.185 scFv	EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNK** **YA**MNWVRQAPGKGLEWVAR**IRSKYNNYAT** YYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYC**VRHGNFGNSYISYWAY**WGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSS**TGAVTSGNY**PNWVQQKP GQAPRGLIG**GTK**FLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGT KLTVL	9

Tumor antigen binding domain (A_2)

[0064] In some embodiments, A_2 comprises an antibody or antibody fragment. In some embodiments, the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment, a single domain antibody, Fab', or a Fab. In some embodiments, the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody. In some embodiments, the antibody or antibody fragment thereof of A_2 is humanized or human. In some embodiments, A_2 is the Fab or Fab'. In some embodiments, the Fab or Fab' comprises (a) a Fab light chain polypeptide and (b) a Fab heavy chain polypeptide. In some embodiments, the second target antigen comprises a tumor antigen. In some embodiments, the antibody or antibody fragment thereof comprises an epidermal growth factor receptor (EGFR) binding domain. In some embodiments, the antibody or antibody fragment thereof comprises a mesothelin binding domain. In some embodiments, A_2 comprises an amino acid sequence disclosed in **Table 3** or a sequence substantially identical thereto (e.g., a sequence that has at least 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence disclosed in Table 3).

Table 3. Exemplary amino acid sequences of Anti-EGFR Fab

Construct Description	Amino Acid Sequence (N to C)	SEQ ID NO:
Anti-EGFR Fab light chain	DILLTQSPVILSVSPGERVSFSCRAS**QSIGTN**IH WYQQRTNGSPRLLIK**YAS**ESISGIPSRFSGSGS GTDFTLSINSVESEDIADYYC**QQNNNWPTT**F GAGTKLELKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC	10
Anti-EGFR Fab heavy chain	QVQLKQSGPGLVQPSQSLSITCTVS**GFSLTNY G**VHWVRQSPGKGLEWLGV**IWSGGNT**DYNT PFTSRLSINKDNSKSQVFFKMNSLQSQDTAIY YC**ARALTYYDYEFAY**WGQGTLVTVSAASTK GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEP KSC	11

Half-life extending molecule (H_1, H_{1a}, H_{1b}, H_{1c})

[0065] In some embodiments, P_1 is further linked to a half-life extending moiety (H_1).

[0066] In some embodiments, the half-life extending moiety is a single-domain antibody.

[0067] In some embodiments, H_1 does not block P_1 binding to CD3. In some embodiments, H_{1a} does not block the anti-CD3 binding domain from binding to the CD3. In some embodiments, H_{1b} does not block the anti-CD3 binding domain from binding to the CD3. In some embodiments, H_{1c} does not block the anti-CD3 binding domain from binding to the CD3. In some embodiments, the half-life extending molecule (H_1, H_{1a}, H_{1b}, or H_{1c}) does not have binding affinity to CD3. In some embodiments, the half-life extending molecule (H_1, H_{1a}, H_{1b}, or H_{1c}) does not have binding affinity to CD3. In some embodiments, the half-life extending molecule (H_1, H_{1a}, H_{1b}, or H_{1c}) does not shield the anti-CD3 binding domain from CD3.

[0068] In some embodiments, H_1, H_{1a}, H_{1b}, or H_{1c} comprise an amino acid sequence that has repetitive sequence motifs. In some embodiments, H_1, H_{1a}, H_{1b}, or H_{1c} comprises an amino acid sequence that has highly ordered secondary structure. "Highly ordered secondary structure," as used in this context, means that at least about 50%, or about 70%, or about 80%, or about 90%, of amino acid residues of H_1 or H_{1a} contribute to secondary structure, as measured or determined by means, including, but not limited to, spectrophotometry (e.g. by circular dichroism spectroscopy in the "far-UV" spectral region (190-250 nm), and computer programs or algorithms, such as the Chou-Fasman algorithm and the Garnier-Osguthorpe-Robson ("GOR") algorithm.

[0069] In some embodiments, H_1, H_{1a}, H_{1b}, or H_{1c} comprises a polymer. In some embodiments, the polymer is polyethylene glycol (PEG). In some embodiments, H_1 or H_{1a} comprises albumin. In some embodiments,

H_1 or H_{1a} comprises a Fc domain. In some embodiments, the albumin is serum albumin. In some embodiments, the albumin is human serum albumin. In some embodiments, H_1, H_{1a}, H_{1b}, or H_{1c} comprises a polypeptide, a ligand, or a small molecule. In some embodiments, the polypeptide, the ligand or the small molecule binds serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1. In some embodiments, the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin. In some embodiments, the circulating immunoglobulin molecule comprises IgGl, IgG2, IgG3, IgG4, sIgA, IgM or IgD. In some embodiments, the serum protein is albumin. In some embodiments, the polypeptide is an antibody. In some embodiments, the antibody comprises a single domain antibody, a single chain variable fragment or a Fab. In some embodiments, the antibody comprises a single domain antibody. In some embodiments, the antibody comprises a single domain antibody that binds to albumin. In some embodiments, the antibody comprises a single domain antibody that binds to human serum albumin. In some embodiments, the antibody is a human or humanized antibody. In some embodiments, the antibody is selected from the group consisting of 645gH1gL1, 645dsgH5gL4, 23-13-A01 -sc02, A10m3 or a fragment thereof, DOM7r-31, DOM7h-11-15, Alb-1, Alb-8, Alb-23, 10G, 10GE, and SA21.

[0070] In some embodiments, H_1 comprises a single domain antibody. In some embodiments, H_1 comprises a single domain antibody that binds to albumin. In some embodiments, H_1 comprises a single domain antibody that binds to human serum albumin. In some embodiments, H_{1a} comprises a single domain antibody. In some embodiments, H_{1a} comprises a single domain antibody that binds to albumin. In some embodiments, H_{1a} comprises a single domain antibody that binds to human serum albumin. In some embodiments, H_{1b} comprises a single domain antibody. In some embodiments, H_{1b} comprises a single domain antibody that binds to albumin. In some embodiments, H_{1b} comprises a single domain antibody that binds to human serum albumin. In some embodiments, H_{1c} comprises a single domain antibody. In some embodiments, H_{1c} comprises a single domain antibody that binds to albumin. In some embodiments, H_{1c} comprises a single domain antibody that binds to human serum albumin.

[0071] In some embodiments, H_1, H_{1a}, H_{1b}, or H_{1c} comprise a modified amino acid or non-natural amino acid, or a modified non-natural amino acid, or a combination thereof. In some embodiments, the modified amino acid or a modified non-natural amino acid comprises a post-translational modification. In some embodiments H_1, H_{1a}, H_{1b}, or H_{1c} comprise a modification including, but not limited to acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. Modifications are made anywhere to H_1, H_{1a}, H_{1b}, or H_{1c} including the peptide backbone, the

amino acid side chains, and the terminus. . In some embodiments, H_1, H_{1a}, H_{1b}, or H_{1c} comprises an amino acid sequence disclosed in **Table 4** or a sequence substantially identical thereto (e.g., a sequence that has at least 90%, 95%, 96%, 97%, 98%, or 99% sequence identity to an amino acid sequence disclosed in Table 4).

Table 4. Exemplary amino acid sequence of half-life extending molecule (H_1 , H_{1a}, H_{1b}, H_{1c})

Construct Description	Amino Acid Sequence (N to C)	SEQ ID NO:
10G single domain antibody	EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSK** **FG**MSWVRQAPGKGLEWVSS**ISGSGRDT**LYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYC**TIGGSLSV**SSQGTLVTVSS	12

Peptide (P_2)

[0072] In some embodiments, P_2 impairs binding of A_2 to the tumor antigen. In some embodiments, P_2 is bound to A_2 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof. In some embodiments, P_2 is bound to A_2 at or near an antigen binding site. In some embodiments, P_2 has less than 70% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 75% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 80% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 85% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 90% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 95% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 98% sequence homology to the tumor antigen. In some embodiments, P_2 has less than 99% sequence homology to the tumor antigen.

[0073] In some embodiments, P_2 comprises a peptide sequence of at least 10 amino acids in length. In some embodiments, P_2 comprises a peptide sequence of at least 10 amino acids in length and no more than 20 amino acids in length. In some embodiments, P_2 comprises a peptide sequence of at least 16 amino acids in length. In some embodiments, P_2 comprises a peptide sequence of no more than 40 amino acids in length. In some embodiments, P_2 comprises at least two cysteine amino acid residues. In some embodiments, P_2 comprises a cyclic peptide or a linear peptide. In some embodiments, P_2 comprises a cyclic peptide.In some embodiments, P_2 comprises a linear peptide.

[0074] In some embodiments, P_2 comprise a modified amino acid or non-natural amino acid, or a modified non-natural amino acid, or a combination thereof. In some embodiments, the modified amino acid or a modified non-natural amino acid comprises a post-translational modification. In some embodiments P_2 comprise a modification including, but not limited to acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation,

glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. Modifications are made anywhere to P_2 including the peptide backbone, the amino acid side chains, and the terminus.

[0075] In some embodiments, P_2 does not comprise albumin or an albumin fragment. In some embodiments, P_2 does not comprise an albumin binding domain.

Cleavable Linker (L_1 or L_2)

[0076] In some embodiments, L_1 or L_2 is a peptide sequence having at least 5 to no more than 50 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 10 to no more than 30 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 10 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 18 amino acids. In some embodiments, L_1 or L_2 is a peptide sequence having at least 26 amino acids.

[0077] In some embodiments, L_1 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1. In some embodiments, L_1 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of 1. In some embodiments, L_1 has a formula selected from the group consisting of $(G_2S)_n$ (SEQ ID NO: 922), $(GS)_n$ (SEQ ID NO: 938), $(GSGGS)_n$ (SEQ ID NO: 939), $(GGGS)_n$ (SEQ ID NO: 940), $(GGGGS)_n$ (SEQ ID NO: 941), and $(GSSGGS)_n$ (SEQ ID NO: 942), wherein n is an integer from 1 to 3.

[0078] In some embodiments, L_1 has a formula of $(G_2S)_n$, wherein n is an integer of least 1. In some embodiments, L_1 has a formula of $(GS)_n$, wherein n is an integer of least 1. In some embodiments, L_1 has a formula of $(GSGGS)_n$ (SEQ ID NO: 917), wherein n is an integer of least 1. In some embodiments, L_1 has a formula of $(GGGS)_n$ (SEQ ID NO: 918), wherein n is an integer of least 1. In some embodiments, L_1 has a formula of $(GGGGS)_n$ (SEQ ID NO: 919), wherein n is an integer of least 1. In some embodiments, L_1 has a formula of $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of least 1.

[0079] In some embodiments, L_1 has a formula of $(G_2S)_n$, wherein n is an integer of 1. In some embodiments, L_1 has a formula of $(GS)_n$, wherein n is an integer of 1. In some embodiments, L_1 has a formula of $(GSGGS)_n$ (SEQ ID NO: 917), wherein n is an integer of 1. In some embodiments, L_1 has a formula of $(GGGS)_n$ (SEQ ID NO: 918), wherein n is an integer of 1. In some embodiments, L_1 has a formula of $(GGGGS)_n$ (SEQ ID NO: 919), wherein n is an integer of 1. In some embodiments, L_1 has a formula of $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of 1.

[0080] In some embodiments, L_1 has a formula of $(G_2S)_n$ (SEQ ID NO: 922), wherein n is an integer from 1 to 3. In some embodiments, L_1 has a formula of $(GS)_n$ (SEQ ID NO: 938), wherein n is an integer from 1 to 3. In some embodiments, L_1 has a formula of $(GSGGS)_n$ (SEQ ID NO: 939), wherein n is an integer from 1 to 3. In some embodiments, L_1 has a formula of $(GGGS)_n$ (SEQ ID NO: 940), wherein n is an integer from 1 to 3. In some embodiments, L_1 has a formula of $(GGGGS)_n$ (SEQ ID NO: 941), wherein n is an integer from

1 to 3. In some embodiments, L_1 has a formula of $(GSSGGS)_n$ (SEQ ID NO: 942), wherein n is an integer from 1 to 3.

[0081] In some embodiments, L_1 is a substrate for a tumor specific protease. In some embodiments, the tumor specific protease is selected from the group consisting of metalloprotease, serine protease, cysteine protease, threonine protease, and aspartic protease. In some embodiments, L_1 comprises a urokinase cleavable amino acid sequence, a matriptase cleavable amino acid sequence, a matrix metalloprotease cleavable amino acid sequence, or a legumain cleavable amino acid sequence. In some embodiments, L_1 comprises an amino acid sequence selected from the group consisting of GGGGSLSGRSDNHGSSGT (SEQ ID NO: 923), GGGGSSGGSGGSGLSGRSDNHGSSGT (SEQ ID NO: 924), ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), ISSGLLAGRSDNH (SEQ ID NO: 928), LSGRSDNH (SEQ ID NO: 929), ISSGLLSGRSDNP (SEQ ID NO: 930), ISSGLLSGRSDNH (SEQ ID NO: 931), LSGRSDNHSPLGLAGS (SEQ ID NO: 932), SPLGLAGSLSGRSDNH (SEQ ID NO: 933), SPLGLSGRSDNH (SEQ ID NO: 934), LAGRSDNHSPLGLAGS (SEQ ID NO: 935), LSGRSDNHVPLSLKMG (SEQ ID NO: 936), and LSGRSDNHVPLSLSMG (SEQ ID NO: 937). In some embodiments, L_1 comprises an amino acid sequence selected from the group consisting of ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), and ISSGLLAGRSDNH (SEQ ID NO: 928).

[0082] In some embodiments, L_2 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1. In some embodiments, L_2 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of 1. In some embodiments, L_2 has a formula selected from the group consisting of $(G_2S)_n$ (SEQ ID NO: 922), $(GS)_n$ (SEQ ID NO: 938), $(GSGGS)_n$ (SEQ ID NO: 939), $(GGGS)_n$ (SEQ ID NO: 940), $(GGGGS)_n$ (SEQ ID NO: 941), and $(GSSGGS)_n$ (SEQ ID NO: 942), wherein n is an integer from 1 to 3.

[0083] In some embodiments, L_2 has a formula of $(G_2S)_n$, wherein n is an integer of least 1. In some embodiments, L_2 has a formula of $(GS)_n$, wherein n is an integer of least 1. In some embodiments, L_2 has a formula of $(GSGGS)_n$ (SEQ ID NO: 917), wherein n is an integer of least 1. In some embodiments, L_2 has a formula of $(GGGS)_n$ (SEQ ID NO: 918), wherein n is an integer of least 1. In some embodiments, L_2 has a formula of $(GGGGS)_n$ (SEQ ID NO: 919), wherein n is an integer of least 1. In some embodiments, L_2 has a formula of $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of least 1.

[0084] In some embodiments, L_2 has a formula of $(G_2S)_n$, wherein n is an integer of 1. In some embodiments, L_2 has a formula of $(GS)_n$, wherein n is an integer of 1. In some embodiments, L_2 has a formula of $(GSGGS)_n$ (SEQ ID NO: 917), wherein n is an integer of 1. In some embodiments, L_2 has a formula of $(GGGS)_n$ (SEQ ID NO: 918), wherein n is an integer of 1. In some embodiments, L_2 has a formula of $(GGGGS)_n$ (SEQ ID NO: 919), wherein n is an integer of 1. In some embodiments, L_2 has a formula of $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of 1.

[0085] In some embodiments, L_2 has a formula of $(G_2S)_n$ (SEQ ID NO: 922), wherein n is an integer from 1 to 3. In some embodiments, L_2 has a formula of $(GS)_n$ (SEQ ID NO: 938), wherein n is an integer from 1 to 3. In some embodiments, L_2 has a formula of $(GSGGS)_n$ (SEQ ID NO: 939), wherein n is an integer from 1 to 3. In some embodiments, L_2 has a formula of $(GGGS)_n$ (SEQ ID NO: 940), wherein n is an integer from 1 to 3. In some embodiments, L_2 has a formula of $(GGGGS)_n$ (SEQ ID NO: 941), wherein n is an integer from 1 to 3. In some embodiments, L_2 has a formula of $(GSSGGS)_n$ (SEQ ID NO: 942), wherein n is an integer from 1 to 3.

[0086] In some embodiments, L_2 is a substrate for a tumor specific protease. In some embodiments, the tumor specific protease is selected from the group consisting of metalloprotease, serine protease, cysteine protease, threonine protease, and aspartic protease. In some embodiments, L_2 comprises a urokinase cleavable amino acid sequence, a matriptase cleavable amino acid sequence, a matrix metalloprotease cleavable amino acid sequence, or a legumain cleavable amino acid sequence. In some embodiments, L_2 comprises an amino acid sequence selected from the group consisting of GGGGSLSGRSDNHGSSGT (SEQ ID NO: 923), GGGGSSGGSGGSGLSGRSDNHGSSGT (SEQ ID NO: 924), ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), ISSGLLAGRSDNH (SEQ ID NO: 928), LSGRSDNH (SEQ ID NO: 929), ISSGLLSGRSDNP (SEQ ID NO: 930), ISSGLLSGRSDNH (SEQ ID NO: 931), LSGRSDNHSPLGLAGS (SEQ ID NO: 932), SPLGLAGSLSGRSDNH (SEQ ID NO: 933), SPLGLSGRSDNH (SEQ ID NO: 934), LAGRSDNHSPLGLAGS (SEQ ID NO: 935), LSGRSDNHVPLSLKMG (SEQ ID NO: 936), and LSGRSDNHVPLSLSMG (SEQ ID NO: 937). In some embodiments, L_2 comprises an amino acid sequence selected from the group consisting of ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), ISSGLLAGRSDNH (SEQ ID NO: 928), or GGGGSGGGSGGISSGLLSGRSDNHGGGS (SEQ ID NO: 943).

[0087] In some embodiments, L_1 or L_2 comprises a modified amino acid or non-natural amino acid, or a modified non-natural amino acid, or a combination thereof. In some embodiments, the modified amino acid or a modified non-natural amino acid comprises a post-translational modification. In some embodiments, L_1 or L_2 comprises a modification including, but not limited, to acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. In some embodiments, modifications are made anywhere to L_1 or L_2 including the peptide backbone, or the amino acid side chains.

Linking moiety (L_3, L_{3a}, L_{3b}, or L_{3c})

[0088] In some embodiments, H_1 comprises a linking moiety (L_3) that connects H_1 to P_1. In some embodiments, H_{1a} comprises a linking moiety (L_{3a}) that connects H_{1a} to P_{1a}. In some embodiments, H_{1b} comprises a linking moiety (L_{3b}) that connects H_{1b} to P_{1b}. In some embodiments, H_{1b} comprises a linking moiety (L_{3c}) that connects H_{1c} to P_{1c}.

[0089] In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} is a peptide sequence having at least 5 to no more than 50 amino acids. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} is a peptide sequence having at least 10 to no more than 30 amino acids. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} is a peptide sequence having at least 10 amino acids. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} is a peptide sequence having at least 18 amino acids. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} is a peptide sequence having at least 26 amino acids.

[0090] In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula selected from the group consisting of $(G_2S)_n$ (SEQ ID NO: 922), $(GS)_n$ (SEQ ID NO: 938), $(GSGGS)_n$ (SEQ ID NO: 939), $(GGGS)_n$ (SEQ ID NO: 940), $(GGGGS)_n$ (SEQ ID NO: 941), and $(GSSGGS)_n$ (SEQ ID NO: 942), wherein n is an integer from 1 to 3.

[0091] In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(G_2S)_n$, wherein n is an integer of least 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GS)_n$, wherein n is an integer of least 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GSGGS)_n$ (SEQ ID NO: 917), wherein n is an integer of least 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GGGS)_n$ (SEQ ID NO: 918), wherein n is an integer of least 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GGGGS)_n$ (SEQ ID NO: 919), wherein n is an integer of least 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of least 1.

[0092] In some embodiments, L_3 or L_{3a} has a formula of $(G_2S)_n$, wherein n is an integer of 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GS)_n$, wherein n is an integer of 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GSGGS)_n$ (SEQ ID NO: 917), wherein n is an integer of 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GGGS)_n$ (SEQ ID NO: 918), wherein n is an integer of 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GGGGS)_n$ (SEQ ID NO: 919), wherein n is an integer of 1. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of 1.

[0093] In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(G_2S)_n$ (SEQ ID NO: 922), wherein n is an integer from 1 to 3. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GS)_n$ (SEQ ID NO: 938), wherein n is an integer from 1 to 3. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GSGGS)_n$ (SEQ ID NO: 939), wherein n is an integer from 1 to 3. In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GGGS)_n$ (SEQ ID NO: 940), wherein n is an integer from 1 to 3. In some embodiments, L_3, L_{3a},

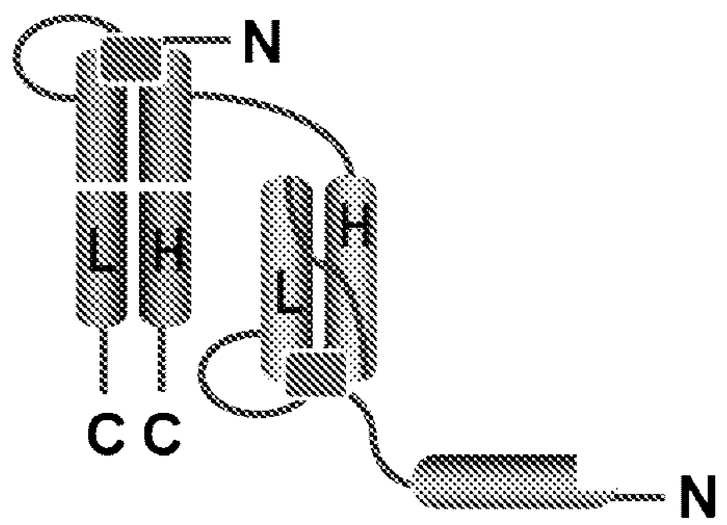
L_{3b}, or L_{3c} has a formula of $(GGGGS)_n$ (SEQ ID NO: 941),, wherein n is an integer from 1 to 3. I In some embodiments, L_3, L_{3a}, L_{3b}, or L_{3c} has a formula of $(GSSGGS)_n$ (SEQ ID NO: 942), wherein n is an integer from 1 to 3.

Configurations

[0094] In some embodiments, the Fab light chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) A_1. In some embodiments, the Fab light chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1. In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1. In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2.

In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2. In some embodiments, the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2. In some embodiments, the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2.

[0095] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 1:

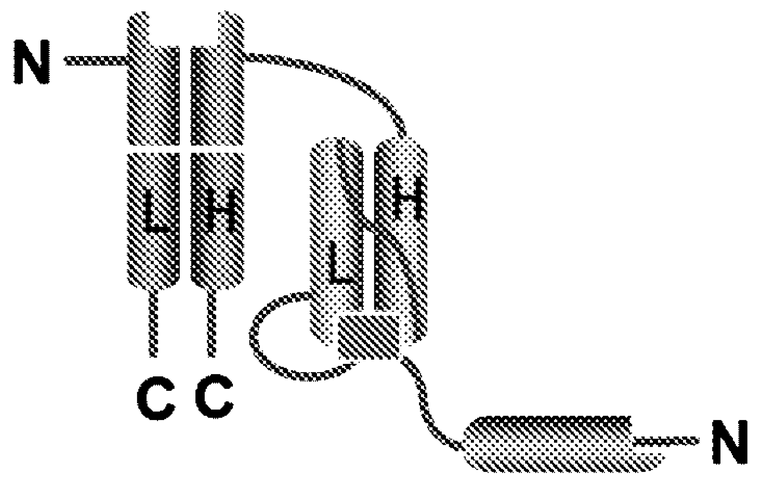


Configuration 1

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide (P_1) wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_1 impairs binding of the scFv to CD3 and P_1 is linked to a N-terminus of the light chain variable domain of the scFv with a linking moiety (L_1) that is a substrate for a

tumor specific protease, and P_1 is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab heavy chain polypeptide is linked to a C terminus of the heavy chain variable domain of the scFv, and wherein the Fab is linked to P_2 and L_2, wherein P_2 comprises a peptide that impairs binding of the Fab to the tumor cell antigen; and L_2 comprises a linking moiety that connects the Fab light chain polypeptide to P_2 and is a substrate for a tumor specific protease.

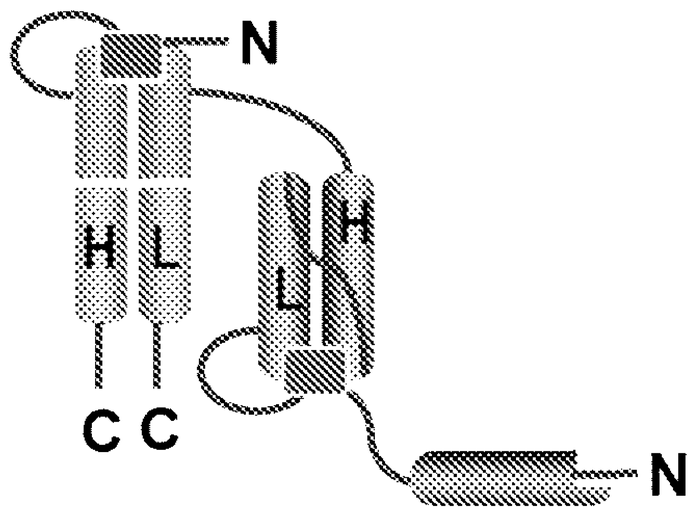
[0096] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 2:



Configuration 2

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein the peptide impairs binding of the scFv to CD3 and the peptide is linked to the light chain variable domain of the scFv with a linking moiety that is a substrate for a tumor specific protease, and the peptide is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide chain and a Fab heavy chain polypeptide chain, and wherein the Fab heavy chain polypeptide chain is linked to a C terminus of the heavy chain variable domain of the scFv.

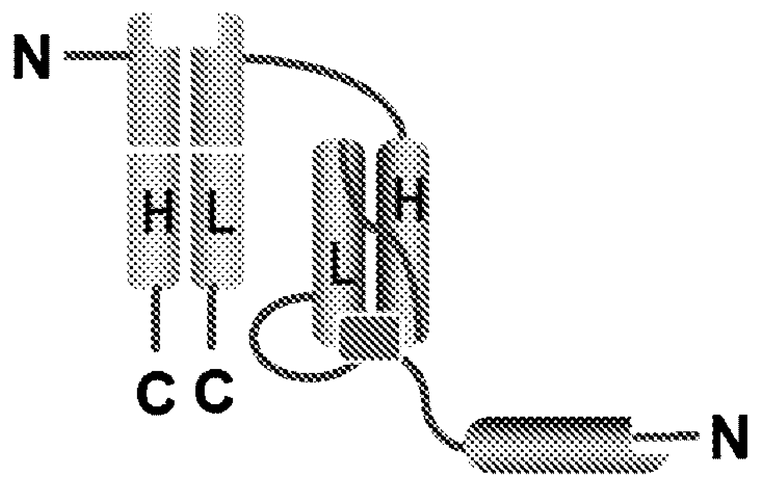
[0097] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 3:



Configuration 3

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide (P_1) wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_1 impairs binding of the scFv to CD3 and P_1 is linked to a N-terminus of the light chain variable domain of the scFv with a linking moiety that is a substrate for a tumor specific protease, and P_1 is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab light chain polypeptide is linked to a C terminus of the heavy chain variable domain of the scFv, and wherein the Fab is linked to P_2 and L_2, wherein P_2 comprises a peptide that impairs binding to the tumor cell antigen; and L_2 comprises a linking moiety that connects the Fab heavy chain polypeptide to P_2 and is a substrate for a tumor specific protease.

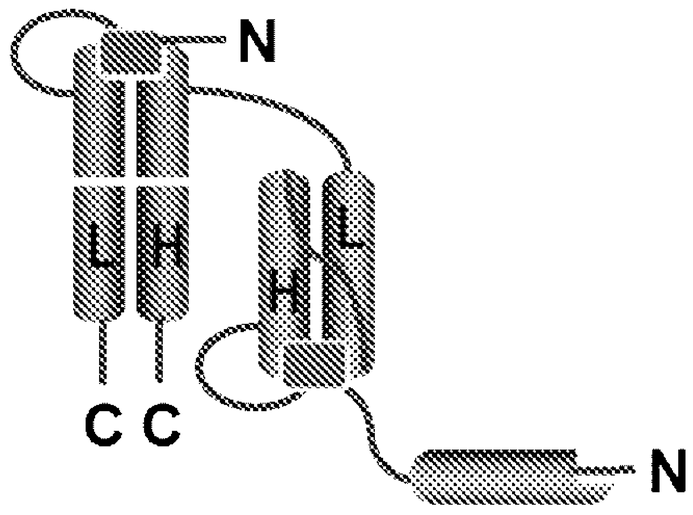
[0098] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 4:



Configuration 4

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is further linked to a peptide wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein the peptide impairs binding of the scFv to CD3 and the peptide is linked to a N-terminus of the light chain variable domain of the scFv with a linking moiety that is a substrate for a tumor specific protease, and the peptide is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab light chain polypeptide is linked to a C terminus of the heavy chain variable domain of the scFv.

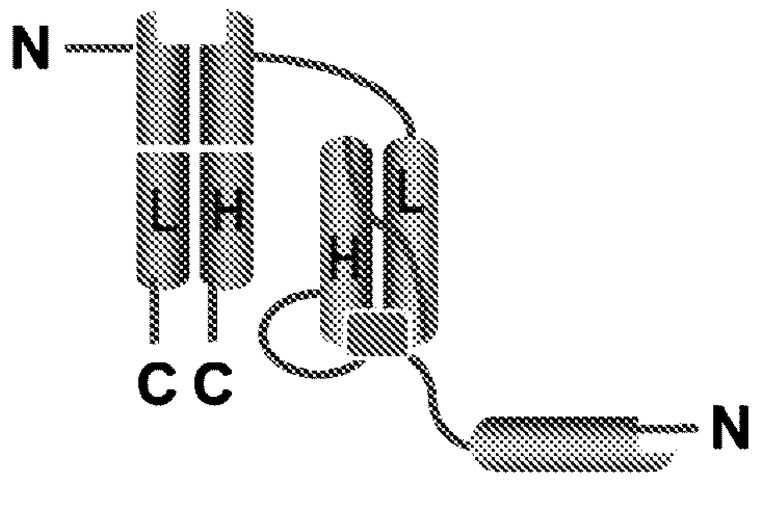
[0099] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 5:



Configuration 5

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide (P_1) wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_1 impairs binding of the scFv to CD3 and P_1 is linked to a N-terminus of the heavy chain variable domain of the scFv with a linking moiety (L_1) that is a substrate for a tumor specific protease, and P_1 is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab heavy chain polypeptide is linked to a C terminus of the light chain variable domain of the scFv, and wherein the Fab is linked to P_2 and L_2, wherein P_2 comprises a peptide that impairs binding of the Fab to the tumor cell antigen; and L_2 comprises a linking moiety that connects the Fab light chain polypeptide to P_2 and is a substrate for a tumor specific protease.

[0100] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 6:

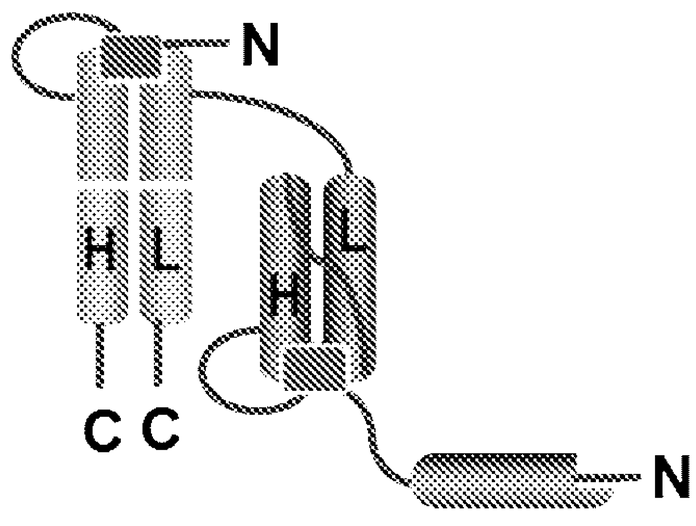


Configuration 6

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein the peptide impairs binding of the scFv to CD3 and the peptide is linked to the heavy chain variable domain of the scFv with a linking moiety that is a substrate for a tumor specific protease, and the peptide is further linked to a half-life extending molecule; and a Fab that binds to a

tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide chain and a Fab heavy chain polypeptide chain, and wherein the Fab heavy chain polypeptide chain is linked to a C terminus of the light chain variable domain of the scFv.

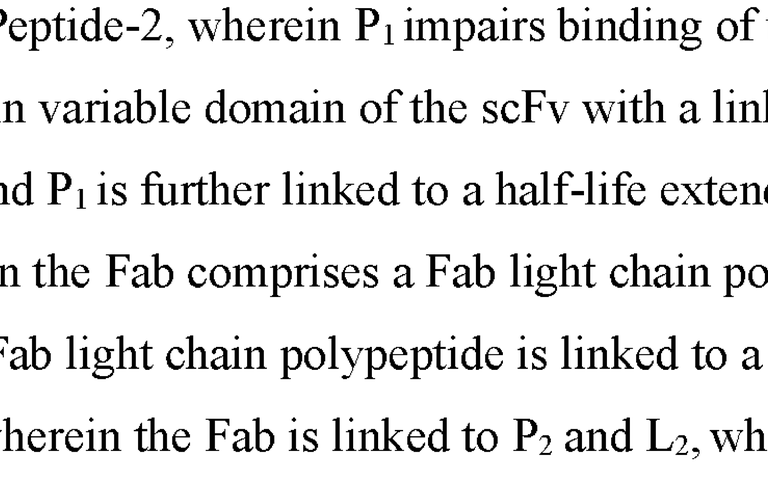
[0101] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 7:



Configuration 7

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide (P_1) wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_1 impairs binding of the scFv to CD3 and P_1 is linked to a N-terminus of the heavy chain variable domain of the scFv with a linking moiety (L_1) that is a substrate for a tumor specific protease, and P_1 is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab light chain polypeptide is linked to a C terminus of the light chain variable domain of the scFv, and wherein the Fab is linked to P_2 and L_2, wherein P_2 comprises a peptide that impairs binding of the Fab to the tumor cell antigen; and L_2 comprises a linking moiety that connects the Fab heavy chain polypeptide to P_2 and is a substrate for a tumor specific protease.

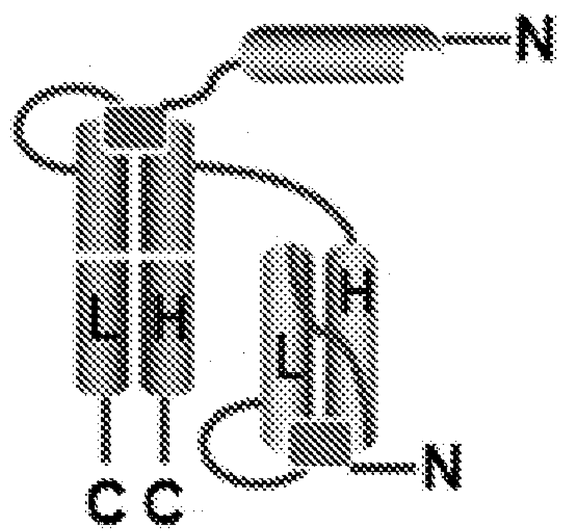
[0102] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 8:



Configuration 8

wherein the polypeptide or polypeptide complex comprises a single chain variable fragment (scFv) comprising a light chain variable domain and a heavy chain variable domain, wherein the scFv is linked to a peptide wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein the peptide impairs binding of the scFv to CD3 and the peptide is linked to a N-terminus of the heavy chain variable domain of the scFv with a linking moiety that is a substrate for a tumor specific protease, and the peptide is further linked to a half-life extending molecule; and a Fab that binds to a tumor cell antigen, wherein the Fab comprises a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab light chain polypeptide is linked to a C terminus of the light chain variable domain of the scFv.

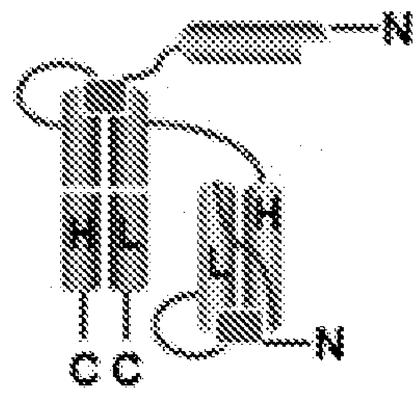
[0103] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 9:



Configuration 9

wherein the polypeptide or polypeptide complex comprises a Fab that binds to a tumor cell antigen, the Fab comprising a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab is linked to a peptide (P_1) that impairs binding of the Fab to the tumor cell antigen and P_1 is linked to a N terminus of the Fab light chain polypeptide with a linking moiety (L_1) that is a substrate for a tumor specific protease, and the P_1 is further linked to a half-life extending molecule; and a single chain variable fragment (scFv) that binds to an effector cell antigen, the scFv comprising a light chain variable domain and a heavy chain variable domain, wherein the heavy chain variable domain of the scFv is linked to an N terminus of the Fab heavy chain polypeptide, wherein the scFv is linked to P_2 and L_2, wherein P_2 comprises a peptide according to an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or P_2 comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_2 impairs binding of the scFv to CD3, and L_2 comprises a linking moiety that connects the light chain variable domain of the scFv to P_2 and is a substrate for a tumor specific protease.

[0104] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 10:

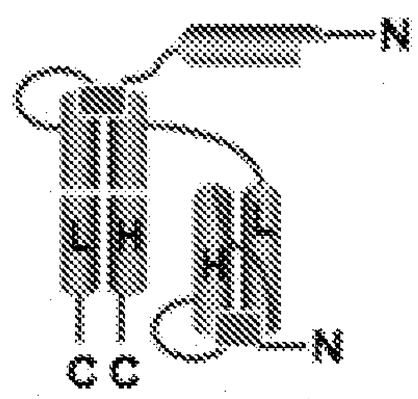


Configuration 10

wherein the polypeptide or polypeptide complex comprises a Fab that binds to a tumor cell antigen, the Fab comprising a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab is linked to a peptide (P_1) that impairs binding of the Fab to the tumor cell antigen and P_1 is linked to a N terminus of the Fab heavy chain polypeptide with a linking moiety (L_1) that is a substrate for a tumor specific protease, and P_1

is further linked to a half-life extending molecule; and a single chain variable fragment (scFv) that binds to an effector cell antigen, the scFv comprising a light chain variable domain and a heavy chain variable domain, wherein the heavy chain variable domain of the scFv is linked to an N terminus of the Fab light chain polypeptide, wherein the scFv further is linked to P_2 and L_2, wherein P_2 comprises a peptide according to an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or P_2 comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_2 impairs binding of the scFv to CD3, and L_2 comprises a linking moiety that connects the light chain variable domain of the scFv to P_2 and is a substrate for a tumor specific protease.

[0105] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 11:



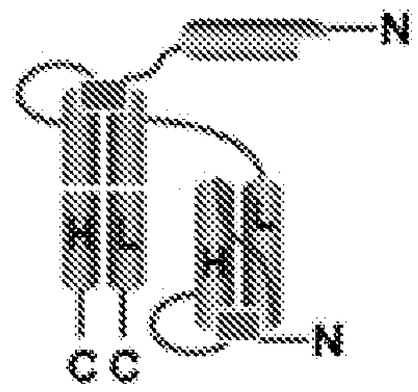
Configuration 11

wherein the polypeptide or polypeptide complex comprises a Fab that binds to a tumor cell antigen, the Fab comprising a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab is linked to a peptide (P_1) that impairs binding of the Fab to the tumor cell antigen and P_1 is linked to a N terminus of the Fab light chain polypeptide with a linking moiety (L_1) that is a substrate for a tumor specific protease, and P_1

is further linked to a half-life extending molecule; and a single chain variable fragment (scFv) that binds to an effector cell antigen, the scFv comprising a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain of the scFv is linked to an N terminus of the Fab heavy

chain polypeptide, wherein the scFv is linked to P_2 and L_2, wherein P_2 comprises a peptide according to an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or P_2 comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_2 impairs binding of the scFv to CD3, and L_2 comprises a linking moiety that connects the heavy chain variable domain of the scFv to P_2 and is a substrate for a tumor specific protease.

[0106] Disclosed herein, in some embodiments, are polypeptides or polypeptide complexes comprising a structural arrangement according to Configuration 12:



Configuration 12

wherein the polypeptide or polypeptide complex comprises a Fab that binds to a tumor cell antigen, the Fab comprising a Fab light chain polypeptide and a Fab heavy chain polypeptide, wherein the Fab is linked to a (P_1) that impairs binding of the Fab to the tumor cell antigen and P_1 is linked to a N terminus of the Fab heavy chain polypeptide with a linking moiety (L_1) that is a substrate for a tumor specific protease, and P_1 is further linked to a half-life extending molecule; and a single chain variable fragment (scFv) that binds to an effector cell antigen, the scFv comprising a light chain variable domain and a heavy chain variable domain, wherein the light chain variable domain of the scFv is linked to an N terminus of the Fab light chain polypeptide, wherein the scFv is linked to P_2 and L_2, wherein P_2 comprises a peptide according to an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or P_2 comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2, wherein P_2 impairs binding of the scFv to CD3, and L_2 comprises a linking moiety that connects the heavy chain variable domain of the scFv to P_2 and is a substrate for a tumor specific protease.

Polypeptides or polypeptide complexes, in some embodiments, comprise a sequence set forth in **Table 5**. In some embodiments, the sequence comprises at least or about 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to any one of SEQ ID NOs: 13-18.

Table 5. Exemplary amino acid sequences of isolated polypeptides or polypeptide complexes (PC) comprising Peptide-1 or Peptide-2

Construct Description	Amino Acid Sequence (N to C)	SEQ ID NO:
PC-1 – light chain	QGQSGQLSCEGWAMNREQCRAGSSGGSGGS GGSGISSGLLSGRSDNHGSSGTDILLTQSPVILS VSPGERVSFSCRAS**QSIGTN**IHWYQQRTNGSP RLLIK**YAS**ESISGIPSRFSGSGSGTDFTLSINSVE SEDIADYYC**QQNNNWPTT**FGAGTKLELKRT	13

	VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	
PC-1 – heavy chain	EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSK FG**MSWVRQAPGKGLEWVSS**ISGSGRDT**LYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYC**TIGGSLSV**SSQGTLVTVSSGGGGSGGG SGGGSQCLGPEWEVCPYGGGGSGGGSGGISS GLLSGRSDNHGGGSEVQLVESGGGLVQPGGS LKLSCAAS**GFTFNKYA**MNWVRQAPGKGLE WVAR**IRSKYNNYAT**YYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYC**VRHGNFGN SYISYWAY**WGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSS**TGA VTSGNY**PNWVQQKPGQAPRGLIG**GTK**FLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYY C**VLWYSNRWV**FGGGTKLTVLGGGGSQVQL KQSGPGLVQPSQSLSITCTVS**GFSLTNYG**VH WVRQSPGKGLEWLGV**IWSGGNT**DYNTPFTS RLSINKDNSKSQVFFKMNSLQSQDTAIYYC**AR ALTYYDYEFAY**WGQGTLVTVSAASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSC	14
PC-2 – light chain	QGQSGQLSCEGWAMNREQCRAGSSGGSGGS GGSGISSGLLSGRSDNHGSSGTDILLTQSPVILS VSPGERVSFSCRAS**QSIGTN**IHWYQQRTNGSP RLLIK**YAS**ESISGIPSRFSGSGSGTDFTLSINSVE SEDIADYYC**QQNNNWPTT**FGAGTKLELKRT VAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDST YSLSSTLTLSKADYEKHKVYACEVTHQGLSSP VTKSFNRGEC	15
PC-2 – heavy chain	EVQLVESGGGLVQPGNSLRLSCAAS**GFTFSK FG**MSWVRQAPGKGLEWVSS**ISGSGRDT**LYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYC**TIGGSLSV**SSQGTLVTVSSGGGGSGGG SGGVYCGPEFDESVGCMGGGGSGGGSGGISS GLLSGRSDNHGGGSEVQLVESGGGLVQPGGS LKLSCAAS**GFTFNKYA**MNWVRQAPGKGLE WVAR**IRSKYNNYAT**YYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYC**VRHGNFGN SYISYWAY**WGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCGSS**TGA VTSGNY**PNWVQQKPGQAPRGLIG**GTK**FLAP GTPARFSGSLLGGKAALTLSGVQPEDEAEYY C**VLWYSNRWV**FGGGTKLTVLGGGGSQVQL KQSGPGLVQPSQSLSITCTVS**GFSLTNYG**VH WVRQSPGKGLEWLGV**IWSGGNT**DYNTPFTS RLSINKDNSKSQVFFKMNSLQSQDTAIYYC**AR ALTYYDYEFAY**WGQGTLVTVSAASTKGPSV FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSC	16
PC-3 – light chain	QILLTQSPVILSVSPGERVSFSCRAS**QSIGTN**IH WYQQRTNGSPRLLIK**YAS**ESISGIPSRFSGSGS	17

	GTDFTLSINSVESEDIADYYC**QQNNNWPTT**F GAGTKLELKRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC	
PC-3 – heavy chain	EVQLVESGGGLVQPGGSLKLSCAAS**GFTFNK YA**MNWVRQAPGKGLEWVAR**IRSKYNNYAT** YYADSVKDRFTISRDDSKNTAYLQMNNLKTE DTAVYYC**VRHGNFGNSYISYWAY**WGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCGSS**TGAVTSGNY**PNWVQQKP GQAPRGLIG**GTK**FLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYC**VLWYSNRWV**FGGGT KLTVLGGGGSQVQLKQSGPGLVQPSQSLSITC TVS**GFSLTNYG**VHWVRQSPGKGLEWLGV**IW SGGNT**DYNTPFTSRLSINKDNSKSQVFFKMNS LQSQDTAIYYC**ARALTYYDYEFAY**WGQGTL VTVSAASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN TKVDKKVEPKSC	18

Polynucleotides Encoding Polypeptides or Polypeptide Complexes

[0107] Disclosed herein, in some embodiments, are isolated recombinant nucleic acid molecules encoding polypeptides or polypeptide complexes as disclosed herein. In some embodiments, the polypeptides or polypeptide complexes comprise an antibody or an antibody fragment.

[0108] Disclosed herein, in some embodiments, are isolated recombinant nucleic acid molecules encoding polypeptide or polypeptide complex comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2, or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to the amino acid sequence of Peptide-1 or Peptide-2. Disclosed herein, in some embodiments, are isolated recombinant nucleic acid molecules encoding polypeptide or polypeptide complex comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Peptide-1 (GSQCLGPEWEVCPY) SEQ ID NO: 1 or Peptide-2 (VYCGPEFDESVGCM) SEQ ID NO: 2.

[0109] Disclosed herein, in some embodiments, are isolated recombinant nucleic acid molecules encoding polypeptides or polypeptide complexes comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to an amino acid sequence selected from SEQ ID NOs: 1-2, 19-55. In some embodiments, the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0110] Disclosed herein, in some embodiments, are isolated recombinant nucleic acid molecules encoding polypeptides or polypeptide complexes comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}-Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L and S. In some embodiments, Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P. In some embodiments, Z_1 is selected from D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; and Z_{14} is selected from D, Y, and N. In some embodiments, the peptide comprises an amino acid sequence of **Table 17**. In some embodiments, the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0111] Disclosed herein, in some embodiments, are isolated recombinant nucleic acid molecules encoding polypeptides or polypeptide complexes comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}- U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; and U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S. In some embodiments, U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E, D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; and U_{14} is selected from D, Y, N, F, I, M, and P. In some embodiments, U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; and U_{14} is selected from D, Y, M, and N. In some

embodiments, the peptide comprises an amino acid sequence of **Table 17**. In some embodiments, the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 2. In some embodiments, the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0112] In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration according to: A_1-L_1-P_1 (Formula I) wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration according to: A_1-L_1-P (Formula I) wherein A_1 is the anti-CD3 binding domain; L_1 is a cleavable linker that is a substrate for a tumor specific protease; P_1 is the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration comprising Formula I: A_1-L_1-P_1 (Formula I) wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3. In some embodiments, the peptide is connected to the anti-CD3 binding domain in a configuration comprising Formula I: A_1-L_1-P_1 (Formula I) wherein A_1 is the anti-CD3 binding domain; L_1 is a cleavable linker that is a substrate for a tumor specific protease; $P_1$is the peptide that impairs binding of the anti-CD3 binding domain to CD3.In some embodiments, A_1 is further linked to a tumor antigen binding domain (A_2). In some embodiments, the polypeptide or polypeptide complex is according to Formula Ia: P_2-L_2-A_2-A_1-L_1-P_1 (Formula Ia) wherein P_2 comprises a peptide that impairs binding of A_2 to a tumor antigen; and L_2 comprises a second cleavable linker that connects A_2 to P_2 and is a substrate for a tumor specific protease.

Pharmaceutical Compositions

[0113] Disclosed herein, in some embodiments, are pharmaceutical compositions comprising: (a) the polypeptides or polypeptide complexes as disclosed herein; and (b) a pharmaceutically acceptable excipient.

[0114] In some embodiments, the polypeptide or polypeptide complex further comprises a detectable label, a therapeutic agent, or a pharmacokinetic modifying moiety. In some embodiments, the detectable label comprises a fluorescent label, a radiolabel, an enzyme, a nucleic acid probe, or a contrast agent.

[0115] For administration to a subject, the polypeptide or polypeptide complex as disclosed herein, may be provided in a pharmaceutical composition together with one or more pharmaceutically acceptable carriers or excipients. The term "pharmaceutically acceptable carrier" includes, but is not limited to, any carrier that does not interfere with the effectiveness of the biological activity of the ingredients and that is not toxic to the patient to whom it is administered. Examples of suitable pharmaceutical carriers are well known in the art and include phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions etc. Such carriers can be formulated by conventional methods and can be administered to the subject at a suitable dose. Preferably, the compositions are sterile. These compositions may also contain adjuvants such as preservative, emulsifying agents and dispersing agents.

Prevention of the action of microorganisms may be ensured by the inclusion of various antibacterial and antifungal agents.

[0116] The pharmaceutical composition may be in any suitable form, (depending upon the desired method of administration). It may be provided in unit dosage form, may be provided in a sealed container and may be provided as part of a kit. Such a kit may include instructions for use. It may include a plurality of said unit dosage forms.

[0117] The pharmaceutical composition may be adapted for administration by any appropriate route, including a parenteral (e.g., subcutaneous, intramuscular, or intravenous) route. Such compositions may be prepared by any method known in the art of pharmacy, for example by mixing the active ingredient with the carrier(s) or excipient(s) under sterile conditions.

[0118] Dosages of the substances of the present disclosure can vary between wide limits, depending upon the disease or disorder to be treated, the age and condition of the individual to be treated, etc. and a physician will ultimately determine appropriate dosages to be used.

[0119] In some embodiments, polypeptides described herein (e.g., antibodies and its binding fragments) are produced using any method known in the art to be useful for the synthesis of polypeptides (e.g., antibodies), in particular, by chemical synthesis or by recombinant expression, and are preferably produced by recombinant expression techniques.

[0120] In some instances, an antibody or its binding fragment thereof is expressed recombinantly, and the nucleic acid encoding the antibody or its binding fragment is assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., 1994, BioTechniques 17:242), which involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligation of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

[0121] Alternatively, a nucleic acid molecule encoding an antibody is optionally generated from a suitable source (e.g., an antibody cDNA library, or cDNA library generated from any tissue or cells expressing the immunoglobulin) by PCR amplification using synthetic primers hybridizable to the 3′ and 5′ ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence.

[0122] In some instances, an antibody or its binding is optionally generated by immunizing an animal, such as a mouse, to generate polyclonal antibodies or, more preferably, by generating monoclonal antibodies, e.g., as described by Kohler and Milstein (1975, Nature 256:495-497) or, as described by Kozbor et al. (1983, Immunology Today 4:72) or Cole et al. (1985 in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). Alternatively, a clone encoding at least the Fab portion of the antibody is optionally obtained by screening Fab expression libraries (e.g., as described in Huse et al., 1989, Science 246:1275-1281) for clones of Fab fragments that bind the specific antigen or by screening antibody libraries (See, e.g., Clackson et al., 1991, Nature 352:624; Hane et al., 1997 Proc. Natl. Acad. Sci. USA 94:4937).

[0123] In some embodiments, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, Proc. Natl. Acad. Sci. 81:851-855; Neuberger et al., 1984, Nature 312:604-608; Takeda et al., 1985, Nature 314:452-454) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with

genes from a human antibody molecule of appropriate biological activity are used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region.

[0124] In some embodiments, techniques described for the production of single chain antibodies (U.S. Pat. No. 4,694,778; Bird, 1988, Science 242:423-42; Huston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; and Ward et al., 1989, Nature 334:544-54) are adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli are also optionally used (Skerra et al., 1988, Science 242:1038-1041).

[0125] In some embodiments, an expression vector comprising the nucleotide sequence of an antibody or the nucleotide sequence of an antibody is transferred to a host cell by conventional techniques (e.g., electroporation, liposomal transfection, and calcium phosphate precipitation), and the transfected cells are then cultured by conventional techniques to produce the antibody. In specific embodiments, the expression of the antibody is regulated by a constitutive, an inducible or a tissue, specific promoter.

[0126] In some embodiments, a variety of host-expression vector systems is utilized to express an antibody, or its binding fragment described herein. Such host-expression systems represent vehicles by which the coding sequences of the antibody is produced and subsequently purified, but also represent cells that are, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody or its binding fragment in situ. These include, but are not limited to, microorganisms such as bacteria (e.g., E. coli and B. subtilis) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing an antibody or its binding fragment coding sequences; yeast (e.g., Saccharomyces Pichia) transformed with recombinant yeast expression vectors containing an antibody or its binding fragment coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing an antibody or its binding fragment coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus (CaMV) and tobacco mosaic virus (TMV)) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing an antibody or its binding fragment coding sequences; or mammalian cell systems (e.g., COS, CHO, BH, 293, 293T, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g. the adenovirus late promoter; the vaccinia virus 7.5K promoter).

[0127] For long-term, high-yield production of recombinant proteins, stable expression is preferred. In some instances, cell lines that stably express an antibody are optionally engineered. Rather than using expression vectors that contain viral origins of replication, host cells are transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells are then allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes

and grow to form foci that in turn are cloned and expanded into cell lines. This method can advantageously be used to engineer cell lines which express the antibody or its binding fragments.

[0128] In some instances, a number of selection systems are used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., 1977, Cell 11:223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, 192, Proc. Natl. Acad. Sci. USA 48:202), and adenine phosphoribosyltransferase (Lowy et al., 1980, Cell 22:817) genes are employed in tk−, hgprt− or aprt− cells, respectively. Also, antimetabolite resistance are used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., 1980, Proc. Natl. Acad. Sci. USA 77:357; O'Hare et al., 1981, Proc. Natl. Acad. Sci. USA 78:1527); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, 1981, Proc. Natl. Acad. Sci. USA 78:2072); neo, which confers resistance to the aminoglycoside G-418 (Clinical Pharmacy 12:488-505; Wu and Wu, 1991, Biotherapy 3:87-95; Tolstoshev, 1993, Ann. Rev. Pharmacol. Toxicol. 32:573-596; Mulligan, 1993, Science 260:926-932; and Morgan and Anderson, 1993, Ann. Rev. Biochem. 62:191-217; May 1993, TIB TECH 11(5):155-215) and hygro, which confers resistance to hygromycin (Santerre et al., 1984, Gene 30:147). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds., 1993, Current Protocols in Molecular Biology, John Wiley & Sons, NY; Kriegler, 1990, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY; and in Chapters 12 and 13, Dracopoli et al. (eds), 1994, Current Protocols in Human Genetics, John Wiley & Sons, NY.; Colberre-Garapin et al., 1981, J. Mol. Biol. 150:1).

[0129] In some instances, the expression levels of an antibody are increased by vector amplification (for a review, see Bebbington and Hentschel, the use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol. 3. (Academic Press, New York, 1987)). When a marker in the vector system expressing an antibody is amplifiable, an increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the nucleotide sequence of the antibody, production of the antibody will also increase (Crouse et al., 1983, Mol. Cell Biol. 3:257).

[0130] In some instances, any method known in the art for purification of an antibody is used, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins.

Expression Vectors

[0131] In some embodiments, vectors include any suitable vectors derived from either a eukaryotic or prokaryotic sources. In some cases, vectors are obtained from bacteria (e.g. E. coli), insects, yeast (e.g. Pichia pastoris), algae, or mammalian sources. Exemplary bacterial vectors include pACYC177, pASK75, pBAD vector series, pBADM vector series, pET vector series, pETM vector series, pGEX vector series, pHAT, pHAT2, pMal-c2, pMal-p2, pQE vector series, pRSET A, pRSET B, pRSET C, pTrcHis2 series, pZA31-Luc, pZE21-MCS-1, pFLAG ATS, pFLAG CTS, pFLAG MAC, pFLAG Shift-12c, pTAC-MAT-1, pFLAG CTC, or pTAC-MAT-2.

[0132] Exemplary insect vectors include pFastBac1, pFastBac DUAL, pFastBac ET, pFastBac HTa, pFastBac HTb, pFastBac HTc, pFastBac M30a, pFastBact M30b, pFastBac, M30c, pVL1392, pVL1393, pVL1393 M10,

pVL1393 M11, pVL1393 M12, FLAG vectors such as pPolh-FLAG1 or pPolh-MAT 2, or MAT vectors such as pPolh-MAT1, or pPolh-MAT2.

[0133] In some cases, yeast vectors include Gateway® pDEST™ 14 vector, Gateway® pDEST™ 15 vector, Gateway® pDEST™ 17 vector, Gateway® pDEST™ 24 vector, Gateway® pYES-DEST52 vector, pBAD-DEST49 Gateway® destination vector, pAO815 Pichia vector, pFLD1 Pichi pastoris vector, pGAPZA,B, & C Pichia pastoris vector, pPIC3.5K Pichia vector, pPIC6 A, B, & C Pichia vector, pPIC9K Pichia vector, pTEF1/Zeo, pYES2 yeast vector, pYES2/CT yeast vector, pYES2/NT A, B, & C yeast vector, or pYES3/CT yeast vector.

[0134] Exemplary algae vectors include pChlamy-4 vector or MCS vector.

[0135] Examples of mammalian vectors include transient expression vectors or stable expression vectors. Mammalian transient expression vectors may include pRK5, p3xFLAG-CMV 8, pFLAG-Myc-CMV 19, pFLAG-Myc-CMV 23, pFLAG-CMV 2, pFLAG-CMV 6a,b,c, pFLAG-CMV 5.1, pFLAG-CMV 5a,b,c, p3xFLAG-CMV 7.1, pFLAG-CMV 20, p3xFLAG-Myc-CMV 24, pCMV-FLAG-MAT1, pCMV-FLAG-MAT2, pBICEP-CMV 3, or pBICEP-CMV 4. Mammalian stable expression vector may include pFLAG-CMV 3, p3xFLAG-CMV 9, p3xFLAG-CMV 13, pFLAG-Myc-CMV 21, p3xFLAG-Myc-CMV 25, pFLAG-CMV 4, p3xFLAG-CMV 10, p3xFLAG-CMV 14, pFLAG-Myc-CMV 22, p3xFLAG-Myc-CMV 26, pBICEP-CMV 1, or pBICEP-CMV 2.

[0136] In some instances, a cell-free system is a mixture of cytoplasmic and/or nuclear components from a cell and is used for in vitro nucleic acid synthesis. In some cases, a cell-free system utilizes either prokaryotic cell components or eukaryotic cell components. Sometimes, a nucleic acid synthesis is obtained in a cell-free system based on for example Drosophila cell, Xenopus egg, or HeLa cells. Exemplary cell-free systems include, but are not limited to, E. coli S30 Extract system, E. coli T7 S30 system, or PURExpress®.

Host Cells

[0137] In some embodiments, a host cell includes any suitable cell such as a naturally derived cell or a genetically modified cell. In some instances, a host cell is a production host cell. In some instances, a host cell is a eukaryotic cell. In other instances, a host cell is a prokaryotic cell. In some cases, a eukaryotic cell includes fungi (e.g., yeast cells), animal cell or plant cell. In some cases, a prokaryotic cell is a bacterial cell. Examples of bacterial cell include gram-positive bacteria or gram-negative bacteria. Sometimes the gram-negative bacteria is anaerobic, rod-shaped, or both.

[0138] In some instances, gram-positive bacteria include Actinobacteria, Firmicutes or Tenericutes. In some cases, gram-negative bacteria include Aquificae, Deinococcus-Thermus, Fibrobacteres–Chlorobi/Bacteroidetes (FCB group), Fusobacteria, Gemmatimonadetes, Nitrospirae, Planctomycetes–Verrucomicrobia/ Chlamydiae (PVC group), Proteobacteria, Spirochaetes or Synergistetes. Other bacteria can be Acidobacteria, Chloroflexi, Chrysiogenetes, Cyanobacteria, Deferribacteres, Dictyoglomi, Thermodesulfobacteria or Thermotogae. A bacterial cell can be Escherichia coli, Clostridium botulinum, or Coli bacilli.

[0139] Exemplary prokaryotic host cells include, but are not limited to, BL21, Mach1™, DH10B™, TOP10, DH5α, DH10Bac™, OmniMax™, MegaX™, DH12S™, INV110, TOP10F', INVαF, TOP10/P3, ccdB Survival, PIR1, PIR2, Stbl2™, Stbl3™, or Stbl4™.

[0140] In some instances, animal cells include a cell from a vertebrate or from an invertebrate. In some cases, an animal cell includes a cell from a marine invertebrate, fish, insects, amphibian, reptile, or mammal. In some cases, a fungus cell includes a yeast cell, such as brewer's yeast, baker's yeast, or wine yeast.

[0141] Fungi include ascomycetes such as yeast, mold, filamentous fungi, basidiomycetes, or zygomycetes. In some instances, yeast includes Ascomycota or Basidiomycota. In some cases, Ascomycota includes Saccharomycotina (true yeasts, e.g. Saccharomyces cerevisiae (baker's yeast)) or Taphrinomycotina (e.g. Schizosaccharomycetes (fission yeasts)). In some cases, Basidiomycota includes Agaricomycotina (e.g. Tremellomycetes) or Pucciniomycotina (e.g. Microbotryomycetes).

[0142] Exemplary yeast or filamentous fungi include, for example, the genus: Saccharomyces, Schizosaccharomyces, Candida, Pichia, Hansenula, Kluyveromyces, Zygosaccharomyces, Yarrowia, Trichosporon, Rhodosporidi, Aspergillus, Fusarium, or Trichoderma. Exemplary yeast or filamentous fungi include, for example, the species: Saccharomyces cerevisiae, Schizosaccharomyces pombe, Candida utilis, Candida boidini, Candida albicans, Candida tropicalis, Candida stellatoidea, Candida glabrata, Candida krusei, Candida parapsilosis, Candida guilliermondii, Candida viswanathii, Candida lusitaniae, Rhodotorula mucilaginosa, Pichia metanolica, Pichia angusta, Pichia pastoris, Pichia anomala, Hansenula polymorpha, Kluyveromyces lactis, Zygosaccharomyces rouxii, Yarrowia lipolytica, Trichosporon pullulans, Rhodosporidium toru-Aspergillus niger, Aspergillus nidulans, Aspergillus awamori, Aspergillus oryzae, Trichoderma reesei, Yarrowia lipolytica, Brettanomyces bruxellensis, Candida stellata, Schizosaccharomyces pombe, Torulaspora delbrueckii, Zygosaccharomyces bailii, Cryptococcus neoformans, Cryptococcus gattii, or Saccharomyces boulardii.

[0143] Exemplary yeast host cells include, but are not limited to, Pichia pastoris yeast strains such as GS115, KM71H, SMD1168, SMD1168H, and X-33; and Saccharomyces cerevisiae yeast strain such as INVSc1.

[0144] In some instances, additional animal cells include cells obtained from a mollusk, arthropod, annelid or sponge. In some cases, an additional animal cell is a mammalian cell, e.g., from a primate, ape, equine, bovine, porcine, canine, feline or rodent. In some cases, a rodent includes mouse, rat, hamster, gerbil, hamster, chinchilla, fancy rat, or guinea pig.

[0145] Exemplary mammalian host cells include, but are not limited to, 293A cell line, 293FT cell line, 293F cells , 293 H cells, CHO DG44 cells, CHO-S cells, CHO-K1 cells, FUT8 KO CHOK1, Expi293F™ cells, Flp-In™ T-REx™ 293 cell line, Flp-In™-293 cell line, Flp-In™-3T3 cell line, Flp-In™-BHK cell line, Flp-In™-CHO cell line, Flp-In™-CV-1 cell line, Flp-In™-Jurkat cell line, FreeStyle™ 293-F cells, FreeStyle™ CHO-S cells, GripTite™ 293 MSR cell line, GS-CHO cell line, HepaRG™ cells, T-REx™ Jurkat cell line, Per.C6 cells, T-REx™-293 cell line, T-REx™-CHO cell line, and T-REx™-HeLa cell line.

[0146] In some instances, a mammalian host cell is a stable cell line, or a cell line that has incorporated a genetic material of interest into its own genome and has the capability to express the product of the genetic material after many generations of cell division. In some cases, a mammalian host cell is a transient cell line, or a cell line that has not incorporated a genetic material of interest into its own genome and does not have the capability to express the product of the genetic material after many generations of cell division.

[0147] Exemplary insect host cells include, but are not limited to, Drosophila S2 cells, Sf9 cells, Sf21 cells, High Five™ cells, and expresSF+® cells.

[0148] In some instances, plant cells include a cell from algae. Exemplary insect cell lines include, but are not limited to, strains from Chlamydomonas reinhardtii 137c, or Synechococcus elongatus PPC 7942.

Articles of Manufacture

[0149] In another aspect of the invention, an article of manufacture containing materials useful for the treatment, prevention and/or diagnosis of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper that is pierceable by a hypodermic injection needle). At least one active agent in the composition is a bispecific antibody comprising a first antigen-binding site that specifically binds to CD3 and a second antigen-binding site that specifically binds to a tumor antigen defined herein before.

[0150] The label or package insert indicates that the composition is used for treating the condition of choice. Moreover, the article of manufacture may comprise (a) a first container with a composition contained therein, wherein the composition comprises the bispecific antibody of the invention; and (b) a second container with a composition contained therein, wherein the composition comprises a further cytotoxic or otherwise therapeutic agent. The article of manufacture in this embodiment of the invention may further comprise a package insert indicating that the compositions can be used to treat a particular condition.

[0151] Alternatively, or additionally, the article of manufacture may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

Certain Definitions

[0152] The terminology used herein is for the purpose of describing particular cases only and is not intended to be limiting. As used herein, the singular forms “a”, “an” and “the” are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the terms “including”, “includes”, “having”, “has”, “with”, or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term “comprising.”

[0153] The term “antibody” is used in the broadest sense and covers fully assembled antibodies, antibody fragments that can bind antigen, for example, Fab, F(ab’)2, Fv, single chain antibodies (scFv), diabodies, antibody chimeras, hybrid antibodies, bispecific antibodies, and the like.

[0154] The term “complementarity determining region” or “CDR” is a segment of the variable region of an antibody that is complementary in structure to the epitope to which the antibody binds and is more variable than the

rest of the variable region. Accordingly, a CDR is sometimes referred to as hypervariable region. A variable region comprises three CDRs. CDR peptides can be obtained by constructing genes encoding the CDR of an antibody of interest. Such genes are prepared, for example, by using the polymerase chain reaction to synthesize the variable region from RNA of antibody-producing cells. See, for example, Larrick et al., *Methods: A Companion to Methods in Enzymology* 2: 106 (1991); Courtenay-Luck, "Genetic Manipulation of Monoclonal Antibodies," in *Monoclonal Antibodies: Production, Engineering and Clinical Application*, Ritter et al. (eds.), pages 166-179 (Cambridge University Press 1995); and Ward et al., "Genetic Manipulation and Expression of Antibodies," in *Monoclonal Antibodies: Principles and Applications*, Birch et al., (eds.), pages 137-185 (Wiley-Liss, Inc. 1995).

[0155] The term "Fab" refers to a protein that contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab′ fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab′ in which the cysteine residue(s) of the constant domains bear a free thiol group. Fab′ fragments are produced by reducing the F(ab')2 fragment's heavy chain disulfide bridge. Other chemical couplings of antibody fragments are also known.

[0156] A "single-chain variable fragment (scFv)" is a fusion protein of the variable regions of the heavy (VH) and light chains (VL) of an antibody, connected with a short linker peptide of ten to about 25 amino acids. The linker is usually rich in glycine for flexibility, as well as serine or threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa. This protein retains the specificity of the original antibody, despite removal of the constant regions and the introduction of the linker. scFv antibodies are, e.g. described in Houston, J. S., Methods in Enzymol. 203 (1991) 46-96). In addition, antibody fragments comprise single chain polypeptides having the characteristics of a VH domain, namely being able to assemble together with a VL domain, or of a VL domain, namely being able to assemble together with a VH domain to a functional antigen binding site and thereby providing the antigen binding property of full length antibodies.

[0157] While preferred embodiments of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the embodiments of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

EMBOIDMENTS

[0158] Embodiment 1 comprises an isolated polypeptide or polypeptide complex comprising a peptide that impairs binding of an anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to an amino acid sequence selected from SEQ ID NOs: 1-2, 19-55.

[0159] Embodiment 2 comprises an isolated polypeptide or polypeptide complex of embodiment 1, wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55.

[0160] Embodiment 3 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-2, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 1.

[0161] Embodiment 4 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-2, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 2.

[0162] Embodiment 5 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-2, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0163] Embodiment 6 comprises an isolated polypeptide or polypeptide complex comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}- Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L and S.

[0164] Embodiment 7 comprises an isolated polypeptide or polypeptide complex of embodiment 6, wherein Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P.

[0165] Embodiment 8 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 6-7, wherein Z_1 is selected from D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; and Z_{14} is selected from D, Y, and N.

[0166] Embodiment 9 comprises an isolated polypeptide or polypeptide complex comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}- U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; and U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S.

[0167] Embodiment 10 comprises an isolated polypeptide or polypeptide complex of embodiment 9, wherein U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E,

D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; and U_{14} is selected from D, Y, N, F, I, M, and P.

[0168] Embodiment 11 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 9-10, wherein U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F;U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; and U_{14} is selected from D, Y, M, and N.

[0169] Embodiment 12 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 6-11, wherein the peptide comprises an amino acid sequence of **Table 17**.

[0170] Embodiment 13 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 6-11, wherein the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55.

[0171] Embodiment 14 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 6 and 9-12, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 2.

[0172] Embodiment 15 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 6-7 and 9-13, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0001] Embodiment 16 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-15, wherein the peptide is connected to the anti-CD3 binding domain in a configuration according to Formula I: A_1-L_1-P_1 wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3.

[0173] Embodiment 17 comprises an isolated polypeptide or polypeptide complex of embodiment 16, wherein P_1 is connected N-terminal to the cleavable linker and A_1 is connected C-terminal to the cleavable linker.

[0174] Embodiment 18 comprises an isolated polypeptide or polypeptide complex of embodiment 16, wherein P_1 is connected C-terminal to the cleavable linker and A_1 is connected N-terminal to the cleavable linker.

[0175] Embodiment 19 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-18, wherein P_1 is bound to A_1 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof.

[0176] Embodiment 20 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-19, wherein A_1 is further linked to a tumor antigen binding domain (A_2).

[0177] Embodiment 21 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-20, wherein the polypeptide or polypeptide complex is according to Formula Ia: P_2-L_2-A_2-A_1-L_1-P_1 wherein P_2 comprises a peptide that impairs binding of A_2 to a tumor antigen; and L_2 comprises a second cleavable linker that connects A_2 to P_2 and is a substrate for a tumor specific protease.

[0178] Embodiment 22 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-21, wherein A_1 comprises an antibody or antibody fragment.

[0179] Embodiment 23 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-22, wherein A_1 comprises an antibody or antibody fragment that is human or humanized.

[0180] Embodiment 24 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-17 and 19-23, wherein L_1 is bound to N-terminus of the antibody or antibody fragment of A_1.

[0181] Embodiment 25 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16 and 18-23, wherein A_2 is bound to N-terminus of the antibody or antibody fragment of A_1.

[0182] Embodiment 26 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16, 18-23, and 25, wherein L_1 is bound to the C-terminus of the antibody or antibody fragment of A_1.

[0183] Embodiment 27 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-17 and 19-24, wherein A_2 is bound to the C-terminus of the antibody or antibody fragment of A_1.

[0184] Embodiment 28 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 22-27, wherein the antibody or antibody fragment of A_1 comprises a single chain variable fragment, a single domain antibody, or a Fab fragment.

[0185] Embodiment 29 comprises an isolated polypeptide or polypeptide complex of embodiment 28, wherein A_1 is the single chain variable fragment (scFv).

[0186] Embodiment 30 comprises an isolated polypeptide or polypeptide complex of embodiment 29, wherein the scFv comprises a scFv heavy chain polypeptide and a scFv light chain polypeptide.

[0187] Embodiment 31 comprises an isolated polypeptide or polypeptide complex of embodiment 28, wherein A_1 is the single domain antibody.

[0188] Embodiment 32 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 22-27, wherein the antibody or antibody fragment thereof comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody.

[0189] Embodiment 33 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-30 and 32, wherein A_1 comprises an anti-CD3e single chain variable fragment.

[0190] Embodiment 34 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-32, wherein A_1 comprises an anti-CD3e single chain variable fragment that has a KD binding of 1 μM or less to CD3 on CD3 expressing cells.

[0191] Embodiment 35 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-30 and 32-34, wherein A_1 comprises a variable light chain and variable heavy chain each of which is capable of specifically binding to human CD3.

[0192] Embodiment 36 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 28-30 and 32-35, wherein A_1 comprises the scFv comprising a scFv heavy chain variable domain and an scFv light chain variable domain comprising complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the scFv heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5; and the scFv light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the scFv light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8.

[0193] Embodiment 37 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-30 and 32-35, wherein A_1 comprises a heavy chain variable domain and a light chain variable domain comprising complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5; and the light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8.

[0194] Embodiment 38 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-37, wherein the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease.

[0195] Embodiment 39 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-38, wherein the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease and A_1 binds to the effector cell.

[0196] Embodiment 40 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 38-39, wherein the effector cell is a T cell.

[0197] Embodiment 41 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 38-40, wherein A_1 binds to a polypeptide that is part of a TCR-CD3 complex on the effector cell.

[0198] Embodiment 42 comprises an isolated polypeptide or polypeptide complex of embodiment 41, wherein the polypeptide that is part of the TCR-CD3 complex is human CD3ε.

[0199] Embodiment 43 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 20-42, wherein A_2 comprises an antibody or antibody fragment.

[0200] Embodiment 44 comprises an isolated polypeptide or polypeptide complex of embodiment 43, wherein the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment, a single domain antibody, Fab', or a Fab.

[0201] Embodiment 45 comprises an isolated polypeptide or polypeptide complex of embodiment 43, wherein the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody.

[0202] Embodiment 46 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 43-45, wherein the antibody or antibody fragment thereof of A_2 is humanized or human.

[0203] Embodiment 47 comprises an isolated polypeptide or polypeptide complex of embodiment 44, wherein A_2 is the Fab or Fab'.

[0002] Embodiment 48 comprises an isolated polypeptide or polypeptide complex of embodiment 47, wherein the Fab or Fab' comprises (a) a Fab light chain polypeptide and (b) a Fab heavy chain polypeptide.

[0204] Embodiment 49 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 20-48, wherein A_2 comprises an epidermal growth factor receptor (EGFR) binding domain.

[0205] Embodiment 50 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 20-48, wherein A_2 comprises a carcinoembryonic antigen-related cell adhesion molecule CEACAM5 binding domain.

[0206] Embodiment 51 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-50, wherein P_1 is further linked to a half-life extending moiety (H_1).

[0207] Embodiment 52 comprises an isolated polypeptide or polypeptide complex of embodiment 51, wherein the half-life extending moiety is a single-domain antibody.

[0208] Embodiment 53 comprises an isolated polypeptide or polypeptide complex of embodiment 51, wherein H_1 comprises a polymer.

[0209] Embodiment 54 comprises an isolated polypeptide or polypeptide complex of embodiment 53, wherein the polymer is polyethylene glycol (PEG).

[0210] Embodiment 55 comprises an isolated polypeptide or polypeptide complex of embodiment 51, wherein H_1 comprises albumin.

[0211] Embodiment 56 comprises an isolated polypeptide or polypeptide complex of embodiment 51, wherein H_1 comprises an Fc domain.

[0212] Embodiment 57 comprises an isolated polypeptide or polypeptide complex of embodiment 55, wherein the albumin is serum albumin.

[0213] Embodiment 58 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 55 and 57, wherein the albumin is human serum albumin.

[0214] Embodiment 59 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 51-58, wherein H_1 comprises a polypeptide, a ligand, or a small molecule.

[0215] Embodiment 60 comprises an isolated polypeptide or polypeptide complex of embodiment 59, wherein the polypeptide, the ligand or the small molecule binds serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1.

[0216] Embodiment 61 comprises an isolated polypeptide or polypeptide complex of embodiment 60, wherein the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin.

[0003] Embodiment 62 comprises an isolated polypeptide or polypeptide complex of embodiment 60, wherein the circulating immunoglobulin molecule comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD.

[0217] Embodiment 63 comprises an isolated polypeptide or polypeptide complex of embodiment 60 or 61, wherein the serum protein is albumin.

[0218] Embodiment 64 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 59-63, wherein the polypeptide is an antibody.

[0219] Embodiment 65 comprises an isolated polypeptide or polypeptide complex of embodiment 64, wherein the antibody comprises a single domain antibody, a single chain variable fragment, or a Fab.

[0220] Embodiment 66 comprises an isolated polypeptide or polypeptide complex of embodiment 65, wherein the single domain antibody comprises a single domain antibody that binds to albumin.

[0221] Embodiment 67 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-66, wherein the single domain antibody is a human or humanized antibody.

[0222] Embodiment 68 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-67, wherein the single domain antibody is 645gH1gL1.

[0223] Embodiment 69 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-67, wherein the single domain antibody is 645dsgH5gL4.

[0224] Embodiment 70 comprises an isolated polypeptide or polypeptide complex of embodiment 65, wherein the single domain antibody is 23-13-A01 -sc02.

[0225] Embodiment 71 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-66, wherein the single domain antibody is A10m3 or a fragment thereof.

[0226] Embodiment 72 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-66, wherein the single domain antibody is DOM7r-31.

[0227] Embodiment 73 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-66, wherein the single domain antibody is DOM7h-11-15.

[0228] Embodiment 74 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-66, wherein the single domain antibody is Alb-1, Alb-8, or Alb-23.

[0229] Embodiment 75 comprises an isolated polypeptide or polypeptide complex of embodiment 65, wherein the single domain antibody is 10G or 10GE.

[0230] Embodiment 76 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 65-66, wherein the single domain antibody is SA21.

[0231] Embodiment 77 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-76, wherein the polypeptide or polypeptide complex comprises a modified amino acid, a non-natural amino acid, a modified non-natural amino acid, or a combination thereof.

[0232] Embodiment 78 comprises an isolated polypeptide or polypeptide complex of embodiment 77, wherein the modified amino acid or modified non-natural amino acid comprises a post-translational modification.

[0233] Embodiment 79 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 51-78, wherein H_1 comprises a linking moiety (L_3) that connects H_1 to P_1.

[0234] Embodiment 80 comprises an isolated polypeptide or polypeptide complex of embodiment 79, wherein L_3 is a peptide sequence having at least 5 to no more than 50 amino acids.

[0235] Embodiment 81 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 79-80, wherein L_3 is a peptide sequence having at least 10 to no more than 30 amino acids.

[0236] Embodiment 82 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 79-81, wherein L_3 is a peptide sequence having at least 10 amino acids.

[0237] Embodiment 83 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 79-82, wherein L_3 is a peptide sequence having at least 18 amino acids.

[0238] Embodiment 84 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 79-83, wherein L_3 is a peptide sequence having at least 26 amino acids.

[0239] Embodiment 85 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 79-84, wherein L_3 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

[0240] Embodiment 86 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 79-84, wherein L_3 comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)).

[0241] Embodiment 87 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, wherein the Fab light chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) of A_1.

[0242] Embodiment 88 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, wherein the Fab heavy chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) A_1.

[0243] Embodiment 89 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, wherein the Fab light chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) of A_1.

[0244] Embodiment 90 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, wherein the Fab heavy chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) A_1.

[0245] Embodiment 91 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, 88, and 90, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1.

[0246] Embodiment 92 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, 87, and 89, wherein the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1.

[0247] Embodiment 93 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, 88, and 90, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1.

[0248] Embodiment 94 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, 87, and 89, wherein the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1.

[0249] Embodiment 95 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-86, 88, 90, and 91, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2.

[0250] Embodiment 96 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 48-87, 89, and 92, wherein the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2.

[0251] Embodiment 97 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-86, 88, 90, and 93, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2.

[0252] Embodiment 98 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 1-87, 89, and 94, wherein the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2.

[0253] Embodiment 99 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-98, wherein P_2 impairs binding of A_2 to the tumor antigen.

[0254] Embodiment 100 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-99, wherein P_2 is bound to A_2 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof.

[0255] Embodiment 101 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-100, wherein P_2 is bound to A_2 at or near an antigen binding site.

[0256] Embodiment 102 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-101, wherein P_2 has less than 70% sequence homology to the tumor antigen.

[0257] Embodiment 103 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-102, wherein P_2 comprises a peptide sequence of at least 10 amino acids in length.

[0258] Embodiment 104 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-103, wherein P_2 comprises a peptide sequence of at least 10 amino acids in length and no more than 20 amino acids in length.

[0259] Embodiment 105 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-104, wherein P_2 comprises a peptide sequence of at least 16 amino acids in length.

[0260] Embodiment 106 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-103 and 105, wherein P_2 comprises a peptide sequence of no more than 40 amino acids in length.

[0261] Embodiment 107 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-106, wherein P_2 comprises at least two cysteine amino acid residues.

[0262] Embodiment 108 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-107, wherein P_2 comprises a cyclic peptide or a linear peptide.

[0263] Embodiment 109 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-108, wherein P_2 comprises a cyclic peptide.

[0264] Embodiment 110 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-108, wherein P_2 comprises a linear peptide.

[0265] Embodiment 111 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-17, 19-24, 27-88, and 91-110, wherein L_1 is bound to N-terminus of A_1.

[0266] Embodiment 112 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16, 18-23, 25-26, 28-86, 89-110, wherein L_1 is bound to C-terminus of A_1.

[0267] Embodiment 113 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-23, 25-26, 28-86, 89-110, and 112, wherein L_2 is bound to N-terminus of A_2.

Embodiment 114 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21, 24, 27-88, and 91-111, wherein L_2 is bound to C-terminus of A_2.

[0268] Embodiment 115 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-114, wherein L_1 or L_2 is a peptide sequence having at least 5 to no more than 50 amino acids.

[0269] Embodiment 116 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-115, wherein L_1 or L_2 is a peptide sequence having at least 10 to no more than 30 amino acids.

[0270] Embodiment 117 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-116, wherein L_1 or L_2 is a peptide sequence having at least 10 amino acids.

[0271] Embodiment 118 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-117, wherein L_1 or L_2 is a peptide sequence having at least 18 amino acids.

[0272] Embodiment 119 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-118, wherein L_1 or L_2 is a peptide sequence having at least 26 amino acids.

[0273] Embodiment 120 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-115, wherein L_1 or L_2 has a formula comprising $(G_2S)_n$ (SEQ ID NO: 922), wherein n is an integer from 1 to 3.

[0274] Embodiment 121 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-120, wherein L_1 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

[0275] Embodiment 122 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-121, wherein P_1 becomes unbound from A_1 when L_1 is cleaved by the tumor specific protease thereby exposing A_1 to CD3.

[0276] Embodiment 123 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 21-122, wherein P_2 becomes unbound from A_2 when L_2 is cleaved by the tumor specific protease thereby exposing A_2 to the tumor antigen.

[0277] Embodiment 124 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-123, wherein the tumor specific protease is selected from the group consisting of metalloprotease, serine protease, cysteine protease, threonine protease, and aspartic protease.

[0278] Embodiment 125 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-124, wherein L_1 or L_2 comprises a urokinase cleavable amino acid sequence, a matriptase cleavable amino acid sequence, a matrix metalloprotease cleavable amino acid sequence, or a legumain cleavable amino acid sequence.

[0279] Embodiment 126 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-119 and 122-125, wherein L_1 or L_2 comprises an amino acid sequence selected from the group consisting of GGGGSLSGRSDNHGSSGT (SEQ ID NO: 923), GGGGSSGGSGGSGLSGRSDNHGSSGT (SEQ ID NO: 924), ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), ISSGLLAGRSDNH (SEQ ID NO: 928), LSGRSDNH (SEQ ID NO: 929), ISSGLLSGRSDNP (SEQ ID NO: 930), ISSGLLSGRSDNH (SEQ ID NO: 931), LSGRSDNHSPLGLAGS (SEQ ID NO: 932), SPLGLAGSLSGRSDNH (SEQ ID NO: 933), SPLGLSGRSDNH (SEQ ID NO: 934), LAGRSDNHSPLGLAGS (SEQ ID NO: 935), LSGRSDNHVPLSLKMG (SEQ ID NO: 936), and LSGRSDNHVPLSLSMG (SEQ ID NO: 937).

[0280] Embodiment 127 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 16-119 and 122-126, wherein L_1 or L_2 comprises an amino acid sequence selected from the group consisting of ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), and ISSGLLAGRSDNH (SEQ ID NO: 928).

[0281] Embodiment 128 comprises a pharmaceutical composition comprising: (i) the polypeptide or polypeptide complex of any one of embodiments 1-127; and (ii) a pharmaceutically acceptable excipient.

[0282] Embodiment 129 comprises an isolated recombinant nucleic acid molecule encoding the polypeptide or polypeptide complex of any one of embodiments 1-127.

[0283] Embodiment 130 comprises an isolated polypeptide or polypeptide complex according to Formula II: L_{1a}-P_{1a}-H_{1a} wherein: L_{1a} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1a} to an anti-CD3 binding domain that binds to CD3 and; P_{1a} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1a} is uncleaved wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to amino acid sequences of SEQ ID NOs: 1-2, and 19-55; and H_{1a} comprises a half-life extending molecule.

[0284] Embodiment 131 comprises an isolated polypeptide or polypeptide complex of embodiment 130, wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2, and 19-55.

[0285] Embodiment 132 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-131, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 1.

[0286] Embodiment 133 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-131, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 2.

[0287] Embodiment 134 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-131, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 54.

[0288] Embodiment 135 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-134, wherein H_{1a} comprises a polymer.

[0289] Embodiment 136 comprises an isolated polypeptide or polypeptide complex of embodiment 135, wherein the polymer is polyethylene glycol (PEG).

[0290] Embodiment 137 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-134, wherein H_{1a} comprises albumin.

[0291] Embodiment 138 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-134, wherein H_{1a} comprises an Fc domain.

[0292] Embodiment 139 comprises an isolated polypeptide or polypeptide complex of embodiment 137, wherein the albumin is serum albumin.

[0293] Embodiment 140 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 137 and 139, wherein the albumin is human serum albumin.

[0294] Embodiment 141 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-140, wherein H_{1a} comprises a polypeptide, a ligand, or a small molecule.

[0295] Embodiment 142 comprises an isolated polypeptide or polypeptide complex of embodiment 141, wherein the polypeptide, the ligand or the small molecule binds a serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1.

[0296] Embodiment 143 comprises an isolated polypeptide or polypeptide complex of embodiment 142, wherein the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin.

[0297] Embodiment 144 comprises an isolated polypeptide or polypeptide complex of embodiment 142, wherein the circulating immunoglobulin molecule comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD.

[0298] Embodiment 145 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 142-143, wherein the serum protein is albumin.

[0004] Embodiment 146 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 141-145, wherein the polypeptide is an antibody.

[0299] Embodiment 147 comprises an isolated polypeptide or polypeptide complex of embodiment 146, wherein the antibody comprises a single domain antibody, a single chain variable fragment or a Fab.

[0300] Embodiment 148 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 146-147, wherein the antibody comprises a single domain antibody that binds to albumin.

[0301] Embodiment 149 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 146-148, wherein the antibody is a human or humanized antibody.

[0302] Embodiment 150 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-149, wherein the single domain antibody is 645gH1gL1.

[0303] Embodiment 151 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-149, wherein the single domain antibody is 645dsgH5gL4.

[0304] Embodiment 152 comprises an isolated polypeptide or polypeptide complex of embodiment 147, wherein the single domain antibody is 23-13-A01 -sc02.

[0305] Embodiment 153 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-148, wherein the single domain antibody is A10m3 or a fragment thereof.

[0306] Embodiment 154 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-148, wherein the single domain antibody is DOM7r-31.

[0307] Embodiment 155 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-148, wherein the single domain antibody is DOM7h-11-15.

[0308] Embodiment 156 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-148, wherein the single domain antibody is Alb-1, Alb-8, or Alb-23.

[0309] Embodiment 157 comprises an isolated polypeptide or polypeptide complex of embodiment 147, wherein the single domain antibody is 10G or 10GE.

[0310] Embodiment 158 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 147-148, wherein the single domain antibody is SA21.

[0311] Embodiment 159 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 130-158, wherein H_{1a} comprises a linking moiety (L_{3a}) that connects H_{1a} to P_{1a}.

[0312] Embodiment 160 comprises an isolated polypeptide or polypeptide complex of embodiment 159, wherein L_{3a} is a peptide sequence having at least 5 to no more than 50 amino acids.

[0313] Embodiment 161 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 159-160, wherein L_{3a} is a peptide sequence having at least 10 to no more than 30 amino acids.

[0005] Embodiment 162 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 159-161, wherein L_{3a} is a peptide sequence having at least 10 amino acids.

[0314] Embodiment 163 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 159-162, wherein L_{3a} is a peptide sequence having at least 18 amino acids.

[0315] Embodiment 164 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 159-163, wherein L_{3a} is a peptide sequence having at least 26 amino acids.

[0316] Embodiment 165 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 159-164, wherein L_{3a} has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

[0317] Embodiment 166 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 159-164, wherein L_{3a} comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)).

[0318] Embodiment 167 comprises an isolated polypeptide or polypeptide complex according to **Formula III**: L_{1b}-P_{1b}-H_{1b} wherein: L_{1b} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1b} to an anti-CD3 binding domain that binds to CD3 and; P_{1b} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1b} is uncleaved wherein the peptide comprises the amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}- Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, and S; and H_{1b} comprises a half-life extending molecule.

[0319] Embodiment 168 comprises an isolated polypeptide or polypeptide complex of embodiment 167, wherein Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P.

[0320] Embodiment 169 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-168, wherein Z_1 is selected from D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and

D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; and Z_{14} is selected from D, Y, and N.

[0321] Embodiment 170 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-169, wherein P_{1b} comprises comprises an amino acid sequence of **Table 17.**

[0322] Embodiment 171 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-170, wherein P_{1b} comprises an amino acid sequences according to any one of SEQ ID NOs: 44-55.

[0323] Embodiment 172 comprises an isolated polypeptide or polypeptide complex of embodiment 167, wherein P_{1b} comprises the amino acid sequences according to SEQ ID NO: 2.

[0324] Embodiment 173 comprises an isolated polypeptide or polypeptide complex of embodiment 167-168, wherein P_{1b} comprises the amino acid sequences according to SEQ ID NO: 54.

[0325] Embodiment 174 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-173, wherein H_{1b} comprises a polymer.

[0326] Embodiment 175 comprises an isolated polypeptide or polypeptide complex of embodiment 174, wherein the polymer is polyethylene glycol (PEG).

[0327] Embodiment 176 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-173, wherein H_{1b} comprises albumin.

[0328] Embodiment 177 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-173, wherein H_{1b} comprises an Fc domain.

[0329] Embodiment 178 comprises an isolated polypeptide or polypeptide complex of embodiment 176, wherein the albumin is serum albumin.

[0330] Embodiment 179 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 176 and 178, wherein the albumin is human serum albumin.

[0331] Embodiment 180 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-179, wherein H_{1b} comprises a polypeptide, a ligand, or a small molecule.

[0332] Embodiment 181 comprises an isolated polypeptide or polypeptide complex of embodiment 180, wherein the polypeptide, the ligand or the small molecule binds a serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1.

[0333] Embodiment 182 comprises an isolated polypeptide or polypeptide complex of embodiment 181, wherein the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin.

[0334] Embodiment 183 comprises an isolated polypeptide or polypeptide complex of embodiment 181, wherein the circulating immunoglobulin molecule comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD.

[0335] Embodiment 184 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 181-182, wherein the serum protein is albumin.

[0336] Embodiment 185 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 180-184, wherein the polypeptide is an antibody.

[0337] Embodiment 186 comprises an isolated polypeptide or polypeptide complex of embodiment 185, wherein the antibody comprises a single domain antibody, a single chain variable fragment or a Fab.

[0338] Embodiment 187 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 185-186, wherein the antibody comprises a single domain antibody that binds to albumin.

[0339] Embodiment 188 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 185-187, wherein the antibody is a human or humanized antibody.

[0006] Embodiment 189 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-188, wherein the single domain antibody is 645gH1gL1.

[0340] Embodiment 190 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-188, wherein the single domain antibody is 645dsgH5gL4.

[0341] Embodiment 191 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186, wherein the single domain antibody is 23-13-A01 -sc02.

[0342] Embodiment 192 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-187, wherein the single domain antibody is A10m3 or a fragment thereof.

[0343] Embodiment 193 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-187, wherein the single domain antibody is DOM7r-31.

[0344] Embodiment 194 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-187, wherein the single domain antibody is DOM7h-11-15.

[0345] Embodiment 195 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-187, wherein the single domain antibody is Alb-1, Alb-8, or Alb-23.

[0346] Embodiment 196 comprises an isolated polypeptide or polypeptide complex of embodiment 186, wherein the single domain antibody is 10G or 10GE.

[0347] Embodiment 197 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 186-187, wherein the single domain antibody is SA21.

[0348] Embodiment 198 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 167-197, wherein H_{1b} comprises a linking moiety (L_{3b}) that connects H_{1b} to P_{1b}.

[0349] Embodiment 199 comprises an isolated polypeptide or polypeptide complex of embodiment 198, wherein L_{3b} is a peptide sequence having at least 5 to no more than 50 amino acids.

[0350] Embodiment 200 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 198-199, wherein L_{3b} is a peptide sequence having at least 10 to no more than 30 amino acids.

[0351] Embodiment 201 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 198-200, wherein L_{3b} is a peptide sequence having at least 10 amino acids.

[0352] Embodiment 202 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 198-201, wherein L_{3b} is a peptide sequence having at least 18 amino acids.

[0353] Embodiment 203 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 198-202, wherein L_{3b} is a peptide sequence having at least 26 amino acids.

[0354] Embodiment 204 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 198-203, wherein L_{3b} has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

[0355] Embodiment 205 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 198-203, wherein L_{3b} comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)).

[0356] Embodiment 206 comprises an isolated polypeptide or polypeptide complex according to **Formula IV**: L_{1c}-P_{1c}-H_{1c} wherein: L_{1c} comprises a tumor specific protease-cleaved linking moiety that when uncleaved connects P_{1c} to an anti-CD3 binding domain that binds to CD3 and; P_{1c} comprises a peptide that impairs binding of the anti-CD3 binding domain to CD3 when L_{1b} is uncleaved wherein the peptide comprises the amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}- U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; and U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S; and H_{1c} comprises a half-life extending molecule.

[0357] Embodiment 207 comprises an isolated polypeptide or polypeptide complex of embodiment 206, wherein U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E, D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; and U_{14} is selected from D, Y, N, F, I, M, and P.

[0358] Embodiment 208 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-207, wherein U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; and U_{14} is selected from D, Y, M, and N.

[0359] Embodiment 209 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-208, wherein P_{1c} comprises comprises an amino acid sequence of **Table 17.**

[0360] Embodiment 210 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-209, wherein P_{1c} comprises an amino acid sequences according to any one of SEQ ID NOs: 44-55.

[0361] Embodiment 211 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-209, wherein P_{1c} comprises the amino acid sequences according to SEQ ID NO: 2.

[0362] Embodiment 212 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-210, wherein P_{1c} comprises the amino acid sequences according to SEQ ID NO: 54.

[0363] Embodiment 213 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-212, wherein H_{1c} comprises a polymer.

[0364] Embodiment 214 comprises an isolated polypeptide or polypeptide complex of embodiment 213, wherein the polymer is polyethylene glycol (PEG).

[0365] Embodiment 215 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-212, wherein H_{1c} comprises albumin.

[0366] Embodiment 216 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-212, wherein H_{1c} comprises an Fc domain.

[0367] Embodiment 217 comprises an isolated polypeptide or polypeptide complex of embodiment 215, wherein the albumin is serum albumin.

[0368] Embodiment 218 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 215 and 217, wherein the albumin is human serum albumin.

[0369] Embodiment 219 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-218, wherein H_{1c} comprises a polypeptide, a ligand, or a small molecule.

[0370] Embodiment 220 comprises an isolated polypeptide or polypeptide complex of embodiment 219, wherein the polypeptide, the ligand or the small molecule binds a serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1.

[0371] Embodiment 221 comprises an isolated polypeptide or polypeptide complex of embodiment 220, wherein the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin.

[0372] Embodiment 222 comprises an isolated polypeptide or polypeptide complex of embodiment 220, wherein the circulating immunoglobulin molecule comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD.

[0373] Embodiment 223 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 220-221, wherein the serum protein is albumin.

[0374] Embodiment 224 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 219-223, wherein the polypeptide is an antibody.

[0375] Embodiment 225 comprises an isolated polypeptide or polypeptide complex of embodiment 224, wherein the antibody comprises a single domain antibody, a single chain variable fragment or a Fab.

[0376] Embodiment 226 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 224-225, wherein the antibody comprises a single domain antibody that binds to albumin.

[0377] Embodiment 227 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 224-226, wherein the antibody is a human or humanized antibody.

[0378] Embodiment 228 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-227, wherein the single domain antibody is 645gH1gL1.

[0379] Embodiment 229 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-227, wherein the single domain antibody is 645dsgH5gL4.

[0380] Embodiment 230 comprises an isolated polypeptide or polypeptide complex of embodiment 225, wherein the single domain antibody is 23-13-A01 -sc02.

[0381] Embodiment 231 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-226, wherein the single domain antibody is A10m3 or a fragment thereof.

[0382] Embodiment 232 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-226, wherein the single domain antibody is DOM7r-31.

[0383] Embodiment 233 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-226, wherein the single domain antibody is DOM7h-11-15.

[0384] Embodiment 234 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-226, wherein the single domain antibody is Alb-1, Alb-8, or Alb-23.

[0385] Embodiment 235 comprises an isolated polypeptide or polypeptide complex of embodiment 225, wherein the single domain antibody is 10G or 10GE.

[0386] Embodiment 236 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 225-226, wherein the single domain antibody is SA21.

[0387] Embodiment 237 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 206-236, wherein H_{1c} comprises a linking moiety (L_{3c}) that connects H_{1c} to P_{1c}.

[0388] Embodiment 238 comprises an isolated polypeptide or polypeptide complex of embodiment 237, wherein L_{3c} is a peptide sequence having at least 5 to no more than 50 amino acids.

[0389] Embodiment 239 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 237-238, wherein L_{3c} is a peptide sequence having at least 10 to no more than 30 amino acids.

[0390] Embodiment 240 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 237-239, wherein L_{3c} is a peptide sequence having at least 10 amino acids.

[0391] Embodiment 241 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 237-240, wherein L_{3c} is a peptide sequence having at least 18 amino acids.

[0392] Embodiment 242 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 237-241, wherein L_{3c} is a peptide sequence having at least 26 amino acids.

[0393] Embodiment 243 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 237-242, wherein L_{3c} has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

[0394] Embodiment 244 comprises an isolated polypeptide or polypeptide complex of any one of embodiments 237-242, wherein L_{3c} comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)).

EXAMPLES

Example 1: Structure activity relationships for Peptide-1 and Peptide 2 by Ala scanning

[0395] Sequence activity relationships were established for Peptide-1 and Peptide-2 by mutating each individual residue within the peptide to alanine and measuring binding and inhibition against SP34.185 scFv. Peptide residues whose alanine mutations significantly weakened binding and inhibition were considered key residues where mutations were not tolerated. Peptide residues whose alanine mutations

performed similarly to the non-mutated sequence were considered non-critical sites where mutations were indeed tolerated.

SP34.185 scFv binding to peptides by ELISA

[0396] Peptides were evaluated for their ability to bind SP34.185 scFv by standard enzyme linked immunosorbent assays (ELISAs). Briefly, biotinylated peptides were captured on neutravidin coated plates, quench with biocytin followed by a washing step. SP34.185 scFv was then titrated onto the peptide captured plates. Plates were then washed and bound SP34.185 scFv was detected using a secondary horse radish peroxidase antibody conjugate. After washing again, plates were developed using standard ELISA techniques and stopped using acid. The concentration of SP34.185 scFv required to achieve 50% maximal signal or EC50 was calculated using Graphpad prism. Data is shown in **Figs. 1A-1F.**

Table 6. Summary of Figure 1B

ELISA	Peptide-1	Peptide-3	Peptide-4	Peptide-5	Peptide-6	Peptide-7	Peptide-8
EC50 nM	1.013	0.9429	1.018	0.9738	1.27	47.5	346.2

Table 7. Summary of Figure 1C

ELISA	Peptide-1	Peptide-9	Peptide-10	Peptide-11	Peptide-12	Peptide-13	Peptide-14
EC50 nM	0.986	310.8	3.134	1,960	4.363	2.76	1.546

Table 8. Summary of Figure 1E

ELISA	Peptide-16	Peptide-17	Peptide-18	Peptide-19	Peptide-20	Peptide-21
EC50 nM	1.356	2.359	30.04	47.50	457.1	4.762

Table 9. Summary of Figure 1F

ELISA	Peptide-22	Peptide-23	Peptide-24	Peptide-25	Peptide-26	Peptide-27
EC50 nM	39.90	2168	1.916	1.948	2.012	1.833

Peptide inhibition of SP34.185 scFv by ELISA

[0397] Peptides were evaluated for their ability to inhibit SP34.185 scFv from binding CD3e by standard enzyme linked immunosorbent assays (ELISAs). Briefly, a fixed concentration of SP34.185 scFv was incubated with varying concentrations of peptides in solution. SP34.185scFv and peptide solutions were incubated for 1hr prior to addition to CD3 coated plates. Binding was allowed to proceed for 30 min prior to washing. After washing, bound SP34.185 scFv was measured using a secondary horse radish peroxidase antibody conjugate. After washing again, plates were developed using standard ELISA techniques and stopped using acid. The concentration of peptide required to inhibit 50% of the SP34.185 scFv CD3 binding signal (IC50) was calculated using Graphpad prism. Data is shown in **Figs. 2A-2F.**

Table 10. Summary of Figure 2B

ELISA	Peptide-1	Peptide-3	Peptide-4	Peptide-5	Peptide-6	Peptide-7	Peptide-8
IC50 uM	0.1926	0.1025	0.2318	0.1905	5.484	>100	>100

Table 11. Summary of Figure 2C

ELISA	Peptide-1	Peptide-9	Peptide-10	Peptide-11	Peptide-12	Peptide-13	Peptide-14
IC50 uM	0.1138	>100	63.18	>100	86.78	36.66	3.009

Table 12. Summary of Figure 2E

ELISA	Peptide-16	Peptide-17	Peptide-18	Peptide-19	Peptide-20	Peptide-21
IC50 uM	0.1473	3.333	>100	>100	>100	41.46

Table 13. Summary of Figure 2F

ELISA	Peptide-22	Peptide-23	Peptide-24	Peptide-25	Peptide-26	Peptide-27
IC50 uM	>100	>100	1.912	0.6992	1.456	0.1180

Table 14. Summary of Peptide Sequences

Peptide-ID	anti-CD3 Panned target	Sequence	SEQ ID NO:
Peptide-1	SP34.185	GSQCLGPEWEVCPY	1
Peptide-3	SP34.185	ASQCLGPEWEVCPY	19
Peptide-4	SP34.185	GAQCLGPEWEVCPY	20
Peptide-5	SP34.185	GSACLGPEWEVCPY	21
Peptide-6	SP34.185	GSQCAGPEWEVCPY	22
Peptide-7	SP34.185	GSQCLAPEWEVCPY	23
Peptide-8	SP34.185	GSQCLGAEWEVCPY	24
Peptide-9	SP34.185	GSQCLGPAWEVCPY	25
Peptide-10	SP34.185	GSQCLGPEAEVCPY	26
Peptide-11	SP34.185	GSQCLGPEWAVCPY	27
Peptide-12	SP34.185	GSQCLGPEWEACPY	28
Peptide-13	SP34.185	GSQCLGPEWEVCAY	29
Peptide-14	SP34.185	GSQCLGPEWEVCPA	30
Peptide-15	SP34.185	GSQCLGPEWEVCPY	31
Peptide-2	SP34.185	VYCGPEFDESVGCM	2
Peptide-16	SP34.185	AYCGPEFDESVGCM	32
Peptide-17	SP34.185	VACGPEFDESVGCM	33

Peptide-18	SP34.185	VYCAPEFDESVGCM	34
Peptide-19	SP34.185	VYCGAEFDESVGCM	35
Peptide-20	SP34.185	VYCGPAFDESVGCM	36
Peptide-21	SP34.185	VYCGPEADESVGCM	37
Peptide-22	SP34.185	VYCGPEFAESVGCM	38
Peptide-23	SP34.185	VYCGPEFDASVGCM	39
Peptide-24	SP34.185	VYCGPEFDEAVGCM	40
Peptide-25	SP34.185	VYCGPEFDESAGCM	41
Peptide-26	SP34.185	VYCGPEFDESVACM	42
Peptide-27	SP34.185	VYCGPEFDESVGCA	43

Example 2: Polypeptide binding to CD3 by ELISA

[0398] Peptide masks were incorporated into bispecific polypeptide molecules via tethering to SP34.185 scFv using a cleavable linker. Polypeptide molecules were then evaluated for their ability to bind CD3 before and after protease treatment via standard enzyme linked immunosorbent assays (ELISAs). Briefly, biotinylated CD3 was captured on neutravidin coated plates, quenched with biocytin, and washed. Polypeptide molecules were treated with protease when indicated. Polypeptide molecules were then titrated in buffer and added to the CD3 captured ELISA plate. After a brief incubation, plates were washed, and bound polypeptide molecules were detected using a standard secondary horse radish peroxidase conjugate antibody. After another wash, ELISA plates were developed and stopped in acid. The concentration of polypeptide requied to achieve a 50% maximal signal (EC50) was calculated in Graphpad prism. Tethering of inhibitory peptides to SP34.185 scFv significantly hindered the ability to bind CD3 relative to the control polypeptide that lacks inhibitory peptide masking.

Table 15. Summary of Figure 3

	PC-1	PC-1+ MTSP1	PC-2	PC-2 + MTSP1	PC-3
EC50 nM	13.66	0.05722	13.28	0.06099	0.05401
Fold shift	252.9x	1.1x	245.9x	1.1x	1x

Example 3: Polypeptide mediated tumor cell killing

Peptide masks were incorporated into bispecific polypeptide molecules via tethering to SP34.185 scFv using a cleavable linker. Bispecific polypeptide molecules' functional activities were then evaluated before and after protease treatment via tumor cell line killing assays. Tumor cell killing was measured using an xCelligence real time cell analyzer (RTCA from Agilent) that relies on surface impedance to monitor cell growth kinetics. Briefly, tumor cell lines were seeded on E-plates and allowed to adhere overnight in a humidified incubator at 37C with 5% carbon dioxide atmosphere. After the overnight incubation, bispecific polypeptide molecules were titrated in cell culture medium and added to the plates. In addition, effector cells such as PBMCs or CD8+ T cells were added to the plate at the indicated effector cell to tumor cell ratio. Bispecific polypeptides were treated with protease when indicated. Plates were then placed back on the

RTCA inside the humidified incubator and impedance measurements (cell index) collected every 10minutes for multiple days. After multiple days, the area under the tumor growth curves (cell index times hours) were plotted against the logarithmic concentration of polypeptide molecule. The concentration of polypeptide molecule required to inhibit tumor cell growth by 50% (IC50) was calculated in Graphpad Prism. Masking of the polypeptide binding domains significantly inhibited functional tumor killing while treatment of masked polypeptides with protease restored functional tumor killing.

Table 16. Summary of Figure 4

	PC-1	PC-1+ MTSP1	PC-2	PC-2 + MTSP1	PC-3
IC50 pM	0.2463	144.3	0.1234	239.5	0.4171
Fold shift	1x	585.9x	1x	1940.8x	control

Example 4: Optimized phage library construction

[0399] Using the peptide sequence activity relationships (SAR) of Example 1, DNA oligo libraries were constructed where codons encoding critical residues within each peptide sequence were minimally mutated and codons encoding non-critical residues were heavily mutated. The resulting oligos were cloned into bacteriophage vectors used to display the SAR guided peptides via fusion to the pIII filament of the bacteriophage. The relevant vectors were then used to produce the phage optimization libraries via amplification in bacteria using standard techniques in the field.

Example 5: Panning of the optimized phage library

[0400] Once the phage optimization libraries were completed, phage libraries were bio-panned using SP34.185 scFv loaded beads. Multiple rounds of panning were performed where bacteriophage was allowed to bind to SP34.185 scFv loaded beads, washed, eluted, and amplified. Additional selective pressure was included during each round of panning using a fixed concentration of CD3, peptide-1, or peptide-2. After panning, phage infected bacteria were plated out and colonies picked into 96 well blocks. Clonal phage was then amplified and separated from bacterial cells via centrifugation. Phage containing supernatants were tested in binding ELISAs against SP34.185 scFv coated plates in the presence or absence of saturating concentration of CD3. Phage able to bind SP34.185 scFv were selected for sequence analysis if the binding signal was reduced in the presence of CD3.

Example 6: Panning ELISAs

[0401] Clonal phage were harvested as crude supernatants and screened via standard enzyme linked immunsorbent assays (ELISAs). Briefly, biotinylated SP34.185 scFv was captured on neutravidin coated plates. Prior to the addition of clonal phage, wells were incubated with blocking buffer and CD3 or blocking buffer alone. Without washing or aspirating, clonal phage supernatants were then added to the wells and incubated for a short time. Wells were then washed followed by detection of bound phage using a horse

radish peroxidase conjugated anti-M13 antibody. Clonal phage of interest were then sent for sequence analysis.

[0402] Phage panning results of Peptide-2 library sequences are shown in **Table 17.**

[0403] Peptide-29 to Peptide-40 were selected for sequence analysis and sequences are shown in **Table 18.** Peptide binding to SP34.185 scFv to CD3 is shown in **Figs. 5A-5B** and summarized in **Tables 19-20**, respectively. Peptide inhibition of SP34.185 scFv binding to CD3 by ELISA is shown in **Figs. 6A-6B** and summarized in **Tables 21-22**, respectively.

[0404] The core sequence motif for Peptide-2 is shown in **Fig. 7**.

Table 17. Clonal Phage Peptide Sequences from the Peptide-2 Optimization Library Panning (-) indicates same amino acid as in Peptide-2 corresponding position (e.g. Phage-1 position).

Phage ID	Amino acid position sequence														Phage binding ELISA			SEQ ID NO:
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	Background signal	SP34.185 scFv signal	SP34.185 scFv signal in presence of CD3	
Phage-1/Peptide 2	V	Y	C	G	P	E	F	D	E	S	V	G	C	M	0.06	2.79	0.09	56
Phage-2	D	D	-	W	-	D	W	E	F	D	F	A	-	A	0.08	2.75	0.09	57
Phage-3	Y	I	-	-	L	D	-	P	D	F	L	Y	-	D	0.08	2.88	0.10	58
Phage-4	F	D	-	W	-	D	W	E	-	Y	F	V	-	D	0.08	2.79	0.09	59
Phage-5	Y	I	-	W	-	D	W	E	-	Y	F	D	-	D	0.08	2.74	0.09	60
Phage-6	N	I	-	W	-	D	W	E	D	D	Y	F	-	F	0.09	2.54	0.09	61
Phage-7	N	F	-	W	-	D	W	E	Y	I	Y	P	-	I	0.07	2.77	0.09	62
Phage-8	-	D	-	W	-	D	W	E	-	D	F	L	-	I	0.08	2.54	0.08	63
Phage-9	H	A	-	W	-	D	W	E	-	Y	F	P	-	N	0.08	2.85	0.09	64
Phage-10	Y	D	-	-	-	D	V	-	-	-	Y	V	-	V	0.09	2.63	0.10	65
Phage-11	I	D	-	W	-	D	W	E	D	D	T	F	-	Y	0.09	2.73	0.08	66
Phage-12	Y	L	-	-	-	D	G	-	-	T	L	A	-	Y	0.08	2.66	0.15	67
Phage-13	-	D	-	-	-	D	G	-	-	-	I	L	-	Y	0.11	2.13	0.08	68
Phage-14	F	I	-	W	-	D	W	E	-	D	Y	F	-	A	0.07	2.44	0.09	69
Phage-15	G	D	-	W	-	D	W	E	W	D	F	Y	-	D	0.07	2.71	0.07	70
Phage-16	Y	L	-	W	-	D	W	E	Y	I	D	L	-	D	0.12	2.67	0.08	71
Phage-17	S	F	-	W	-	D	W	E	-	Y	F	D	-	D	0.10	2.60	0.07	72
Phage-18	D	D	-	W	-	D	W	E	-	Y	A	S	-	D	0.09	2.57	0.07	73
Phage-19	N	L	-	W	-	D	W	E	Y	P	F	F	-	D	0.09	2.52	0.09	74
Phage-20	F	D	-	W	-	D	W	E	-	-	F	V	-	D	0.08	2.34	0.09	75
Phage-21	D	I	-	-	-	D	G	-	-	T	I	I	-	D	0.13	2.30	0.10	76
Phage-22	D	D	-	W	-	D	W	E	Y	Y	A	V	-	D	0.09	2.28	0.09	77
Phage-23	Y	D	-	W	-	D	W	E	-	Y	S	N	-	D	0.10	2.17	0.08	78
Phage-24	I	N	-	W	-	D	W	E	D	Y	F	F	-	D	0.07	2.16	0.07	79

Phage-25	N	I	-	W	-	D	W	E	D	D	T	F	-	F	0.06	2.87	0.07	80
Phage-26	N	I	-	W	-	D	W	E	P	N	S	F	-	F	0.09	2.87	0.08	81
Phage-27	Y	D	-	-	-	-	M	-	-	-	I	D	-	F	0.09	2.39	0.08	82
Phage-28	D	F	-	W	-	D	W	E	F	P	F	I	-	H	0.11	2.73	0.12	83
Phage-29	D	F	-	-	-	-	M	-	-	-	I	T	-	I	0.07	2.36	0.08	84
Phage-30	Y	D	-	-	-	-	-	-	-	-	T	V	-	I	0.10	2.32	0.08	85
Phage-31	H	D	-	W	-	D	W	E	W	D	I	F	-	I	0.07	2.26	0.08	86
Phage-32	H	A	-	W	-	D	W	E	-	Y	N	P	-	N	0.11	2.71	0.11	87
Phage-33	D	V	-	W	-	D	W	E	W	D	F	F	-	N	0.08	2.65	0.08	88
Phage-34	N	-	-	W	-	D	W	E	Y	Y	I	P	-	N	0.10	2.57	0.08	89
Phage-35	I	I	-	W	-	D	W	E	F	I	D	Y	-	N	0.08	2.10	0.07	90
Phage-36	S	L	-	W	-	D	W	E	Y	D	I	A	-	P	0.07	2.53	0.08	91
Phage-37	D	L	-	-	-	-	L	-	-	-	I	F	-	P	0.08	2.49	0.09	92
Phage-38	T	N	-	W	-	D	W	E	W	V	L	P	-	P	0.14	2.47	0.10	93
Phage-39	I	E	-	W	-	D	W	E	P	N	Y	F	-	P	0.13	2.29	0.09	94
Phage-40	I	F	-	W	-	D	W	E	D	Y	-	D	-	P	0.07	2.28	0.07	95
Phage-41	I	D	-	W	-	D	W	E	Y	D	F	F	-	P	0.07	2.26	0.08	96
Phage-42	L	F	-	W	-	D	W	E	D	-	F	F	-	P	0.18	2.11	0.13	97
Phage-43	-	D	-	W	-	D	W	E	D	Y	A	D	-	T	0.11	2.20	0.10	98
Phage-44	-	I	-	W	-	D	W	E	Q	Y	F	P	-	V	0.11	2.34	0.09	99
Phage-45	I	E	-	W	-	D	W	E	P	I	Y	P	-	Y	0.09	2.85	0.09	100
Phage-46	I	T	-	W	-	D	W	E	V	Y	F	P	-	Y	0.07	2.55	0.08	101
Phage-47	I	D	-	W	-	D	W	E	Y	I	H	P	-	Y	0.06	2.51	0.09	102
Phage-48	I	D	-	W	-	D	W	E	Y	I	N	P	-	Y	0.12	2.50	0.12	103
Phage-49	A	D	-	W	-	D	W	E	-	A	F	P	-	Y	0.09	2.44	0.09	104
Phage-50	I	D	-	W	-	D	W	E	Y	I	Y	P	-	Y	0.09	2.31	0.07	105
Phage-51	N	I	-	W	-	D	W	E	D	D	N	F	-	F	0.09	2.08	0.09	106
Phage-52	Y	D	-	W	-	D	W	E	Y	V	D	A	-	Y	0.09	2.06	0.09	107
Phage-53	F	-	-	-	-	D	G	-	-	-	Y	V	-	D	0.09	2.03	0.11	108
Phage-54	D	I	-	W	-	D	W	E	Y	I	N	I	-	S	0.11	2.02	0.11	109
Phage-55	F	V	-	W	-	D	W	E	D	F	N	F	-	D	0.07	2.01	0.08	110
Phage-56	F	A	-	W	-	D	W	E	D	Y	-	A	-	D	0.07	2.01	0.09	111
Phage-57	D	N	-	W	-	D	W	E	Y	D	F	F	-	V	0.08	1.99	0.09	112
Phage-58	Y	D	-	W	-	D	W	E	-	Y	N	D	-	A	0.09	1.96	0.11	113
Phage-59	D	D	-	-	-	D	G	-	-	T	I	I	-	V	0.07	1.91	0.09	114
Phage-60	F	P	-	W	-	D	W	E	-	Y	A	I	-	D	0.10	1.89	0.10	115
Phage-61	P	D	-	-	-	D	G	-	-	-	L	F	-	T	0.12	1.86	0.07	116

Phage-62	D	N	-	W	-	D	W	E	Y	D	Y	F	-	V	0.07	1.83	0.07	117
Phage-63	I	F	-	W	-	D	W	E	-	F	Y	D	-	Y	0.12	1.82	0.08	118
Phage-64	A	D	-	W	-	D	W	E	-	Y	F	P	-	N	0.08	1.82	0.08	119
Phage-65	H	T	-	W	-	D	W	E	D	D	I	F	-	N	0.12	1.81	0.10	120
Phage-66	F	A	-	W	-	D	W	E	-	A	F	L	-	L	0.09	1.80	0.09	121
Phage-67	Y	D	-	-	-	-	L	-	-	-	I	A	-	D	0.08	1.77	0.08	122
Phage-68	N	S	-	W	-	D	W	E	Y	D	I	I	-	D	0.08	1.77	0.10	123
Phage-69	F	A	-	W	-	D	W	E	-	V	A	P	-	Y	0.07	1.75	0.07	124
Phage-70	L	D	-	-	-	D	G	-	-	T	L	T	-	Y	0.10	1.75	0.12	125
Phage-71	-	L	-	W	-	D	W	E	-	F	Y	D	-	P	0.07	1.74	0.09	126
Phage-72	H	A	-	W	-	V	W	E	-	Y	F	P	-	N	0.07	1.72	0.08	127
Phage-73	N	E	-	W	-	N	G	E	P	T	F	P	-	T	0.08	1.71	0.07	128
Phage-74	L	T	-	-	-	D	G	-	-	T	L	Y	-	D	0.08	1.70	0.07	129
Phage-75	Y	D	-	-	-	-	Y	-	-	-	-	P	-	I	0.13	1.67	0.09	130
Phage-76	I	E	-	W	-	D	W	E	P	N	S	F	-	D	0.09	1.66	0.08	131
Phage-77	Y	D	-	-	-	-	L	-	-	-	I	H	-	Y	0.12	1.66	0.09	132
Phage-78	I	-	-	-	-	-	-	-	-	-	T	I	-	N	0.08	1.63	0.08	133
Phage-79	I	-	-	-	-	-	V	E	-	A	Y	L	-	Y	0.09	1.62	0.10	134
Phage-80	F	D	-	-	-	D	G	-	-	T	-	Y	-	D	0.09	1.61	0.08	135
Phage-81	I	D	-	-	-	D	G	-	-	T	I	S	-	Y	0.08	1.57	0.11	136
Phage-82	N	-	-	-	-	-	-	-	-	-	S	T	-	L	0.10	1.55	0.11	137
Phage-83	Y	D	-	-	-	D	G	-	-	-	Y	F	-	D	0.08	1.53	0.08	138
Phage-84	N	F	-	W	-	D	W	E	Y	F	N	D	-	N	0.09	1.53	0.09	139
Phage-85	-	L	-	W	-	D	W	E	A	F	F	D	-	D	0.07	1.47	0.07	140
Phage-86	I	-	-	-	-	-	W	E	W	P	-	A	-	N	0.16	1.47	0.10	141
Phage-87	-	F	-	W	-	D	W	E	D	N	F	F	-	N	0.08	1.46	0.10	142
Phage-88	-	V	-	W	-	D	W	E	T	F	F	P	-	D	0.08	1.46	0.08	143
Phage-89	D	N	-	-	-	D	G	-	-	T	Y	I	-	N	0.10	1.45	0.09	144
Phage-90	D	N	-	W	-	D	W	E	Y	N	F	F	-	V	0.07	1.45	0.08	145
Phage-91	F	-	-	-	-	-	V	E	-	D	Y	L	-	I	0.10	1.43	0.10	146
Phage-92	D	N	-	W	-	D	W	E	Y	D	I	F	-	V	0.07	1.43	0.07	147
Phage-93	I	D	-	-	-	-	-	-	-	-	I	A	-	P	0.08	1.42	0.08	148
Phage-94	Y	F	-	-	-	-	V	E	-	Y	T	L	-	F	0.10	1.42	0.10	149
Phage-95	F	-	-	-	-	-	-	-	-	-	A	P	-	N	0.06	1.37	0.08	150
Phage-96	F	D	-	-	-	-	V	E	-	Y	F	Y	-	A	0.11	1.36	0.08	151
Phage-97	D	F	-	W	-	D	W	E	D	F	F	F	-	A	0.18	1.35	0.12	152
Phage-98	F	F	-	-	-	D	G	-	-	T	L	S	-	N	0.08	1.35	0.09	153

Phage-99	F	I	-	-	-	-	-	-	-	-	-	A	-	L	0.14	1.35	0.09	154
Phage-100	Y	D	-	-	-	-	-	-	-	A	I	-	-	Y	0.09	1.32	0.10	155
Phage-101	Y	I	-	W	-	D	W	E	-	Y	L	Y	-	P	0.10	1.32	0.15	156
Phage-102	F	D	-	W	-	D	W	E	-	P	T	T	-	H	0.08	1.31	0.08	157
Phage-103	Y	D	-	W	-	D	W	E	D	F	P	I	-	D	0.14	1.31	0.10	158
Phage-104	-	V	-	W	-	D	W	E	Y	I	D	D	-	S	0.08	1.30	0.07	159
Phage-105	I	N	-	W	-	D	W	E	V	I	S	F	-	D	0.12	1.30	0.08	160
Phage-106	L	S	-	W	-	D	W	E	-	V	T	P	-	L	0.10	1.29	0.10	161
Phage-107	F	A	-	W	-	D	W	E	-	V	D	I	-	Y	0.09	1.28	0.08	162
Phage-108	Y	D	-	-	-	-	M	-	-	-	I	V	-	D	0.10	1.25	0.08	163
Phage-109	Y	D	-	W	-	D	W	E	V	F	I	V	-	D	0.06	1.25	0.07	164
Phage-110	D	N	-	W	-	D	W	E	H	N	F	F	-	V	0.10	1.25	0.08	165
Phage-111	Y	D	-	-	-	D	G	-	-	-	I	Y	-	P	0.07	1.23	0.08	166
Phage-112	Y	D	-	-	-	-	-	E	F	P	Y	Y	-	F	0.12	1.23	0.12	167
Phage-113	A	D	-	-	-	-	Y	-	-	-	-	P	-	V	0.11	1.22	0.09	168
Phage-114	F	L	-	-	-	-	V	E	-	V	H	Y	-	S	0.08	1.22	0.10	169
Phage-115	T	D	-	W	-	D	W	E	Y	I	T	S	-	S	0.08	1.22	0.08	170
Phage-116	A	F	-	-	-	-	L	-	-	-	I	T	-	D	0.09	1.21	0.09	171
Phage-117	N	D	-	W	-	D	W	E	-	Y	F	S	-	Y	0.09	1.19	0.09	172
Phage-118	F	D	-	-	-	-	W	E	I	V	T	D	-	Y	0.08	1.19	0.09	173
Phage-119	N	L	-	-	-	-	M	-	-	-	I	I	-	P	0.13	1.19	0.11	174
Phage-120	D	L	-	-	-	-	M	-	-	-	I	Y	-	D	0.10	1.19	0.14	175
Phage-121	F	D	-	-	-	D	G	V	-	D	Y	I	-	D	0.09	1.18	0.09	176
Phage-122	Y	A	-	W	-	D	W	E	-	D	F	A	-	Y	0.11	1.18	0.08	177
Phage-123	H	D	-	-	-	-	M	-	-	-	I	V	-	V	0.10	1.17	0.10	178
Phage-124	-	F	-	-	-	-	-	E	F	I	F	L	-	A	0.07	1.17	0.08	179
Phage-125	Y	D	-	-	-	-	L	-	-	-	I	L	-	D	0.08	1.16	0.09	180
Phage-126	S	V	-	W	-	D	W	E	-	F	Y	S	-	D	0.11	1.16	0.10	181
Phage-127	P	-	-	-	-	D	G	-	-	T	A	I	-	T	0.13	1.16	0.10	182
Phage-128	D	D	-	-	-	-	L	E	W	Y	Y	P	-	Y	0.09	1.16	0.08	183
Phage-129	F	I	-	-	-	-	-	-	-	-	L	P	-	N	0.08	1.14	0.09	184
Phage-130	I	D	-	-	-	-	-	-	-	-	L	P	-	D	0.11	1.14	0.33	185
Phage-131	F	L	-	-	-	-	-	E	-	D	A	P	-	Y	0.08	1.13	0.08	186
Phage-132	I	F	-	-	-	D	G	-	-	T	H	I	-	H	0.10	1.13	0.07	187
Phage-133	-	F	-	W	-	D	W	E	Y	I	D	F	-	N	0.10	1.11	0.21	188
Phage-134	I	F	-	-	-	-	Y	-	-	-	L	H	-	I	0.12	1.11	0.11	189
Phage-135	H	L	-	W	-	D	W	E	W	Y	-	D	-	P	0.08	1.11	0.10	190

Phage-136	F	I	-	-	-	-	M	-	-	-	I	A	-	N	0.08	1.11	0.09	191
Phage-137	I	F	-	-	-	-	V	E	M	I	F	L	-	N	0.09	1.10	0.08	192
Phage-138	Y	D	-	-	-	-	W	E	F	P	-	D	-	I	0.11	1.09	0.11	193
Phage-139	N	L	-	-	-	-	L	-	-	-	I	T	-	F	0.10	1.09	0.08	194
Phage-140	F	-	-	-	-	-	V	E	D	F	Y	F	-	Y	0.08	1.09	0.08	195
Phage-141	D	-	-	-	-	-	-	-	-	-	L	I	-	N	0.11	1.07	0.11	196
Phage-142	D	-	-	-	-	-	-	-	-	-	L	P	-	D	0.08	1.07	0.08	197
Phage-143	A	I	-	-	-	-	L	-	-	-	I	A	-	P	0.09	1.07	0.09	198
Phage-144	-	I	-	-	-	-	V	E	D	Y	N	L	-	Y	0.08	1.07	0.09	199
Phage-145	H	T	-	W	-	D	W	E	D	Y	T	V	-	P	0.10	1.06	0.09	200
Phage-146	S	D	-	W	-	D	W	E	Y	F	Y	D	-	N	0.10	1.06	0.08	201
Phage-147	-	F	-	-	-	D	G	-	-	T	-	H	-	D	0.09	1.05	0.08	202
Phage-148	D	-	-	-	-	-	Y	-	-	-	-	H	-	I	0.09	1.05	0.08	203
Phage-149	A	D	-	-	-	D	G	-	-	-	I	I	-	H	0.07	1.05	0.08	204
Phage-150	F	-	-	-	-	-	L	-	-	-	L	T	-	V	0.10	1.05	0.08	205
Phage-151	I	L	-	-	-	-	V	E	-	D	Y	Y	-	Y	0.11	1.04	0.09	206
Phage-152	H	L	-	W	-	D	W	E	-	Y	H	S	-	D	0.09	1.04	0.09	207
Phage-153	I	F	-	W	-	D	W	E	D	Y	N	F	-	T	0.08	1.04	0.11	208
Phage-154	I	V	-	-	-	D	G	-	-	T	L	I	-	H	0.12	1.04	0.11	209
Phage-155	A	D	-	W	-	D	W	E	W	D	Y	T	-	D	0.12	1.03	0.11	210
Phage-156	I	T	-	-	-	-	-	-	-	-	T	T	-	N	0.20	1.02	0.21	211
Phage-157	Y	H	-	W	-	D	W	E	-	Y	T	S	-	D	0.20	1.02	0.09	212
Phage-158	N	-	-	-	-	-	V	E	-	Y	A	L	-	T	0.11	1.01	0.10	213
Phage-159	F	I	-	-	-	-	M	-	-	-	I	H	-	D	0.15	1.00	0.19	214
Phage-160	D	N	-	W	-	D	W	E	-	F	A	V	-	P	0.14	1.00	0.10	215
Phage-161	Y	D	-	-	-	-	L	-	-	T	-	V	-	D	0.10	1.00	0.09	216
Phage-162	Y	D	-	-	-	-	-	-	-	-	I	A	-	Y	0.08	0.99	0.08	217
Phage-163	I	D	-	W	-	D	W	E	Y	T	-	H	-	D	0.07	0.97	0.09	218
Phage-164	D	D	-	-	-	-	L	-	-	-	I	I	-	I	0.09	0.96	0.09	219
Phage-165	-	-	-	-	-	-	Y	-	-	-	S	F	-	F	0.09	0.91	0.08	220
Phage-166	F	N	-	W	-	D	W	E	D	P	Y	F	-	V	0.09	0.86	0.07	221
Phage-167	Y	D	-	-	-	-	Y	-	-	-	S	Y	-	S	0.08	0.82	0.07	222
Phage-168	-	A	-	W	-	D	W	E	Y	T	D	S	-	F	0.13	0.79	0.09	223
Phage-169	T	D	-	-	-	-	-	-	-	-	-	A	-	Y	0.10	0.77	0.09	224
Phage-170	T	D	-	W	-	D	W	E	F	Y	A	D	-	D	0.07	0.75	0.08	225
Phage-171	Y	D	-	-	-	-	L	-	-	-	-	I	-	H	0.09	0.69	0.09	226
Phage-172	S	D	-	-	-	D	G	-	-	-	I	I	-	T	0.07	0.69	0.07	227

Phage-173	Y	-	-	-	-	-	-	-	-	-	I	D	-	D	0.08	0.67	0.09	228
Phage-174	F	F	-	-	-	-	I	-	-	-	I	A	-	V	0.08	0.62	0.09	229
Phage-175	D	-	-	-	-	-	-	-	-	-	T	F	-	D	0.16	0.60	0.10	230
Phage-176	Y	D	-	-	-	-	W	E	W	P	I	D	-	V	0.10	0.59	0.10	231
Phage-177	F	-	-	-	-	-	I	E	L	F	S	F	-	Y	0.13	0.59	0.11	232
Phage-178	Y	-	-	-	-	-	V	-	-	-	I	T	-	P	0.15	0.42	0.11	233
Phage-179	I	L	-	-	-	-	-	-	-	-	I	N	-	N	0.09	0.37	0.25	234
Phage-180	-	V	-	-	-	A	M	G	Q	H	Y	L	-	D	0.08	0.09	0.08	235
Phage-181	-	V	-	-	T	K	M	G	-	H	Y	L	-	S	0.08	0.08	0.08	236
Phage-182	Y	D	-	W	-	D	W	E	Y	V	Y	A	-	Y	0.08	0.98	0.08	237
Phage-183	D	L	-	-	-	-	L	-	-	-	-	N	-	D	0.09	0.98	0.08	238
Phage-184	Y	-	-	-	-	-	-	-	-	-	T	V	-	Y	0.14	0.97	0.16	239
Phage-185	L	D	-	W	-	D	W	E	W	P	Y	S	-	N	0.08	0.96	0.09	240
Phage-186	F	I	-	W	-	D	W	E	D	D	F	F	-	Y	0.08	0.96	0.09	241
Phage-187	D	L	-	-	-	-	V	E	W	Y	F	F	-	N	0.11	0.95	0.10	242
Phage-188	Y	D	-	-	-	-	L	-	-	-	I	V	-	F	0.07	0.94	0.08	243
Phage-189	L	N	-	W	-	V	W	E	D	D	-	F	-	Y	0.09	0.92	0.09	244
Phage-190	F	N	-	W	-	D	W	E	D	P	N	F	-	V	0.09	0.91	0.09	245
Phage-191	-	I	-	W	-	D	W	E	D	D	Y	F	-	P	0.10	0.91	0.13	246
Phage-192	F	L	-	-	-	-	-	-	-	-	S	V	-	Y	0.10	0.91	0.08	247
Phage-193	Y	D	-	-	-	-	L	-	-	-	I	F	-	Y	0.10	0.91	0.09	248
Phage-194	H	L	-	-	-	D	G	-	-	-	F	T	-	F	0.11	0.90	0.10	249
Phage-195	Y	F	-	-	-	-	M	-	-	-	L	Y	-	I	0.08	0.90	0.08	250
Phage-196	Y	-	-	-	-	-	V	E	-	Y	A	N	-	Y	0.07	0.90	0.07	251
Phage-197	N	T	-	-	-	-	-	-	-	-	T	A	-	Y	0.16	0.90	0.58	252
Phage-198	I	D	-	W	-	D	W	E	-	A	F	N	-	Y	0.09	0.90	0.08	253
Phage-199	A	-	-	-	-	-	L	E	-	F	F	L	-	T	0.09	0.89	0.08	254
Phage-200	I	-	-	-	-	-	V	E	-	V	H	H	-	Y	0.08	0.89	0.08	255
Phage-201	F	F	-	-	-	-	-	-	-	-	-	A	-	D	0.10	0.89	0.11	256
Phage-202	Y	D	-	-	-	-	L	-	-	T	I	I	-	A	0.08	0.89	0.08	257
Phage-203	I	L	-	-	-	-	W	E	Y	P	L	D	-	S	0.09	0.89	0.10	258
Phage-204	F	I	-	-	-	-	-	-	-	-	T	T	-	N	0.09	0.88	0.10	259
Phage-205	F	-	-	-	-	-	L	-	-	-	-	S	-	D	0.17	0.88	0.15	260
Phage-206	H	L	-	-	-	-	L	-	-	-	-	T	-	F	0.10	0.87	0.10	261
Phage-207	L	I	-	-	-	-	V	E	D	Y	S	L	-	H	0.09	0.87	0.09	262
Phage-208	Y	F	-	-	-	-	M	-	-	-	-	Y	-	D	0.08	0.87	0.08	263
Phage-209	H	-	-	-	-	-	M	-	-	-	I	Y	-	I	0.13	0.87	0.09	264

Phage-210	F	D	-	-	-	-	L	-	-	-	I	N	-	D	0.08	0.87	0.09	265
Phage-211	Y	-	-	-	-	-	V	E	-	Y	I	Y	-	T	0.07	0.87	0.08	266
Phage-212	L	A	-	W	-	V	R	E	-	I	N	A	-	I	0.08	0.85	0.07	267
Phage-213	I	D	-	W	-	D	W	E	D	I	T	F	-	D	0.08	0.85	0.08	268
Phage-214	I	V	-	-	-	-	L	-	-	-	I	T	-	P	0.11	0.85	0.15	269
Phage-215	F	-	-	-	-	-	-	E	L	P	A	D	-	D	0.08	0.85	0.09	270
Phage-216	F	D	-	-	-	-	-	-	-	-	N	P	-	F	0.10	0.85	0.09	271
Phage-217	D	A	-	W	-	D	W	E	-	Y	S	S	-	D	0.10	0.83	0.10	272
Phage-218	D	H	-	W	-	D	W	E	P	N	Y	F	-	V	0.08	0.83	0.09	273
Phage-219	D	-	-	W	-	D	W	E	I	N	Y	I	-	F	0.09	0.83	0.10	274
Phage-220	I	-	-	W	-	D	W	E	Y	V	Y	A	-	N	0.10	0.82	0.09	275
Phage-221	D	F	-	-	-	-	V	E	-	D	Y	L	-	D	0.07	0.82	0.08	276
Phage-222	H	D	-	-	-	D	G	R	-	D	Y	D	-	A	0.11	0.82	0.09	277
Phage-223	L	A	-	W	-	D	W	E	D	D	Y	F	-	V	0.08	0.82	0.09	278
Phage-224	D	I	-	W	-	D	W	E	D	Y	L	P	-	V	0.10	0.82	0.10	279
Phage-225	I	L	-	-	-	-	I	E	V	Y	A	L	-	P	0.08	0.81	0.10	280
Phage-226	I	F	-	-	-	-	W	E	F	-	-	L	-	N	0.10	0.81	0.11	281
Phage-227	T	-	-	-	-	-	V	E	D	F	S	L	-	V	0.07	0.80	0.08	282
Phage-228	F	I	-	-	-	-	W	E	F	V	D	A	-	F	0.11	0.80	0.09	283
Phage-229	F	A	-	W	-	D	W	E	-	D	S	P	-	D	0.06	0.80	0.07	284
Phage-230	I	L	-	-	-	-	V	E	-	L	I	F	-	P	0.12	0.80	0.08	285
Phage-231	F	-	-	-	-	-	V	E	-	Y	I	Y	-	Y	0.08	0.80	0.08	286
Phage-232	D	S	-	-	-	-	L	-	-	-	I	I	-	D	0.10	0.79	0.09	287
Phage-233	F	L	-	-	-	D	G	-	-	T	S	V	-	D	0.11	0.79	0.08	288
Phage-234	F	N	-	W	-	N	G	E	P	T	Y	F	-	V	0.11	0.79	0.08	289
Phage-235	L	A	-	W	-	V	W	E	Y	P	-	T	-	I	0.09	0.78	0.09	290
Phage-236	D	-	-	-	-	-	V	E	-	D	-	Y	-	Y	0.09	0.78	0.09	291
Phage-237	I	T	-	W	-	D	W	E	-	Y	A	N	-	T	0.08	0.77	0.07	292
Phage-238	F	F	-	-	-	D	G	-	-	T	Y	S	-	I	0.15	0.77	0.13	293
Phage-239	T	D	-	W	-	D	W	E	Y	A	T	S	-	D	0.09	0.76	0.09	294
Phage-240	F	N	-	-	-	D	G	Y	-	D	Y	L	-	D	0.10	0.76	0.11	295
Phage-241	Y	D	-	W	-	D	W	E	V	D	F	H	-	P	0.11	0.76	0.08	296
Phage-242	N	I	-	W	-	D	W	E	D	D	S	F	-	F	0.08	0.76	0.08	297
Phage-243	A	T	-	-	-	-	-	-	-	-	I	-	-	S	0.13	0.75	0.09	298
Phage-244	S	-	-	-	-	-	-	-	-	-	T	F	-	D	0.10	0.74	0.09	299
Phage-245	P	I	-	-	-	-	Y	-	-	-	D	V	-	A	0.08	0.74	0.08	300
Phage-246	Y	-	-	-	-	D	G	-	-	Y	N	S	-	I	0.11	0.74	0.11	301

Phage-247	-	D	-	W	-	D	W	E	V	F	I	A	-	D	0.11	0.74	0.10	302
Phage-248	D	L	-	-	-	-	V	E	-	V	N	L	-	L	0.12	0.74	0.10	303
Phage-249	F	D	-	-	-	-	M	-	-	-	T	T	-	F	0.09	0.74	0.09	304
Phage-250	N	F	-	W	-	D	W	E	P	I	Y	F	-	T	0.13	0.74	0.14	305
Phage-251	-	D	-	-	-	D	G	-	-	-	F	F	-	L	0.08	0.73	0.08	306
Phage-252	-	D	-	-	-	D	G	-	-	T	A	F	-	I	0.10	0.73	0.09	307
Phage-253	N	I	-	-	-	-	M	-	-	-	L	V	-	I	0.10	0.73	0.09	308
Phage-254	I	I	-	-	-	-	-	-	-	-	F	F	-	F	0.08	0.73	0.09	309
Phage-255	N	F	-	-	-	-	Y	-	-	-	I	S	-	I	0.10	0.73	0.38	310
Phage-256	H	L	-	-	-	-	I	E	-	A	D	I	-	N	0.11	0.73	0.51	311
Phage-257	D	-	-	-	-	-	V	E	-	D	Y	L	-	D	0.08	0.72	0.09	312
Phage-258	D	-	-	-	-	-	L	-	-	-	I	N	-	D	0.11	0.72	0.10	313
Phage-259	F	-	-	-	-	-	L	-	-	-	L	F	-	V	0.09	0.72	0.08	314
Phage-260	P	D	-	-	-	-	W	E	F	Y	-	T	-	N	0.12	0.72	0.08	315
Phage-261	F	D	-	-	-	-	-	E	Y	I	Y	A	-	T	0.09	0.72	0.08	316
Phage-262	D	-	-	-	-	-	-	-	-	-	S	I	-	N	0.12	0.72	0.11	317
Phage-263	D	F	-	-	-	-	V	E	-	Y	I	F	-	F	0.08	0.72	0.07	318
Phage-264	P	V	-	W	-	D	W	E	Y	V	S	S	-	D	0.08	0.71	0.08	319
Phage-265	Y	I	-	-	-	-	R	-	-	-	N	L	-	L	0.09	0.71	0.09	320
Phage-266	Y	D	-	-	-	-	L	-	-	-	I	V	-	D	0.11	0.71	0.11	321
Phage-267	H	D	-	W	-	D	W	E	D	F	Y	F	-	V	0.09	0.71	0.08	322
Phage-268	H	-	-	-	-	-	Y	-	-	-	I	D	-	Y	0.12	0.71	0.10	323
Phage-269	L	F	-	-	-	-	M	P	-	D	I	F	-	N	0.08	0.71	0.08	324
Phage-270	H	D	-	-	-	-	L	E	F	H	Y	A	-	Y	0.10	0.71	0.12	325
Phage-271	D	F	-	-	-	-	L	-	-	-	I	N	-	F	0.08	0.70	0.08	326
Phage-272	Y	F	-	-	-	-	L	-	-	-	I	A	-	N	0.10	0.70	0.10	327
Phage-273	T	D	-	W	-	D	W	E	D	D	I	I	-	D	0.10	0.70	0.08	328
Phage-274	Y	D	-	-	-	-	L	-	-	-	I	Y	-	F	0.09	0.70	0.08	329
Phage-275	Y	-	-	W	-	D	W	W	-	Y	-	T	-	D	0.10	0.70	0.11	330
Phage-276	P	I	-	-	-	-	L	E	-	-	Y	L	-	N	0.13	0.69	0.52	331
Phage-277	F	D	-	-	-	-	-	-	-	-	I	V	-	Y	0.12	0.69	0.11	332
Phage-278	-	L	-	-	-	D	G	I	-	F	F	D	-	P	0.09	0.68	0.07	333
Phage-279	A	-	-	-	-	-	Y	-	-	-	L	T	-	V	0.07	0.68	0.07	334
Phage-280	D	F	-	-	-	-	L	-	-	-	I	I	-	A	0.14	0.68	0.14	335
Phage-281	Y	D	-	-	-	-	-	-	-	-	L	D	-	N	0.08	0.68	0.08	336
Phage-282	A	I	-	-	-	-	-	-	-	-	-	A	-	D	0.14	0.67	0.08	337
Phage-283	L	L	-	-	-	D	G	V	-	D	F	F	-	D	0.10	0.67	0.10	338

Phage-284	N	F	-	-	-	-	L	P	-	D	I	F	-	F	0.12	0.66	0.13	339
Phage-285	F	-	-	-	-	-	V	E	-	V	S	L	-	N	0.08	0.66	0.08	340
Phage-286	Y	D	-	-	-	D	G	Y	-	A	F	Y	-	H	0.12	0.66	0.10	341
Phage-287	N	F	-	-	-	-	I	E	F	D	Y	L	-	D	0.08	0.65	0.08	342
Phage-288	D	-	-	-	-	D	G	V	-	D	F	I	-	N	0.06	0.65	0.08	343
Phage-289	T	D	-	W	-	D	W	E	Y	I	Y	S	-	S	0.08	0.65	0.07	344
Phage-290	F	-	-	-	-	-	-	E	-	I	T	N	-	I	0.14	0.65	0.11	345
Phage-291	F	D	-	W	-	D	W	E	-	-	F	F	-	H	0.07	0.64	0.08	346
Phage-292	D	F	-	-	-	D	G	-	-	-	-	F	-	P	0.08	0.63	0.08	347
Phage-293	H	N	-	-	-	-	L	-	-	-	L	V	-	D	0.13	0.63	0.09	348
Phage-294	I	-	-	-	-	D	G	A	-	D	Y	T	-	D	0.07	0.63	0.07	349
Phage-295	F	D	-	-	-	-	-	E	F	P	-	I	-	F	0.08	0.62	0.08	350
Phage-296	Y	N	-	-	-	-	L	-	-	-	-	T	-	D	0.09	0.62	0.08	351
Phage-297	F	D	-	-	-	-	L	-	-	-	I	H	-	A	0.07	0.62	0.08	352
Phage-298	D	I	-	-	-	-	V	E	-	Y	F	L	-	F	0.15	0.61	0.10	353
Phage-299	F	D	-	-	-	-	V	-	-	-	L	T	-	F	0.10	0.61	0.09	354
Phage-300	F	D	-	-	-	-	I	E	-	F	H	L	-	F	0.08	0.61	0.08	355
Phage-301	A	-	-	-	-	-	L	-	-	-	I	I	-	D	0.12	0.61	0.10	356
Phage-302	Y	N	-	-	-	-	L	-	-	-	I	T	-	N	0.09	0.61	0.10	357
Phage-303	F	D	-	W	-	D	W	E	-	P	-	D	-	L	0.08	0.61	0.07	358
Phage-304	D	V	-	-	-	-	L	-	-	-	-	L	-	P	0.08	0.60	0.08	359
Phage-305	N	-	-	-	-	-	L	-	-	-	L	P	-	P	0.09	0.60	0.08	360
Phage-306	Y	-	-	W	-	D	W	E	Y	D	I	F	-	S	0.08	0.60	0.10	361
Phage-307	D	D	-	-	-	-	-	-	-	-	T	Y	-	N	0.08	0.60	0.09	362
Phage-308	F	-	-	-	-	-	-	E	-	V	F	H	-	Y	0.09	0.60	0.09	363
Phage-309	T	D	-	W	-	D	W	E	-	Y	F	L	-	D	0.07	0.60	0.09	364
Phage-310	-	-	-	-	-	-	W	E	-	-	Y	L	-	P	0.09	0.60	0.09	365
Phage-311	D	D	-	-	-	N	G	Y	A	T	F	I	-	Y	0.06	0.59	0.08	366
Phage-312	F	L	-	-	-	-	I	E	D	D	T	H	-	Y	0.16	0.59	0.38	367
Phage-313	F	A	-	W	-	D	W	E	-	T	I	P	-	H	0.08	0.59	0.08	368
Phage-314	-	L	-	-	-	-	-	-	-	-	Y	N	-	Y	0.10	0.58	0.08	369
Phage-315	Y	D	-	-	-	-	-	-	-	-	I	S	-	I	0.09	0.58	0.09	370
Phage-316	Y	D	-	-	-	-	-	-	-	-	-	N	-	Y	0.12	0.57	0.10	371
Phage-317	A	I	-	W	-	D	W	E	-	F	-	D	-	Y	0.10	0.57	0.09	372
Phage-318	L	T	-	W	-	V	R	E	-	I	F	A	-	D	0.07	0.57	0.08	373
Phage-319	-	L	-	-	-	-	-	-	-	-	Y	Y	-	N	0.09	0.57	0.09	374
Phage-320	N	V	-	-	-	-	Y	-	-	-	A	P	-	N	0.07	0.56	0.08	375

Phage-321	H	D	-	-	-	-	-	-	-	-	I	S	-	V	0.11	0.55	0.09	376
Phage-322	F	D	-	-	-	-	L	-	-	T	-	D	-	N	0.12	0.55	0.41	377
Phage-323	Y	F	-	-	-	-	V	E	-	H	F	Y	-	Y	0.09	0.55	0.08	378
Phage-324	D	-	-	-	-	-	L	-	-	-	I	I	-	H	0.09	0.54	0.09	379
Phage-325	D	D	-	-	-	-	V	P	-	D	I	T	-	Y	0.11	0.54	0.08	380
Phage-326	D	N	-	-	-	-	L	-	-	-	-	V	-	D	0.10	0.54	0.08	381
Phage-327	-	H	-	W	-	D	W	E	P	N	Y	V	-	D	0.10	0.54	0.08	382
Phage-328	D	-	-	-	-	-	L	-	-	-	L	F	-	L	0.09	0.53	0.09	383
Phage-329	D	D	-	-	-	-	L	-	-	-	-	V	-	A	0.08	0.53	0.11	384
Phage-330	A	A	-	-	-	-	L	-	-	-	I	V	-	D	0.13	0.53	0.09	385
Phage-331	D	F	-	-	-	-	-	E	-	I	N	N	-	F	0.14	0.52	0.48	386
Phage-332	Y	-	-	-	-	-	-	-	-	-	N	A	-	Y	0.08	0.52	0.07	387
Phage-333	-	L	-	-	-	-	-	-	-	-	N	S	-	Y	0.10	0.52	0.11	388
Phage-334	Y	D	-	-	-	-	-	-	-	-	I	D	-	D	0.09	0.52	0.09	389
Phage-335	D	S	-	-	-	-	-	E	F	Y	Y	V	-	F	0.11	0.52	0.14	390
Phage-336	Y	I	-	-	-	-	L	-	-	-	L	I	-	H	0.10	0.52	0.08	391
Phage-337	F	D	-	-	-	-	V	E	-	D	Y	F	-	Y	0.11	0.52	0.10	392
Phage-338	F	D	-	-	-	-	Y	-	-	-	L	Y	-	F	0.08	0.52	0.07	393
Phage-339	-	L	-	-	-	D	G	-	-	Y	S	F	-	H	0.10	0.51	0.10	394
Phage-340	I	P	-	-	-	-	M	-	-	-	-	V	-	N	0.12	0.51	0.09	395
Phage-341	I	I	-	-	-	D	G	Y	-	D	F	T	-	D	0.12	0.51	0.09	396
Phage-342	I	F	-	-	-	-	L	-	-	-	I	I	-	Y	0.11	0.51	0.08	397
Phage-343	-	D	-	-	-	-	-	-	-	-	Y	D	-	Y	0.18	0.51	0.18	398
Phage-344	L	S	-	-	-	-	M	-	-	-	L	Y	-	D	0.12	0.51	0.08	399
Phage-345	Y	D	-	W	-	D	W	E	Y	N	I	D	-	T	0.08	0.51	0.09	400
Phage-346	N	H	-	-	-	D	G	-	-	T	I	V	-	F	0.09	0.51	0.08	401
Phage-347	N	F	-	-	-	-	L	-	-	-	I	P	-	H	0.11	0.50	0.12	402
Phage-348	F	H	-	-	-	-	I	E	-	Y	A	L	-	D	0.08	0.50	0.09	403
Phage-349	-	-	-	-	-	-	V	E	D	Y	N	L	-	Y	0.07	0.50	0.08	404
Phage-350	-	-	-	-	-	D	G	-	-	L	A	N	-	Y	0.09	0.50	0.08	405
Phage-351	L	I	-	-	-	V	I	A	-	D	L	P	-	N	0.17	0.50	0.26	406
Phage-352	D	I	-	-	-	-	I	P	-	D	-	S	-	D	0.10	0.50	0.08	407
Phage-353	I	-	-	-	-	-	W	E	-	A	D	Y	-	D	0.11	0.50	0.45	408
Phage-354	I	D	-	W	-	D	W	E	D	D	S	I	-	Y	0.10	0.50	0.10	409
Phage-355	-	L	-	-	-	-	V	E	D	F	T	L	-	D	0.09	0.50	0.11	410
Phage-356	L	-	-	-	-	V	I	E	-	I	Y	Y	-	Y	0.09	0.49	0.09	411
Phage-357	F	F	-	-	-	-	-	E	V	H	S	D	-	N	0.14	0.49	0.38	412

Phage-358	N	D	-	-	-	-	V	E	L	V	S	D	-	N	0.10	0.49	0.08	413
Phage-359	D	L	-	-	-	-	L	-	-	-	T	V	-	D	0.09	0.49	0.08	414
Phage-360	I	P	-	-	-	-	V	E	D	Y	N	L	-	N	0.08	0.49	0.08	415
Phage-361	Y	-	-	-	-	-	L	E	W	P	-	V	-	N	0.10	0.49	0.10	416
Phage-362	Y	D	-	-	-	-	L	-	-	-	-	I	-	N	0.08	0.49	0.10	417
Phage-363	-	-	-	-	-	D	G	-	-	-	F	D	-	A	0.08	0.49	0.08	418
Phage-364	N	D	-	-	-	-	W	E	D	T	Y	F	-	L	0.08	0.49	0.10	419
Phage-365	P	-	-	-	-	-	M	E	-	L	S	N	-	S	0.13	0.48	0.16	420
Phage-366	D	D	-	-	-	-	-	E	V	I	S	D	-	Y	0.15	0.48	0.10	421
Phage-367	D	L	-	-	-	-	-	P	-	D	-	P	-	D	0.08	0.48	0.08	422
Phage-368	I	-	-	-	-	-	-	-	-	-	F	V	-	Y	0.11	0.48	0.10	423
Phage-369	A	-	-	-	-	-	Y	E	V	F	A	D	-	N	0.10	0.48	0.11	424
Phage-370	I	D	-	-	-	-	Y	-	-	-	-	D	-	L	0.09	0.48	0.09	425
Phage-371	H	I	-	W	-	D	W	E	-	F	H	D	-	N	0.07	0.48	0.08	426
Phage-372	Y	D	-	-	-	-	L	-	-	T	I	T	-	L	0.08	0.48	0.08	427
Phage-373	Y	L	-	-	-	-	L	-	-	T	I	L	-	N	0.09	0.48	0.08	428
Phage-374	F	F	-	-	-	-	-	E	-	A	F	L	-	F	0.10	0.48	0.14	429
Phage-375	I	L	-	-	-	-	L	-	-	-	F	T	-	A	0.07	0.47	0.08	430
Phage-376	F	H	-	-	-	-	V	E	L	Y	T	D	-	N	0.09	0.47	0.08	431
Phage-377	N	L	-	-	-	-	V	E	-	Y	N	F	-	Y	0.08	0.47	0.08	432
Phage-378	F	D	-	-	-	-	V	E	-	T	Y	Y	-	F	0.21	0.47	0.09	433
Phage-379	-	F	-	-	-	-	-	E	-	D	H	Y	-	Y	0.12	0.47	0.37	434
Phage-380	A	I	-	-	-	-	W	E	V	V	A	D	-	N	0.11	0.47	0.11	435
Phage-381	F	I	-	W	-	D	W	E	-	D	N	Y	-	N	0.12	0.47	0.25	436
Phage-382	I	-	-	-	-	-	-	-	-	-	F	I	-	D	0.08	0.47	0.10	437
Phage-383	N	L	-	-	-	-	V	E	D	V	Y	D	-	H	0.12	0.47	0.43	438
Phage-384	H	-	-	-	-	-	V	E	-	Y	H	N	-	N	0.09	0.47	0.09	439
Phage-385	D	I	-	-	-	-	Y	-	-	-	Y	S	-	T	0.09	0.47	0.09	440
Phage-386	D	-	-	-	-	-	L	-	-	T	L	I	-	A	0.13	0.46	0.10	441
Phage-387	I	A	-	-	-	-	M	P	-	D	I	D	-	Y	0.12	0.46	0.09	442
Phage-388	I	D	-	-	-	-	L	-	-	-	I	F	-	D	0.10	0.46	0.10	443
Phage-389	Y	F	-	-	-	D	V	E	-	D	F	A	-	D	0.11	0.46	0.11	444
Phage-390	Y	N	-	-	-	-	W	E	Y	A	I	L	-	D	0.12	0.46	0.34	445
Phage-391	I	-	-	-	-	-	V	E	D	Y	I	V	-	N	0.14	0.46	0.22	446
Phage-392	Y	D	-	-	-	-	I	-	-	-	T	P	-	A	0.07	0.46	0.07	447
Phage-393	D	T	-	W	-	D	W	E	H	I	Y	A	-	D	0.09	0.46	0.09	448
Phage-394	D	I	-	-	-	-	M	-	-	-	-	T	-	N	0.13	0.45	0.12	449

Phage-395	Y	D	-	W	-	D	W	E	R	Y	F	P	-	I	0.10	0.45	0.09	450
Phage-396	H	L	-	-	-	-	L	-	-	-	-	A	-	S	0.13	0.45	0.11	451
Phage-397	Y	D	-	-	-	D	G	-	-	T	T	I	-	A	0.09	0.45	0.09	452
Phage-398	Y	-	-	-	-	-	Y	E	D	V	L	D	-	F	0.07	0.45	0.08	453
Phage-399	D	F	-	-	-	-	M	-	-	T	I	S	-	D	0.14	0.45	0.10	454
Phage-400	I	L	-	-	-	-	L	-	-	-	L	V	-	D	0.08	0.44	0.07	455
Phage-401	L	I	-	-	-	-	W	E	V	I	T	N	-	D	0.12	0.44	0.40	456
Phage-402	Y	D	-	-	-	-	-	-	-	Y	F	-	-	P	0.09	0.44	0.09	457
Phage-403	A	L	-	-	-	-	V	E	V	Y	D	V	-	V	0.08	0.44	0.08	458
Phage-404	Y	H	-	W	-	D	W	E	D	V	N	F	-	Y	0.10	0.44	0.09	459
Phage-405	F	L	-	-	-	M	G	G	L	T	F	Y	-	Y	0.09	0.44	0.08	460
Phage-406	I	I	-	-	-	-	-	-	-	Y	-	-	-	F	0.09	0.43	0.19	461
Phage-407	F	F	-	-	-	-	M	-	-	-	-	H	-	F	0.11	0.43	0.09	462
Phage-408	A	F	-	-	-	-	-	-	-	-	L	F	-	A	0.09	0.43	0.09	463
Phage-409	N	-	-	-	-	D	G	-	-	T	N	I	-	D	0.08	0.43	0.08	464
Phage-410	Y	L	-	-	-	-	W	E	W	V	H	N	-	L	0.13	0.43	0.09	465
Phage-411	A	T	-	-	-	D	G	-	-	-	H	I	-	A	0.08	0.43	0.09	466
Phage-412	-	-	-	-	-	-	V	E	V	L	D	Y	-	D	0.07	0.42	0.08	467
Phage-413	I	H	-	-	-	-	W	E	F	Y	T	D	-	D	0.08	0.42	0.08	468
Phage-414	D	D	-	-	-	-	L	-	-	T	-	A	-	D	0.13	0.42	0.32	469
Phage-415	Y	L	-	-	-	-	-	-	-	-	I	D	-	N	0.11	0.42	0.17	470
Phage-416	L	L	-	-	-	-	V	E	D	V	F	A	-	Y	0.09	0.42	0.09	471
Phage-417	Y	D	-	-	-	-	L	-	-	-	L	T	-	D	0.08	0.42	0.08	472
Phage-418	F	D	-	-	-	-	L	-	-	T	-	N	-	Y	0.09	0.41	0.09	473
Phage-419	F	A	-	W	-	D	W	E	-	I	N	D	-	H	0.08	0.41	0.09	474
Phage-420	Y	-	-	-	-	-	Y	E	-	D	I	Y	-	N	0.09	0.41	0.09	475
Phage-421	N	V	-	-	-	-	V	E	D	Y	T	F	-	Y	0.09	0.40	0.08	476
Phage-422	A	-	-	-	-	-	L	E	-	Y	D	F	-	T	0.12	0.40	0.08	477
Phage-423	F	D	-	-	-	-	I	-	-	-	T	I	-	T	0.08	0.40	0.09	478
Phage-424	N	L	-	-	-	-	L	-	-	T	L	V	-	A	0.10	0.40	0.09	479
Phage-425	Y	S	-	W	-	D	W	E	-	Y	L	A	-	N	0.08	0.40	0.08	480
Phage-426	G	I	-	-	-	-	V	E	D	Y	N	Y	-	D	0.09	0.40	0.10	481
Phage-427	F	F	-	-	-	-	L	-	-	-	-	N	-	H	0.07	0.40	0.07	482
Phage-428	Y	-	-	-	-	-	Y	E	-	D	F	Y	-	F	0.11	0.40	0.09	483
Phage-429	L	-	-	-	-	-	Y	-	-	-	T	D	-	Y	0.11	0.40	0.10	484
Phage-430	D	-	-	-	-	-	V	E	-	D	F	L	-	Y	0.10	0.40	0.08	485
Phage-431	T	L	-	-	-	-	V	E	L	Y	I	F	-	D	0.08	0.40	0.09	486

Phage-432	F	-	-	-	-	-	-	E	Q	I	A	D	-	Y	0.11	0.40	0.09	487
Phage-433	D	D	-	-	-	-	V	E	-	Y	H	L	-	D	0.11	0.40	0.18	488
Phage-434	D	-	-	-	-	-	L	E	D	V	T	L	-	H	0.13	0.39	0.09	489
Phage-435	-	L	-	-	-	-	V	E	D	V	N	L	-	Y	0.09	0.39	0.08	490
Phage-436	D	I	-	-	-	-	L	-	-	T	I	D	-	Y	0.09	0.39	0.09	491
Phage-437	T	-	-	-	-	-	V	E	-	D	I	N	-	Y	0.08	0.39	0.08	492
Phage-438	I	V	-	W	-	D	W	E	-	Y	P	N	-	D	0.08	0.39	0.08	493
Phage-439	S	D	-	-	-	-	L	-	-	-	I	I	-	T	0.11	0.39	0.10	494
Phage-440	Y	D	-	-	-	-	L	P	-	D	Y	D	-	N	0.15	0.39	0.10	495
Phage-441	N	L	-	W	-	D	W	E	-	Y	Y	A	-	D	0.12	0.39	0.17	496
Phage-442	D	D	-	-	-	-	L	-	-	-	L	P	-	H	0.10	0.39	0.08	497
Phage-443	S	L	-	-	-	D	G	Q	-	D	Y	T	-	F	0.08	0.39	0.08	498
Phage-444	L	I	-	W	-	D	W	E	-	Y	N	F	-	T	0.13	0.39	0.11	499
Phage-445	F	H	-	-	-	D	G	-	-	T	-	P	-	I	0.08	0.39	0.08	500
Phage-446	F	D	-	-	-	-	W	E	W	I	Y	D	-	F	0.08	0.38	0.08	501
Phage-447	I	-	-	-	-	-	W	-	-	-	L	D	-	D	0.08	0.38	0.09	502
Phage-448	L	I	-	-	-	-	I	-	-	-	A	S	-	N	0.10	0.38	0.11	503
Phage-449	T	S	-	W	V	D	W	E	-	F	S	D	-	I	0.11	0.38	0.34	504
Phage-450	Y	-	-	-	-	-	V	E	-	D	Y	V	-	D	0.10	0.38	0.08	505
Phage-451	D	D	-	-	-	-	Q	E	F	I	Y	A	-	I	0.09	0.38	0.08	506
Phage-452	A	D	-	W	-	D	W	E	-	Y	A	D	-	Y	0.11	0.38	0.10	507
Phage-453	Y	-	-	-	-	-	-	-	-	-	I	H	-	I	0.08	0.38	0.07	508
Phage-454	S	E	-	W	-	D	W	E	P	F	F	D	-	N	0.08	0.37	0.09	509
Phage-455	Y	H	-	-	-	-	M	-	-	-	L	I	-	T	0.07	0.37	0.07	510
Phage-456	S	D	-	W	-	D	W	E	D	A	Y	F	-	I	0.09	0.37	0.07	511
Phage-457	-	D	-	-	-	-	V	E	-	Y	Y	H	-	D	0.08	0.37	0.08	512
Phage-458	D	N	-	-	-	-	Y	-	-	-	I	A	-	N	0.10	0.37	0.10	513
Phage-459	L	-	-	-	-	V	-	E	F	Y	D	Y	-	Y	0.08	0.37	0.10	514
Phage-460	Y	T	-	-	-	-	M	-	-	-	-	T	-	I	0.09	0.37	0.08	515
Phage-461	N	F	-	W	-	D	W	E	V	N	S	F	-	D	0.09	0.37	0.08	516
Phage-462	N	A	-	W	-	D	W	E	Y	I	D	F	-	N	0.12	0.36	0.09	517
Phage-463	Y	N	-	-	-	-	M	-	-	-	I	F	-	S	0.09	0.36	0.07	518
Phage-464	L	D	-	-	-	-	L	-	-	-	I	T	-	Y	0.08	0.36	0.09	519
Phage-465	H	-	-	-	-	-	-	-	-	-	I	N	-	D	0.11	0.36	0.08	520
Phage-466	I	I	-	-	-	-	L	P	-	D	Y	V	-	T	0.08	0.36	0.08	521
Phage-467	D	I	-	-	-	-	-	-	-	-	I	D	-	S	0.08	0.36	0.08	522
Phage-468	P	-	-	-	-	-	-	-	-	-	-	L	-	F	0.10	0.36	0.09	523

Phage-469	-	F	-	-	-	-	-	-	-	-	-	D	-	Y	0.07	0.36	0.08	524
Phage-470	Y	D	-	W	-	D	W	E	-	A	L	P	-	A	0.08	0.36	0.08	525
Phage-471	D	D	-	W	-	D	W	E	D	Y	-	F	-	F	0.10	0.36	0.10	526
Phage-472	H	F	-	-	-	-	W	E	L	F	S	D	-	Y	0.11	0.36	0.11	527
Phage-473	I	T	-	W	-	D	W	E	V	N	F	P	-	Y	0.07	0.35	0.07	528
Phage-474	P	D	-	-	-	-	L	-	-	-	I	T	-	N	0.20	0.35	0.16	529
Phage-475	N	L	-	W	-	D	W	E	A	F	F	P	-	Y	0.08	0.35	0.07	530
Phage-476	F	-	-	-	-	-	-	E	Y	I	R	D	-	Y	0.08	0.35	0.07	531
Phage-477	F	F	-	-	-	-	-	-	-	-	I	I	-	D	0.09	0.35	0.10	532
Phage-478	-	L	-	-	-	K	G	G	P	T	Y	N	-	S	0.08	0.35	0.10	533
Phage-479	L	A	-	W	-	V	W	E	-	P	G	H	-	D	0.11	0.35	0.10	534
Phage-480	D	-	-	-	-	-	V	E	D	V	N	D	-	Y	0.07	0.35	0.08	535
Phage-481	D	-	-	-	-	-	-	E	-	A	H	Y	-	N	0.08	0.35	0.07	536
Phage-482	-	L	-	-	-	-	L	-	-	T	L	T	-	I	0.08	0.35	0.07	537
Phage-483	Y	-	-	-	-	-	I	E	D	Y	N	L	-	N	0.10	0.34	0.09	538
Phage-484	Y	I	-	-	-	-	V	E	-	Y	Y	N	-	F	0.13	0.34	0.14	539
Phage-485	D	I	-	-	-	-	L	-	-	-	I	F	-	F	0.08	0.34	0.09	540
Phage-486	D	I	-	-	-	-	V	E	-	D	Y	L	-	Y	0.07	0.34	0.08	541
Phage-487	T	L	-	-	-	-	-	E	-	D	A	P	-	I	0.10	0.34	0.08	542
Phage-488	N	-	-	W	-	D	W	E	Y	I	N	S	-	V	0.14	0.34	0.09	543
Phage-489	N	D	-	-	-	-	V	E	-	Y	Y	Y	-	T	0.07	0.34	0.09	544
Phage-490	I	T	-	-	-	-	M	-	-	-	I	D	-	N	0.08	0.34	0.08	545
Phage-491	Y	-	-	-	-	-	M	A	-	D	L	I	-	D	0.10	0.34	0.29	546
Phage-492	I	D	-	-	-	-	L	-	-	-	I	V	-	T	0.11	0.33	0.09	547
Phage-493	H	T	-	W	-	D	W	E	W	D	-	Y	-	D	0.08	0.33	0.07	548
Phage-494	I	H	-	-	-	-	W	E	L	I	D	D	-	L	0.08	0.33	0.10	549
Phage-495	Y	T	-	-	-	-	L	-	-	-	I	T	-	T	0.08	0.33	0.08	550
Phage-496	F	H	-	-	-	-	V	E	-	T	-	Y	-	F	0.11	0.33	0.09	551
Phage-497	D	-	-	-	-	-	L	-	-	-	L	I	-	N	0.07	0.33	0.08	552
Phage-498	I	-	-	-	-	-	-	-	-	-	D	Y	-	I	0.08	0.33	0.10	553
Phage-499	D	L	-	-	-	-	I	E	-	D	L	V	-	T	0.09	0.33	0.09	554
Phage-500	N	I	-	-	-	-	L	Q	-	D	I	V	-	P	0.09	0.33	0.09	555
Phage-501	N	N	-	-	-	-	M	-	-	-	I	T	-	Y	0.08	0.33	0.08	556
Phage-502	H	T	-	-	-	-	L	-	-	-	I	V	-	V	0.08	0.33	0.08	557
Phage-503	Y	-	-	-	-	-	I	E	D	I	L	V	-	T	0.12	0.33	0.23	558
Phage-504	N	T	-	-	-	-	-	E	F	V	H	L	-	P	0.07	0.33	0.11	559
Phage-505	D	I	-	-	-	-	M	-	-	-	T	V	-	D	0.10	0.33	0.09	560

Phage-506	A	I	-	-	-	-	V	E	I	V	N	Y	-	Y	0.09	0.32	0.07	561
Phage-507	H	L	-	-	-	-	V	E	D	P	T	A	-	V	0.10	0.32	0.28	562
Phage-508	A	D	-	-	-	-	L	-	-	-	I	S	-	T	0.10	0.32	0.09	563
Phage-509	F	D	-	-	-	-	L	-	-	-	-	I	-	D	0.07	0.32	0.09	564
Phage-510	D	V	-	-	-	-	-	-	-	-	I	D	-	N	0.10	0.32	0.08	565
Phage-511	Y	L	-	-	-	-	V	E	-	I	S	I	-	F	0.08	0.32	0.07	566
Phage-512	S	A	-	-	-	-	-	-	-	-	L	H	-	V	0.10	0.31	0.30	567
Phage-513	H	L	-	W	-	D	W	E	-	D	S	A	-	N	0.08	0.31	0.08	568
Phage-514	H	T	-	W	-	D	W	E	Y	D	Y	D	-	F	0.10	0.31	0.08	569
Phage-515	Y	D	-	-	-	-	W	E	-	V	A	L	-	N	0.10	0.31	0.10	570
Phage-516	T	L	-	-	-	-	I	E	-	Y	I	V	-	Y	0.09	0.31	0.23	571
Phage-517	S	-	-	-	-	-	-	-	-	-	I	F	-	T	0.09	0.31	0.09	572
Phage-518	D	I	-	-	-	-	-	-	-	-	L	H	-	Y	0.08	0.31	0.08	573
Phage-519	L	F	-	-	-	-	-	E	-	A	Y	L	-	I	0.08	0.31	0.08	574
Phage-520	I	F	-	-	-	-	I	E	-	D	F	V	-	T	0.10	0.31	0.10	575
Phage-521	D	D	-	-	-	-	W	E	Y	Y	-	A	-	V	0.08	0.31	0.08	576
Phage-522	D	D	-	-	-	-	L	-	-	T	T	I	-	Y	0.10	0.31	0.09	577
Phage-523	A	S	-	-	-	-	L	-	-	-	I	A	-	D	0.10	0.31	0.09	578
Phage-524	Y	L	-	-	-	-	V	E	D	Y	D	Y	-	Y	0.08	0.31	0.09	579
Phage-525	D	L	-	-	-	-	W	E	-	T	I	F	-	A	0.12	0.30	0.09	580
Phage-526	D	F	-	-	-	D	G	E	-	F	Y	I	-	P	0.12	0.30	0.11	581
Phage-527	-	-	-	-	-	-	V	E	-	N	I	L	-	H	0.15	0.30	0.17	582
Phage-528	D	-	-	-	-	-	V	E	-	N	Y	F	-	F	0.12	0.30	0.21	583
Phage-529	N	D	-	W	-	D	W	Y	-	F	L	S	-	D	0.10	0.30	0.10	584
Phage-530	R	D	-	W	-	D	W	E	V	P	Y	F	-	D	0.08	0.30	0.09	585
Phage-531	N	L	-	-	-	-	V	E	-	A	-	Y	-	Y	0.10	0.30	0.13	586
Phage-532	F	D	-	W	-	D	G	E	L	N	Y	L	-	T	0.23	0.30	0.08	587
Phage-533	Y	-	-	-	-	-	V	E	D	V	N	L	-	I	0.18	0.30	0.10	588
Phage-534	D	N	-	-	-	-	Y	-	-	-	I	T	-	L	0.11	0.29	0.09	589
Phage-535	L	N	-	W	-	D	W	E	-	D	Y	S	-	N	0.09	0.29	0.09	590
Phage-536	P	T	-	-	-	-	V	E	-	L	L	S	-	N	0.12	0.29	0.26	591
Phage-537	D	H	-	-	-	-	V	E	L	I	F	Y	-	H	0.11	0.29	0.08	592
Phage-538	F	H	-	-	-	-	L	-	-	-	I	F	-	Y	0.08	0.29	0.08	593
Phage-539	F	D	-	-	-	-	L	E	-	T	-	V	-	P	0.16	0.29	0.16	594
Phage-540	D	F	-	-	-	-	L	-	-	-	L	P	-	A	0.08	0.29	0.08	595
Phage-541	D	S	-	-	-	-	L	-	-	-	I	Y	-	D	0.09	0.29	0.09	596
Phage-542	A	D	-	W	-	D	W	E	-	F	L	L	-	F	0.12	0.29	0.10	597

Phage-543	I	L	-	-	-	-	V	E	-	L	D	F	-	N	0.10	0.28	0.08	598
Phage-544	F	F	-	-	-	-	-	E	-	I	F	L	-	Y	0.09	0.28	0.07	599
Phage-545	Y	N	-	-	-	D	G	-	-	-	Y	D	-	H	0.07	0.28	0.07	600
Phage-546	D	N	-	-	-	-	L	-	-	T	I	T	-	F	0.11	0.28	0.11	601
Phage-547	H	N	-	-	-	D	G	-	-	A	F	I	-	N	0.09	0.28	0.23	602
Phage-548	D	-	-	-	-	-	V	E	-	D	L	V	-	P	0.10	0.28	0.23	603
Phage-549	D	-	-	-	-	-	L	-	-	-	L	N	-	F	0.08	0.28	0.07	604
Phage-550	D	-	-	-	-	-	-	Q	-	D	F	H	-	H	0.11	0.28	0.27	605
Phage-551	Y	D	-	-	-	-	W	E	F	T	D	D	-	I	0.10	0.28	0.18	606
Phage-552	D	I	-	-	-	-	Y	E	-	D	I	I	-	Y	0.14	0.28	0.19	607
Phage-553	F	D	-	-	-	-	L	-	-	T	-	P	-	P	0.11	0.28	0.08	608
Phage-554	N	-	-	-	-	-	L	-	-	T	S	V	-	D	0.09	0.28	0.26	609
Phage-555	Y	-	-	-	-	-	W	E	F	-	F	D	-	D	0.17	0.28	0.11	610
Phage-556	Y	A	-	-	-	-	L	-	-	-	-	T	-	D	0.09	0.28	0.08	611
Phage-557	F	L	-	-	-	-	V	E	Q	D	Y	F	-	V	0.08	0.28	0.10	612
Phage-558	D	N	-	-	-	-	-	-	-	-	-	R	-	D	0.09	0.27	0.26	613
Phage-559	N	D	-	-	-	D	G	I	-	T	-	D	-	Y	0.10	0.27	0.24	614
Phage-560	Y	F	-	-	-	-	V	E	D	Y	N	D	-	F	0.08	0.27	0.09	615
Phage-561	N	L	-	-	-	-	-	-	-	-	I	F	-	Y	0.10	0.27	0.07	616
Phage-562	I	D	-	W	-	D	W	E	-	Y	I	P	-	T	0.10	0.27	0.08	617
Phage-563	I	-	-	-	-	D	G	-	-	-	F	I	-	A	0.07	0.27	0.08	618
Phage-564	D	-	-	-	-	-	-	-	-	-	-	V	-	Y	0.08	0.27	0.07	619
Phage-565	-	F	-	-	-	-	W	E	D	I	T	D	-	D	0.13	0.27	0.09	620
Phage-566	L	D	-	-	-	-	V	-	-	T	F	T	-	H	0.08	0.26	0.08	621
Phage-567	D	D	-	-	-	-	Y	-	-	-	F	A	-	H	0.13	0.26	0.10	622
Phage-568	I	-	-	-	-	-	Y	Q	-	D	L	P	-	N	0.12	0.26	0.11	623
Phage-569	L	D	-	-	-	-	V	E	-	Y	N	Y	-	V	0.09	0.26	0.08	624
Phage-570	Y	V	-	-	-	-	-	-	-	-	S	A	-	N	0.14	0.26	0.08	625
Phage-571	T	P	-	-	-	-	L	E	-	A	I	-	-	Y	0.10	0.26	0.10	626
Phage-572	Y	F	-	-	-	-	-	-	-	-	A	D	-	N	0.08	0.26	0.08	627
Phage-573	D	D	-	-	-	-	-	E	-	D	I	I	-	D	0.12	0.26	0.25	628
Phage-574	L	-	-	-	-	V	V	E	-	L	N	H	-	N	0.08	0.26	0.09	629
Phage-575	-	I	-	-	-	D	G	E	-	L	I	A	-	A	0.09	0.26	0.27	630
Phage-576	F	A	-	W	-	D	W	Q	-	T	Y	V	-	N	0.09	0.25	0.08	631
Phage-577	Y	I	-	-	-	-	V	E	F	L	F	F	-	N	0.08	0.25	0.08	632
Phage-578	T	Q	-	-	-	K	G	E	P	T	Y	H	-	Y	0.12	0.25	0.12	633
Phage-579	N	-	-	-	-	-	V	E	-	Y	H	N	-	D	0.10	0.25	0.17	634

Phage-580	-	-	-	-	-	-	W	E	F	F	S	D	-	A	0.08	0.25	0.07	635
Phage-581	F	-	-	-	-	-	L	E	-	-	F	F	-	Y	0.10	0.25	0.22	636
Phage-582	D	-	-	-	-	-	I	E	-	N	F	Y	-	Y	0.13	0.25	0.09	637
Phage-583	Y	A	-	-	-	-	V	E	-	Y	-	Y	-	A	0.08	0.25	0.09	638
Phage-584	-	D	-	-	-	-	L	-	-	-	I	I	-	D	0.08	0.25	0.07	639
Phage-585	N	D	-	-	-	-	M	-	-	-	I	A	-	Y	0.07	0.25	0.07	640
Phage-586	-	-	-	-	-	-	-	-	-	Y	L	A	-	A	0.09	0.25	0.21	641
Phage-587	-	I	-	-	-	-	-	-	-	-	A	N	-	D	0.08	0.25	0.09	642
Phage-588	L	T	-	W	-	D	W	E	-	D	F	F	-	N	0.07	0.24	0.07	643
Phage-589	F	-	-	-	-	-	Q	E	-	I	N	Y	-	Y	0.10	0.24	0.23	644
Phage-590	T	-	-	-	-	-	L	E	-	F	F	L	-	Y	0.13	0.24	0.08	645
Phage-591	P	D	-	-	-	-	L	-	-	-	-	A	-	H	0.12	0.24	0.09	646
Phage-592	N	D	-	-	-	-	-	E	-	I	I	F	-	V	0.09	0.24	0.24	647
Phage-593	Y	I	-	-	-	-	-	-	-	-	F	Y	-	N	0.25	0.24	0.08	648
Phage-594	H	A	-	-	-	-	L	-	-	-	L	L	-	N	0.20	0.24	0.07	649
Phage-595	Y	-	-	-	-	-	W	E	-	A	-	L	-	A	0.09	0.24	0.21	650
Phage-596	A	F	-	-	-	-	V	E	-	Y	D	L	-	N	0.10	0.24	0.16	651
Phage-597	Y	N	-	-	-	-	-	-	-	-	-	A	-	S	0.15	0.23	0.09	652
Phage-598	Y	L	-	-	-	-	V	E	D	D	T	L	-	A	0.08	0.23	0.09	653
Phage-599	A	V	-	-	-	-	-	-	-	-	-	N	-	D	0.08	0.23	0.08	654
Phage-600	N	-	-	-	-	-	W	E	V	Y	S	L	-	P	0.13	0.23	0.08	655
Phage-601	D	F	-	-	-	-	V	E	-	D	T	Y	-	H	0.07	0.23	0.07	656
Phage-602	I	S	-	-	-	-	Y	E	W	D	Y	A	-	N	0.08	0.23	0.10	657
Phage-603	-	N	-	-	-	-	L	-	-	-	I	I	-	Y	0.08	0.23	0.08	658
Phage-604	Y	D	-	-	-	-	-	-	-	T	A	P	-	Y	0.07	0.23	0.08	659
Phage-605	Y	L	-	-	-	-	-	E	-	N	F	L	-	T	0.09	0.23	0.22	660
Phage-606	F	D	-	-	-	-	V	-	-	-	-	D	-	A	0.08	0.22	0.09	661
Phage-607	Y	D	-	-	-	-	Q	E	-	I	S	F	-	N	0.09	0.22	0.09	662
Phage-608	I	D	-	-	-	-	I	E	L	Y	D	D	-	F	0.09	0.22	0.09	663
Phage-609	T	F	-	-	-	-	L	-	-	-	-	Y	-	Y	0.08	0.22	0.07	664
Phage-610	F	F	-	-	-	-	I	-	-	-	N	A	-	V	0.09	0.22	0.07	665
Phage-611	Y	H	-	W	-	D	W	E	P	I	Y	I	-	I	0.12	0.22	0.10	666
Phage-612	A	I	-	-	-	-	Y	E	-	D	H	Y	-	Y	0.08	0.22	0.08	667
Phage-613	P	L	-	-	-	D	G	F	-	N	Y	N	-	F	0.12	0.22	0.08	668
Phage-614	F	P	-	W	-	D	W	E	W	D	N	N	-	H	0.09	0.22	0.09	669
Phage-615	-	D	-	-	-	D	G	-	-	L	A	A	-	H	0.10	0.22	0.11	670
Phage-616	-	D	-	W	-	D	W	E	-	Y	Y	S	-	D	0.08	0.22	0.07	671

Phage-617	-	-	-	-	-	-	Y	-	-	-	Y	D	-	T	0.07	0.21	0.10	672
Phage-618	N	L	-	-	-	-	W	E	N	F	A	D	-	F	0.08	0.21	0.08	673
Phage-619	Y	L	-	-	-	-	L	E	V	F	F	V	-	D	0.12	0.21	0.10	674
Phage-620	I	F	-	-	-	-	L	E	D	Y	S	I	-	F	0.09	0.21	0.08	675
Phage-621	D	-	-	-	-	-	L	E	Q	Y	D	L	-	F	0.09	0.21	0.08	676
Phage-622	L	L	-	-	-	V	N	E	D	P	L	D	-	Y	0.11	0.21	0.13	677
Phage-623	I	D	-	-	-	-	-	-	-	-	-	F	-	Y	0.08	0.21	0.08	678
Phage-624	I	I	-	-	-	-	V	E	-	I	D	I	-	S	0.08	0.21	0.08	679
Phage-625	I	A	-	W	-	D	W	E	D	Y	S	S	-	P	0.08	0.21	0.11	680
Phage-626	Y	-	-	-	-	-	V	E	D	I	N	D	-	I	0.09	0.21	0.07	681
Phage-627	N	I	-	-	-	-	M	-	-	-	I	D	-	I	0.08	0.21	0.07	682
Phage-628	F	D	-	W	-	D	W	E	-	L	-	S	-	Y	0.07	0.21	0.08	683
Phage-629	Y	F	-	-	-	-	W	E	D	H	F	F	-	D	0.09	0.21	0.19	684
Phage-630	T	-	-	-	-	-	-	E	-	D	S	Y	-	D	0.12	0.20	0.09	685
Phage-631	N	L	-	-	-	-	V	E	L	I	D	I	-	S	0.11	0.20	0.09	686
Phage-632	D	N	-	-	-	-	W	E	-	V	Y	L	-	N	0.08	0.20	0.08	687
Phage-633	F	L	-	-	-	-	-	-	-	-	D	L	-	F	0.08	0.20	0.09	688
Phage-634	H	I	-	-	-	-	Q	-	-	-	I	-	-	T	0.09	0.20	0.19	689
Phage-635	F	D	-	W	-	D	W	E	D	N	S	Y	-	D	0.10	0.20	0.09	690
Phage-636	T	A	-	-	-	-	W	E	F	D	F	N	-	D	0.08	0.20	0.07	691
Phage-637	H	H	-	W	-	D	W	E	D	Y	S	T	-	P	0.10	0.20	0.11	692
Phage-638	Y	-	-	-	-	-	-	-	-	-	-	N	-	F	0.07	0.20	0.08	693
Phage-639	L	H	-	W	-	D	W	E	-	I	D	I	-	D	0.08	0.20	0.09	694
Phage-640	D	I	-	-	-	D	G	Q	-	D	F	V	-	S	0.08	0.20	0.09	695
Phage-641	D	V	-	W	-	D	W	E	V	N	Y	F	-	D	0.09	0.20	0.07	696
Phage-642	-	N	-	-	-	-	M	-	-	-	I	D	-	A	0.12	0.20	0.10	697
Phage-643	D	N	-	-	-	-	-	-	-	A	T	V	-	N	0.11	0.19	0.19	698
Phage-644	D	L	-	-	-	-	-	E	-	V	H	N	-	N	0.08	0.19	0.08	699
Phage-645	-	N	-	-	-	-	-	-	-	-	S	Y	-	F	0.13	0.19	0.09	700
Phage-646	N	I	-	W	-	D	W	E	-	D	N	F	-	S	0.08	0.19	0.08	701
Phage-647	F	V	-	-	-	-	W	E	V	Y	D	D	-	D	0.08	0.19	0.08	702
Phage-648	A	-	-	-	-	-	L	E	V	V	H	L	-	V	0.10	0.19	0.17	703
Phage-649	P	F	-	-	-	-	M	-	-	T	I	D	-	Y	0.07	0.19	0.09	704
Phage-650	L	L	-	-	-	V	M	E	D	V	F	A	-	Y	0.08	0.19	0.08	705
Phage-651	D	L	-	-	-	-	-	-	-	-	T	N	-	Y	0.07	0.19	0.08	706
Phage-652	H	D	-	-	-	-	M	E	-	Y	Y	L	-	P	0.10	0.18	0.10	707
Phage-653	T	D	-	-	-	-	Y	-	-	-	I	I	-	P	0.08	0.18	0.09	708

Phage-654	-	L	-	W	-	D	W	E	D	Y	A	D	-	N	0.09	0.18	0.08	709
Phage-655	N	D	-	-	-	-	L	-	-	-	L	T	-	D	0.07	0.18	0.09	710
Phage-656	I	-	-	-	-	-	L	-	-	-	I	A	-	Y	0.11	0.18	0.08	711
Phage-657	N	-	-	-	-	-	V	E	-	F	N	F	-	H	0.11	0.18	0.14	712
Phage-658	D	V	-	-	-	-	I	E	-	Y	S	F	-	I	0.08	0.18	0.09	713
Phage-659	D	L	-	-	-	-	V	E	-	I	T	D	-	A	0.10	0.18	0.12	714
Phage-660	H	D	-	-	-	-	-	-	-	-	-	F	-	I	0.12	0.18	0.12	715
Phage-661	P	L	-	-	-	V	L	E	-	D	I	Y	-	Y	0.10	0.18	0.13	716
Phage-662	D	L	-	-	-	-	-	E	D	I	I	D	-	N	0.10	0.18	0.11	717
Phage-663	D	-	-	-	-	-	V	E	V	P	S	N	-	N	0.10	0.18	0.18	718
Phage-664	I	I	-	-	-	-	L	-	-	-	T	A	-	D	0.10	0.18	0.09	719
Phage-665	D	H	-	-	-	-	-	-	-	-	-	N	-	D	0.10	0.18	0.14	720
Phage-666	F	D	-	-	-	-	-	-	-	-	L	Y	-	S	0.07	0.18	0.07	721
Phage-667	F	A	-	W	-	D	W	E	-	V	Y	I	-	Y	0.08	0.18	0.08	722
Phage-668	L	-	-	-	-	-	-	-	-	-	L	D	-	S	0.08	0.18	0.09	723
Phage-669	D	L	-	-	-	-	L	E	-	A	F	L	-	A	0.09	0.18	0.08	724
Phage-670	F	A	-	-	-	-	L	-	-	T	L	T	-	L	0.10	0.18	0.08	725
Phage-671	F	D	-	-	-	-	V	E	-	I	S	N	-	D	0.17	0.18	0.10	726
Phage-672	-	H	-	-	-	-	L	E	Y	P	F	D	-	N	0.09	0.17	0.16	727
Phage-673	A	-	-	-	-	-	-	E	-	H	T	T	-	N	0.10	0.17	0.15	728
Phage-674	L	-	-	-	-	V	S	E	Q	F	T	F	-	I	0.08	0.17	0.08	729
Phage-675	D	-	-	-	-	-	L	-	-	-	Y	D	-	N	0.10	0.17	0.09	730
Phage-676	F	-	-	-	-	-	W	E	-	F	D	V	-	I	0.13	0.17	0.15	731
Phage-677	F	T	-	-	-	-	V	E	-	Y	D	H	-	I	0.08	0.17	0.09	732
Phage-678	Y	N	-	-	-	-	-	-	-	-	-	T	-	F	0.12	0.17	0.11	733
Phage-679	A	V	-	-	-	-	N	-	-	-	N	S	-	A	0.08	0.17	0.08	734
Phage-680	I	-	-	W	-	D	W	E	V	P	N	D	-	A	0.10	0.17	0.09	735
Phage-681	Y	F	-	-	-	-	-	E	-	F	F	H	-	Y	0.12	0.17	0.12	736
Phage-682	Y	V	-	-	-	D	G	-	-	-	S	F	-	D	0.12	0.17	0.12	737
Phage-683	I	S	-	-	-	-	V	E	-	F	F	Y	-	Y	0.10	0.17	0.08	738
Phage-684	L	I	-	-	-	V	-	E	-	D	-	Y	-	D	0.17	0.17	0.15	739
Phage-685	-	-	-	-	-	-	V	E	D	H	N	Y	-	A	0.14	0.17	0.16	740
Phage-686	L	D	-	-	-	-	-	E	F	V	Y	I	-	A	0.08	0.17	0.10	741
Phage-687	Y	D	-	-	-	-	-	E	-	D	L	P	-	I	0.17	0.17	0.11	742
Phage-688	D	V	-	-	-	-	V	E	-	D	Y	Y	-	D	0.10	0.17	0.14	743
Phage-689	N	D	-	W	-	D	W	E	Y	D	N	V	-	V	0.08	0.17	0.10	744
Phage-690	D	L	-	-	-	-	-	E	V	A	N	D	-	N	0.10	0.16	0.16	745

Phage-691	H	D	-	-	-	-	L	-	-	-	I	S	-	N	0.09	0.16	0.07	746
Phage-692	L	D	-	W	-	D	W	E	-	T	T	H	-	D	0.08	0.16	0.08	747
Phage-693	I	I	-	-	-	-	V	E	-	D	D	Y	-	L	0.09	0.16	0.09	748
Phage-694	Y	-	-	W	-	D	W	E	-	V	I	I	-	D	0.09	0.16	0.09	749
Phage-695	F	D	-	-	-	-	I	-	-	Y	T	N	-	N	0.12	0.16	0.09	750
Phage-696	I	T	-	-	-	-	L	-	-	T	I	N	-	D	0.08	0.16	0.11	751
Phage-697	D	S	-	-	-	-	V	E	-	D	I	Y	-	I	0.07	0.16	0.08	752
Phage-698	Y	L	-	-	-	-	-	-	-	-	G	N	-	H	0.07	0.16	0.08	753
Phage-699	D	N	-	-	-	-	L	P	-	D	Y	F	-	D	0.08	0.16	0.10	754
Phage-700	-	L	-	-	-	-	-	E	-	V	S	N	-	N	0.11	0.16	0.08	755
Phage-701	-	D	-	W	-	D	W	E	-	D	I	V	-	D	0.10	0.16	0.09	756
Phage-702	-	-	-	W	-	D	W	E	D	N	F	P	-	Y	0.07	0.16	0.07	757
Phage-703	D	-	-	-	-	-	V	E	-	H	F	N	-	H	0.08	0.16	0.08	758
Phage-704	A	D	-	-	-	-	I	E	-	D	A	Y	-	Y	0.12	0.16	0.09	759
Phage-705	I	L	-	W	-	D	W	E	D	A	T	F	-	Y	0.09	0.16	0.07	760
Phage-706	I	H	-	W	-	D	W	E	D	F	N	I	-	P	0.09	0.16	0.08	761
Phage-707	T	I	-	-	-	-	V	E	D	Y	N	D	-	I	0.07	0.16	0.07	762
Phage-708	D	D	-	-	-	-	L	-	-	-	-	A	-	I	0.08	0.16	0.08	763
Phage-709	D	D	-	W	-	D	W	E	D	H	I	F	-	F	0.13	0.16	0.08	764
Phage-710	-	N	-	-	-	-	V	E	-	I	I	F	-	D	0.12	0.15	0.12	765
Phage-711	I	F	-	W	-	D	W	E	D	D	T	V	-	I	0.08	0.15	0.09	766
Phage-712	I	I	-	-	-	-	-	E	-	I	S	D	-	L	0.12	0.15	0.15	767
Phage-713	F	D	-	-	-	-	V	E	-	Y	N	D	-	D	0.11	0.15	0.09	768
Phage-714	N	D	-	-	-	-	L	-	-	T	L	Y	-	I	0.08	0.15	0.10	769
Phage-715	A	I	-	-	-	-	L	E	-	D	I	S	-	N	0.12	0.15	0.17	770
Phage-716	H	L	-	-	-	-	-	-	-	-	T	N	-	Y	0.07	0.15	0.07	771
Phage-717	S	-	-	-	-	-	L	-	-	-	-	A	-	I	0.10	0.15	0.11	772
Phage-718	L	-	-	-	-	-	-	E	Q	L	A	D	-	T	0.08	0.15	0.08	773
Phage-719	I	D	-	-	-	-	L	-	-	-	I	A	-	N	0.07	0.15	0.08	774
Phage-720	F	D	-	-	-	D	G	Q	-	D	L	V	-	N	0.10	0.15	0.08	775
Phage-721	N	L	-	-	-	-	-	E	-	F	F	D	-	Y	0.09	0.15	0.15	776
Phage-722	S	I	-	-	-	-	L	Q	-	D	I	V	-	P	0.09	0.14	0.14	777
Phage-723	N	P	-	-	-	-	Y	-	-	-	A	H	-	D	0.08	0.14	0.08	778
Phage-724	Y	D	-	-	-	-	L	-	-	Y	Y	N	-	N	0.12	0.14	0.11	779
Phage-725	-	D	-	-	-	-	L	-	-	T	I	F	-	D	0.07	0.14	0.08	780
Phage-726	D	N	-	-	-	-	L	-	-	-	-	T	-	T	0.09	0.14	0.10	781
Phage-727	-	D	-	-	-	-	L	-	-	-	S	Y	-	D	0.10	0.14	0.13	782

Phage-728	Y	-	-	-	-	-	-	E	F	I	D	F	-	F	0.07	0.14	0.07	783
Phage-729	Y	D	-	W	-	D	W	E	V	I	T	Y	-	N	0.08	0.14	0.09	784
Phage-730	F	D	-	-	-	-	I	E	-	D	F	F	-	V	0.06	0.14	0.07	785
Phage-731	I	F	-	W	-	D	W	-	D	I	N	F	-	D	0.10	0.14	0.14	786
Phage-732	N	F	-	-	-	-	L	P	-	D	I	T	-	Y	0.37	0.14	0.09	787
Phage-733	S	L	-	-	-	-	-	E	-	Y	Y	H	-	L	0.09	0.14	0.07	788
Phage-734	A	S	-	-	-	-	L	-	-	-	L	D	-	L	0.12	0.14	0.13	789
Phage-735	S	F	-	-	-	-	R	E	W	D	L	A	-	Y	0.09	0.14	0.08	790
Phage-736	H	L	-	-	-	-	-	E	D	V	L	D	-	I	0.08	0.14	0.12	791
Phage-737	L	D	-	-	-	D	G	-	-	F	Y	Y	-	L	0.20	0.14	0.09	792
Phage-738	D	N	-	W	-	D	W	E	-	D	I	A	-	T	0.16	0.14	0.11	793
Phage-739	S	D	-	-	-	-	L	-	-	T	I	H	-	I	0.09	0.14	0.08	794
Phage-740	N	S	-	-	-	D	G	-	-	-	-	D	-	L	0.08	0.14	0.08	795
Phage-741	D	L	-	-	-	-	L	-	-	-	T	L	-	I	0.07	0.14	0.08	796
Phage-742	F	D	-	-	-	-	S	-	-	-	F	N	-	Y	0.09	0.14	0.11	797
Phage-743	D	L	-	-	-	-	-	E	-	D	D	I	-	Y	0.12	0.14	0.13	798
Phage-744	H	A	-	-	-	-	-	E	-	D	T	Y	-	F	0.10	0.14	0.14	799
Phage-745	S	D	-	-	-	-	L	-	-	-	-	A	-	I	0.11	0.14	0.08	800
Phage-746	I	V	-	-	-	-	L	P	-	D	Y	N	-	Y	0.09	0.13	0.11	801
Phage-747	D	L	-	-	-	-	-	-	-	-	F	I	-	F	0.09	0.13	0.08	802
Phage-748	Y	D	-	-	-	-	-	-	-	T	L	T	-	N	0.13	0.13	0.08	803
Phage-749	Y	D	-	-	-	-	V	E	-	I	-	N	-	D	0.11	0.13	0.12	804
Phage-750	-	F	-	-	-	-	I	E	D	D	H	V	-	I	0.07	0.13	0.07	805
Phage-751	F	I	-	-	-	-	W	E	D	D	Y	A	-	S	0.12	0.13	0.12	806
Phage-752	N	F	-	-	-	-	-	-	-	-	-	-	-	N	0.10	0.13	0.09	807
Phage-753	N	L	-	-	-	-	V	E	-	I	L	I	-	D	0.07	0.13	0.07	808
Phage-754	D	S	-	-	-	-	V	E	-	Y	D	L	-	N	0.11	0.13	0.08	809
Phage-755	T	L	-	-	-	-	-	E	-	I	T	D	-	N	0.09	0.13	0.08	810
Phage-756	T	V	-	-	-	K	M	E	M	N	S	T	-	D	0.09	0.13	0.09	811
Phage-757	-	H	-	W	-	D	W	E	D	A	-	S	-	N	0.10	0.12	0.11	812
Phage-758	D	L	-	-	-	D	G	N	-	L	D	F	-	F	0.08	0.12	0.08	813
Phage-759	D	L	-	-	-	D	G	E	-	H	Y	Y	-	D	0.09	0.12	0.07	814
Phage-760	F	N	-	-	-	-	V	E	-	I	L	L	-	T	0.11	0.12	0.12	815
Phage-761	H	-	-	-	-	-	V	E	N	I	N	D	-	I	0.09	0.12	0.07	816
Phage-762	I	D	-	-	-	-	L	-	-	-	-	I	-	D	0.09	0.12	0.08	817
Phage-763	I	F	-	-	-	-	I	E	Q	P	A	L	-	Y	0.08	0.12	0.09	818
Phage-764	Y	D	-	-	-	-	-	Q	-	D	L	V	-	P	0.10	0.12	0.08	819

Phage-765	H	A	-	W	-	D	W	E	-	P	N	Y	-	D	0.13	0.12	0.09	820
Phage-766	N	V	-	W	-	D	W	E	-	D	Y	N	-	Y	0.11	0.12	0.10	821
Phage-767	S	F	-	-	Q	-	L	G	D	N	Y	D	-	I	0.09	0.12	0.12	822
Phage-768	D	D	-	-	-	-	L	-	-	T	T	V	-	Y	0.08	0.12	0.09	823
Phage-769	N	F	-	-	-	-	W	E	V	A	T	L	-	L	0.09	0.12	0.14	824
Phage-770	D	L	-	-	-	-	V	E	-	D	T	Y	-	N	0.09	0.11	0.07	825
Phage-771	A	L	-	-	-	-	V	E	Q	V	D	L	-	T	0.08	0.11	0.08	826
Phage-772	D	D	-	-	-	-	L	-	-	-	-	N	-	N	0.08	0.11	0.08	827
Phage-773	I	F	-	-	-	-	-	E	Q	I	I	Y	-	D	0.09	0.11	0.11	828
Phage-774	S	D	-	W	-	D	W	E	-	V	Y	Y	-	S	0.09	0.11	0.10	829
Phage-775	F	F	-	-	-	D	G	-	-	V	A	I	-	D	0.09	0.11	0.07	830
Phage-776	D	D	-	W	-	D	W	E	D	D	-	Y	-	Y	0.11	0.11	0.07	831
Phage-777	Y	D	-	-	-	-	-	-	-	T	-	V	-	P	0.08	0.11	0.08	832
Phage-778	S	-	-	-	-	-	L	-	-	-	-	N	-	V	0.10	0.11	0.08	833
Phage-779	A	F	-	V	S	F	Q	Q	S	L	P	H	-	D	0.09	0.11	0.10	834
Phage-780	-	N	-	-	-	-	V	E	-	Y	F	V	-	F	0.09	0.11	0.09	835
Phage-781	T	N	-	W	-	D	W	E	-	D	F	A	-	V	0.07	0.11	0.08	836
Phage-782	D	D	-	-	-	-	-	E	-	I	I	L	-	F	0.08	0.10	0.08	837
Phage-783	N	S	-	-	-	-	L	E	D	Y	H	L	-	P	0.08	0.10	0.10	838
Phage-784	I	H	-	-	-	D	S	-	G	F	D	F	-	D	0.09	0.10	0.08	839
Phage-785	F	D	-	-	-	-	L	E	-	D	H	L	-	F	0.08	0.10	0.08	840
Phage-786	T	V	-	W	-	D	-	E	-	Y	A	D	-	D	0.10	0.10	0.08	841
Phage-787	Y	F	-	W	-	D	W	E	-	A	A	D	-	L	0.09	0.10	0.09	842
Phage-788	-	S	-	-	-	-	-	-	-	-	-	D	-	I	0.08	0.10	0.07	843
Phage-789	A	V	-	-	-	-	L	P	-	D	I	V	-	Y	0.08	0.10	0.08	844
Phage-790	-	L	-	-	-	-	V	E	-	Y	H	L	-	A	0.08	0.10	0.30	845
Phage-791	S	L	-	W	-	D	W	E	-	V	D	N	-	F	0.12	0.10	0.11	846
Phage-792	T	I	-	-	-	D	G	Q	-	D	Y	N	-	H	0.07	0.10	0.07	847
Phage-793	F	L	-	-	-	-	G	E	P	T	Y	L	-	T	0.12	0.10	0.09	848
Phage-794	D	D	-	W	L	-	Q	H	D	I	Y	V	-	A	0.10	0.10	0.08	849
Phage-795	I	F	-	-	-	-	V	E	-	V	A	F	-	F	0.07	0.10	0.08	850
Phage-796	A	L	-	-	-	-	V	E	D	D	Y	D	-	L	0.09	0.10	0.09	851
Phage-797	D	D	-	-	-	-	I	E	L	Y	L	T	-	A	0.08	0.10	0.08	852
Phage-798	T	D	-	W	-	D	W	E	D	D	S	I	-	D	0.07	0.10	0.07	853
Phage-799	S	I	-	-	-	-	L	E	-	I	F	L	-	N	0.08	0.10	0.08	854
Phage-800	N	D	-	-	-	-	L	E	-	D	I	L	-	F	0.07	0.10	0.09	855
Phage-801	D	D	-	-	-	-	L	-	-	T	Y	S	-	Y	0.09	0.09	0.08	856

Phage-802	F	V	-	-	-	-	W	E	-	I	D	L	-	I	0.10	0.09	0.09	857
Phage-803	Y	D	-	-	-	-	L	-	-	-	L	S	-	P	0.07	0.09	0.07	858
Phage-804	N	L	-	-	-	-	L	-	-	-	I	I	-	P	0.08	0.09	0.08	859
Phage-805	I	D	-	W	-	D	W	E	-	F	N	N	-	F	0.08	0.09	0.09	860
Phage-806	A	-	-	-	-	-	L	E	-	H	D	Y	-	Y	0.08	0.09	0.09	861
Phage-807	D	D	-	S	-	Q	-	-	Q	I	D	L	-	D	0.14	0.09	0.09	862
Phage-808	S	-	-	-	-	-	S	-	-	-	I	Y	-	Y	0.08	0.09	0.07	863
Phage-809	S	L	-	-	-	-	-	Q	-	D	A	P	-	N	0.07	0.09	0.07	864
Phage-810	D	A	-	-	-	-	L	-	-	T	T	H	-	D	0.09	0.09	0.08	865
Phage-811	N	D	-	-	-	-	V	E	-	V	A	D	-	F	0.07	0.09	0.08	866
Phage-812	Y	I	-	-	-	-	-	E	Q	D	Y	F	-	F	0.08	0.09	0.08	867
Phage-813	T	D	-	-	-	D	G	-	-	T	N	Y	-	F	0.11	0.09	0.08	868
Phage-814	Y	D	-	-	-	-	V	-	-	-	-	L	-	P	0.08	0.09	0.08	869
Phage-815	I	D	-	-	-	-	-	-	-	-	A	Y	-	T	0.08	0.09	0.08	870
Phage-816	F	D	-	-	-	-	-	E	-	F	F	H	-	Y	0.09	0.09	0.09	871
Phage-817	F	P	-	-	-	-	I	E	-	Y	D	Y	-	V	0.09	0.09	0.08	872
Phage-818	A	D	-	-	-	I	-	E	S	I	D	I	-	V	0.09	0.09	0.07	873
Phage-819	I	S	-	-	-	D	L	W	P	T	D	I	-	T	0.10	0.09	0.10	874
Phage-820	D	D	-	-	-	D	G	-	-	V	H	T	-	N	0.09	0.09	0.07	875
Phage-821	I	D	-	W	-	D	W	E	G	-	F	A	-	N	0.09	0.09	0.08	876
Phage-822	L	N	-	-	-	D	G	-	-	T	F	Y	-	D	0.08	0.08	0.07	877
Phage-823	I	H	-	-	-	-	L	G	A	Y	I	S	-	S	0.08	0.08	0.09	878
Phage-824	T	I	-	W	-	D	W	E	-	D	Y	F	-	Y	0.08	0.08	0.08	879
Phage-825	H	S	-	L	A	Q	-	-	Q	D	L	V	-	I	0.07	0.08	0.07	880
Phage-826	N	N	-	A	S	D	L	S	-	D	N	S	-	I	0.07	0.08	0.08	881
Phage-827	-	N	-	W	-	D	W	E	-	D	-	A	-	N	0.09	0.08	0.07	882
Phage-828	-	-	-	-	-	-	L	-	-	-	F	Y	-	F	0.08	0.08	0.07	883
Phage-829	L	F	-	-	T	V	L	-	-	F	F	D	-	D	0.07	0.08	0.07	884
Phage-830	F	D	-	-	-	-	L	-	-	-	-	S	-	A	0.08	0.08	0.07	885
Phage-831	Y	-	-	-	-	-	V	E	-	N	-	Y	-	I	0.07	0.08	0.08	886
Phage-832	D	-	-	-	-	-	L	-	D	-	T	I	-	H	0.12	0.08	0.10	887
Phage-833	-	F	-	-	-	Q	W	A	-	A	N	A	-	F	0.09	0.08	0.07	888
Phage-834	F	T	-	-	-	-	Y	-	-	-	I	T	-	P	0.09	0.08	0.09	889
Phage-835	L	N	-	-	-	V	N	-	-	-	S	V	-	I	0.07	0.08	0.08	890
Phage-836	A	I	-	W	-	D	W	E	-	F	S	D	-	H	0.07	0.08	0.07	891
Phage-837	Y	-	-	-	V	D	L	G	A	N	-	Y	-	Y	0.10	0.08	0.09	892
Phage-838	H	-	-	-	-	-	V	E	-	D	Y	H	-	D	0.07	0.08	0.07	893

Phage-839	N	D	-	-	S	L	Q	Y	D	I	P	T	-	V	0.08	0.08	0.07	894
Phage-840	Y	V	-	R	-	Q	L	-	V	Y	H	Y	-	N	0.15	0.08	0.07	895
Phage-841	H	D	-	-	-	D	G	-	-	-	I	I	-	S	0.08	0.08	0.07	896
Phage-842	F	D	-	-	-	-	L	-	-	T	I	I	-	P	0.08	0.08	0.08	897
Phage-843	-	D	-	-	S	D	R	G	-	N	A	A	-	H	0.07	0.08	0.07	898
Phage-844	N	I	-	L	A	Q	-	N	-	D	P	T	-	N	0.07	0.08	0.08	899
Phage-845	T	N	-	-	S	K	S	Q	V	-	D	H	-	I	0.10	0.08	0.09	900
Phage-846	N	H	-	H	-	Q	-	W	-	L	T	N	-	N	0.09	0.07	0.07	901
Phage-847	L	L	-	H	-	Q	G	-	L	Y	H	L	-	H	0.09	0.07	0.08	902
Phage-848	T	N	-	D	S	K	L	E	G	D	D	N	-	F	0.09	0.07	0.07	903
Phage-849	N	D	-	-	-	-	M	-	-	-	L	L	-	D	0.08	0.07	0.07	904
Phage-850	F	H	-	-	-	-	V	-	-	-	I	N	-	N	0.07	0.07	0.07	905
Phage-851	D	F	-	-	-	D	G	-	-	T	Y	V	-	S	0.07	0.07	0.08	906
Phage-852	-	S	-	-	-	Q	-	-	-	N	N	T	-	N	0.07	0.07	0.08	907
Phage-853	-	-	-	H	L	-	S	E	Q	F	D	I	-	I	0.08	0.07	0.08	908
Phage-854	D	D	-	-	-	-	W	E	F	V	F	F	-	D	0.08	0.07	0.08	909
Phage-855	Y	N	-	E	Q	Q	Q	-	-	D	P	S	-	I	0.07	0.07	0.07	910
Phage-856	N	T	-	-	T	-	Q	H	-	F	N	-	-	L	0.08	0.07	0.08	911
Phage-857	H	P	-	Q	-	G	-	E	-	V	D	Y	-	V	0.08	0.07	0.08	912
Phage-858	-	A	-	S	R	Q	L	G	-	D	A	Y	-	N	0.07	0.07	0.07	913
Phage-859	D	I	-	-	A	Q	E	V	H	V	Y	T	-	P	0.07	0.07	0.07	914
Phage-860	F	F	-	E	G	N	L	-	A	Y	L	L	-	L	0.08	0.07	0.08	915
Phage-861	Y	-	-	-	-	D	G	E	-	N	I	V	-	D	0.07	0.07	0.07	916

Table 18. Summary of Peptide Sequences

Peptide-ID	anti-CD3 Panned target	Sequence	SEQ ID NO:
Peptide-29	SP34.185	DDCWPDWEFDFACA	44
Peptide-30	SP34.185	YICGLDFPDFLYCD	45
Peptide-31	SP34.185	FDCWPDWEEYFVCD	46
Peptide-32	SP34.185	YICWPDWEEYFDCD	47
Peptide-33	SP34.185	NICWPDWEDDYFCF	48
Peptide-34	SP34.185	NFCWPDWEYIYPCI	49
Peptide-35	SP34.185	VDCWPDWEEDFLCI	50
Peptide-36	SP34.185	HACWPDWEEYFPCN	51
Peptide-37	SP34.185	YDCGPDVDESYVCV	52
Peptide-38	SP34.185	IDCWPDWEDDTFCY	53
Peptide-39	SP34.185	YLCGPDGDETLACY	54
Peptide-40	SP34.185	VDCGPDGDESILCY	55

Table 19. Summary of Figure 5A

ELISA	Peptide-29	Peptide-30	Peptide-31	Peptide-32	Peptide-33	Peptide-34	Peptide-2
EC50 nM	2.163	1.564	2.035	1.713	2.174	2.752	1.972

Table 20. Summary of Figure 5B

ELISA	Peptide-35	Peptide-36	Peptide-37	Peptide-38	Peptide-39	Peptide-40	Peptide-2
EC50 nM	2.804	2.695	344.3	1.652	1.286	1.895	1.623

Table 21. Summary of Figure 6A

ELISA	Peptide-29	Peptide-30	Peptide-31	Peptide-32	Peptide-33	Peptide-34	Peptide-2
IC50 uM	7.9	3.2	8.5	6.5	17.2	11.7	0.28

Table 22. Summary of Figure 6A

ELISA	Peptide-35	Peptide-36	Peptide-37	Peptide-38	Peptide-39	Peptide-40	Peptide-2
IC50 uM	17.3	15.2	>100	2.9	0.01	0.35	0.15

CLAIMS

WHAT IS CLAIMED IS:

1. An isolated polypeptide or polypeptide complex comprising a peptide that impairs binding of an anti-CD3 binding domain to cluster of differentiation 3 (CD3) wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2 and 19-55 or the peptide comprises 1, 2, or 3, amino acid substitutions, additions, or deletions relative to an amino acid sequence selected from SEQ ID NOs: 1-2 and 19-55.

2. The isolated polypeptide or polypeptide complex of claim 1, wherein the peptide comprises an amino acid sequence selected from SEQ ID NOs: 1-2 and 19-55.

3. The isolated polypeptide or polypeptide complex of claim 2, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 1.

4. The isolated polypeptide or polypeptide complex of claim 2, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 2.

5. The isolated polypeptide or polypeptide complex of claim 2, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 54.

6. An isolated polypeptide or polypeptide complex comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to Z_1-Z_2-C- Z_4-P-Z_6-Z_7-Z_8- Z_9-Z_{10}-Z_{11}- Z_{12}-C-Z_{14} and Z_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; Z_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S; Z_4 is selected from G and W; Z_6 is selected from E, D, V, and P; Z_7 is selected from W, L, F, V, G, M, I, and Y; Z_8 is selected from E, D, P, and Q; Z_9 is selected from E, D, Y, V, F, W, P, L, and Q; Z_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; Z_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; Z_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, and H; and Z_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L and S.

7. The isolated polypeptide or polypeptide complex of claim 6, wherein Z_1 is selected from D, Y, F, I, and N; Z_2 is selected from D, Y, L, F, I, and N; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, F, and V; Z_8 is selected from E and D; Z_9 is selected from E, D, Y, and V; Z_{10} is selected from S, D, Y, T, and I; Z_{11} is selected from I, Y, F, V, L, and T; Z_{12} is selected from F, D, Y, L, I, V, A, and N; and Z_{14} is selected from D, Y, N, F, I, and P.

8. The isolated polypeptide or polypeptide complex of claim 7, wherein Z_1 is selected from D, Y, and F; Z_2 is selected from D, Y, L, and F; Z_4 is selected from G and W; Z_6 is selected from E and D; Z_7 is selected from W, L, and F; Z_8 is selected from E and D; Z_9 is selected from E and D; Z_{10} is selected from S, D, and Y; Z_{11} is selected from I, Y, and F; Z_{12} is selected from F, D, Y, and L; and Z_{14} is selected from D, Y, and N.

9. An isolated polypeptide or polypeptide complex comprising an anti-CD3 binding domain that is linked to a peptide that impairs binding of the anti-CD3 binding domain to CD3 wherein the peptide comprises an amino acid sequence according to U_1-U_2-C- U_4-P-U_6-U_7-U_8- U_9-U_{10}-U_{11}-U_{12}-C-U_{14} and U_1 is selected from D, Y, F, I, N, V, H, L, A, T, S, and P; U_2 is selected from D, Y, L, F, I, N, A, V, H, T, and S;

U_4 is selected from G and W; U_6 is selected from E, D, V, and P; U_7 is selected from W, L, F, V, G, M, I, and Y; U_8 is selected from E, D, P, and Q; U_9 is selected from E, D, Y, V, F, W, P, L, and Q; U_{10} is selected from S, D, Y, T, I, F, V, N, A, P, L, and H; U_{11} is selected from I, Y, F, V, L, T, N, S, D, A, and H; U_{12} is selected from F, D, Y, L, I, V, A, N, T, P, S, G, and H; and U_{14} is selected from D, Y, N, F, I, P, V, A, T, H, L, M, and S.

10. The isolated polypeptide or polypeptide complex of claim 9, wherein U_1 is selected from D, Y, F, I, V, and N; U_2 is selected from D, Y, L, F, I, and N; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, F, G, and V; U_8 is selected from E and D; U_9 is selected from E, D, Y, and V; U_{10} is selected from S, D, Y, T, and I; U_{11} is selected from I, Y, F, V, L, and T; U_{12} is selected from F, D, Y, L, I, V, A, G, and N; and U_{14} is selected from D, Y, N, F, I, M, and P.

11. The isolated polypeptide or polypeptide complex of claim 10, wherein U_1 is selected from D, Y, V, and F; U_2 is selected from D, Y, L, and F; U_4 is selected from G and W; U_6 is selected from E and D; U_7 is selected from W, L, G, and F; U_8 is selected from E and D; U_9 is selected from E and D; U_{10} is selected from S, D, T, and Y; U_{11} is selected from I, Y, V, L, and F; U_{12} is selected from F, D, Y, G, A, and L; and U_{14} is selected from D, Y, M, and N.

12. The isolated polypeptide or polypeptide complex of claim 9, wherein the peptide comprises an amino acid sequence of **Table 17**.

13. The isolated polypeptide or polypeptide complex of claim 9, wherein the peptide comprises an amino acid sequence according to any one of SEQ ID NOs: 44-55.

14. The isolated polypeptide or polypeptide complex of claim 11, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 2.

15. The isolated polypeptide or polypeptide complex of claim 11, wherein the peptide comprises the amino acid sequence of SEQ ID NO: 54.

16. The isolated polypeptide or polypeptide complex of claim 9, wherein the peptide is connected to the anti-CD3 binding domain in a configuration according to Formula I: A_1-L_1-P_1 wherein A_1 comprises the anti-CD3 binding domain; L_1 comprises a cleavable linker that is a substrate for a tumor specific protease; and P_1 comprises the peptide that impairs binding of the anti-CD3 binding domain to CD3.

17. The isolated polypeptide or polypeptide complex of claim 16, wherein P_1 is connected N-terminal to the cleavable linker and A_1 is connected C-terminal to the cleavable linker.

18. The isolated polypeptide or polypeptide complex of claim 16, wherein P_1 is connected C-terminal to the cleavable linker and A_1 is connected N-terminal to the cleavable linker.

19. The isolated polypeptide or polypeptide complex of claim 16, wherein P_1 is bound to A_1 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof.

20. The isolated polypeptide or polypeptide complex of claim 16, wherein A_1 is further linked to a tumor antigen binding domain (A_2).

21. The isolated polypeptide or polypeptide complex of claim 16, wherein the polypeptide or polypeptide complex is according to Formula Ia: P_2-L_2-A_2-A_1-L_1-P_1 wherein P_2 comprises a peptide that impairs binding of A_2 to a tumor antigen; and L_2 comprises a second cleavable linker that connects A_2 to P_2 and is a substrate for a tumor specific protease.

22. The isolated polypeptide or polypeptide complex of claim 21, wherein A_1 comprises an antibody or antibody fragment.

23. The isolated polypeptide or polypeptide complex of claim 21, wherein A_1 comprises an antibody or antibody fragment that is human or humanized.

24. The isolated polypeptide or polypeptide complex of claim 22, wherein L_1 is bound to a N-terminus of the antibody or antibody fragment of A_1.

25. The isolated polypeptide or polypeptide complex of claim 22, wherein A_2 is bound to a N-terminus of the antibody or antibody fragment of A_1.

26. The isolated polypeptide or polypeptide complex of claim 22, wherein L_1 is bound to a C-terminus of the antibody or antibody fragment of A_1.

27. The isolated polypeptide or polypeptide complex of claim 22, wherein A_2 is bound to a C-terminus of the antibody or antibody fragment of A_1.

28. The isolated polypeptide or polypeptide complex of claim 22, wherein the antibody or antibody fragment of A_1 comprises a single chain variable fragment, a single domain antibody, or a Fab fragment.

29. The isolated polypeptide or polypeptide complex of claim 28, wherein A_1 is the single chain variable fragment (scFv).

30. The isolated polypeptide or polypeptide complex of claim 29, wherein the scFv comprises a scFv heavy chain polypeptide and a scFv light chain polypeptide.

31. The isolated polypeptide or polypeptide complex of claim 28, wherein A_1 is the single domain antibody.

32. The isolated polypeptide or polypeptide complex of claim 23, wherein the antibody or antibody fragment thereof comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody.

33. The isolated polypeptide or polypeptide complex of claim 32, wherein A_1 comprises an anti-CD3e single chain variable fragment.

34. The isolated polypeptide or polypeptide complex of claim 22, wherein A_1 comprises an anti-CD3e single chain variable fragment that has a KD binding of 1 μM or less to CD3 on CD3 expressing cells.

35. The isolated polypeptide or polypeptide complex of claim 22, wherein A_1 comprises a variable light chain and variable heavy chain each of which is capable of specifically binding to human CD3.

36. The isolated polypeptide or polypeptide complex of claim 30, wherein A_1 comprises the scFv comprising a scFv heavy chain variable domain and an scFv light chain variable domain comprising

complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the scFv heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5; and the scFv light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the scFv light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8.

37. The isolated polypeptide or polypeptide complex of claim 22, wherein A_1 comprises a heavy chain variable domain and a light chain variable domain comprising complementarity determining regions (CDRs): HC-CDR1, HC-CDR2, and HC-CDR3, wherein the HC-CDR1, the HC-CDR2, and the HC-CDR3 of the heavy chain variable domain comprise: HC-CDR1: SEQ ID NO: 3; HC-CDR2: SEQ ID NO: 4; HC-CDR3: SEQ ID NO: 5; and the light chain variable domain comprises complementarity determining regions (CDRs): LC-CDR1, LC-CDR2, and LC-CDR3, wherein the LC-CDR1, the LC-CDR2, and the LC-CDR3 of the light chain variable domain comprise: LC-CDR1: SEQ ID NO: 6; LC-CDR2: SEQ ID NO: 7; and LC-CDR3: SEQ ID NO: 8.

38. The isolated polypeptide or polypeptide complex of claim 16, wherein the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease.

39. The isolated polypeptide or polypeptide complex of claim 16, wherein the polypeptide or polypeptide complex of formula I binds to an effector cell when L_1 is cleaved by the tumor specific protease and A_1 binds to the effector cell.

40. The isolated polypeptide or polypeptide complex of claim 39, wherein the effector cell is a T cell.

41. The isolated polypeptide or polypeptide complex of claim 40, wherein A_1 binds to a polypeptide that is part of a TCR-CD3 complex on the effector cell.

42. The isolated polypeptide or polypeptide complex of claim 41, wherein the polypeptide that is part of the TCR-CD3 complex is human CD3ε.

43. The isolated polypeptide or polypeptide complex of claim 30, wherein A_2 comprises an antibody or antibody fragment.

44. The isolated polypeptide or polypeptide complex of claim 43, wherein the antibody or antibody fragment thereof of A_2 comprises a single chain variable fragment, a single domain antibody, Fab', or a Fab.

45. The isolated polypeptide or polypeptide complex of claim 43, wherein the antibody or antibody fragment of A_2 comprises a single chain variable fragment (scFv), a heavy chain variable domain (VH domain), a light chain variable domain (VL domain), or a variable domain (VHH) of a camelid derived single domain antibody.

46. The isolated polypeptide or polypeptide complex of claim 43, wherein the antibody or antibody fragment of A_2 is humanized or human.

47. The isolated polypeptide or polypeptide complex of claim 44, wherein A_2 is the Fab or Fab'.

48. The isolated polypeptide or polypeptide complex of claim 47, wherein the Fab or Fab' comprises (a) a Fab light chain polypeptide and (b) a Fab heavy chain polypeptide.

49. The isolated polypeptide or polypeptide complex of claim 48, wherein A_2 comprises an epidermal growth factor receptor (EGFR) binding domain.

50. The isolated polypeptide or polypeptide complex of claim 48, wherein A_2 comprises a carcinoembryonic antigen-related cell adhesion molecule CEACAM5 binding domain.

51. The isolated polypeptide or polypeptide complex of claim 48, wherein P_1 is further linked to a half-life extending moiety (H_l).

52. The isolated polypeptide or polypeptide complex of claim 51, wherein the half-life extending moiety is a single-domain antibody.

53. The isolated polypeptide or polypeptide complex of claim 51, wherein H_l comprises a polymer.

54. The isolated polypeptide or polypeptide complex of claim 53, wherein the polymer is polyethylene glycol (PEG).

55. The isolated polypeptide or polypeptide complex of claim 51, wherein H_l comprises albumin.

56. The isolated polypeptide or polypeptide complex of claim 51, wherein H_l comprises an Fc domain.

57. The isolated polypeptide or polypeptide complex of claim 55, wherein the albumin is serum albumin.

58. The isolated polypeptide or polypeptide complex of claim 57, wherein the albumin is human serum albumin.

59. The isolated polypeptide or polypeptide complex of claim 51, wherein H_l comprises a polypeptide, a ligand, or a small molecule.

60. The isolated polypeptide or polypeptide complex of claim 59, wherein the polypeptide, the ligand or the small molecule binds serum protein or a fragment thereof, a circulating immunoglobulin or a fragment thereof, or CD35/CR1.

61. The isolated polypeptide or polypeptide complex of claim 60, wherein the serum protein comprises a thyroxine-binding protein, a transthyretin, a 1-acid glycoprotein, a transferrin, transferrin receptor or a transferrin-binding portion thereof, a fibrinogen, or an albumin.

62. The isolated polypeptide or polypeptide complex of claim 60, wherein the circulating immunoglobulin comprises IgGl, IgG2, IgG3, IgG4, slgA, IgM or IgD.

63. The isolated polypeptide or polypeptide complex of claim 60, wherein the serum protein is albumin.

64. The isolated polypeptide or polypeptide complex of claim 59, wherein the polypeptide is an antibody.

65. The isolated polypeptide or polypeptide complex of claim 64, wherein the antibody comprises a single domain antibody, a single chain variable fragment, or a Fab.

66. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody comprises a single domain antibody that binds to albumin.

67. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is a human or humanized antibody.

68. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is 645gH1gL1.

69. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is 645dsgH5gL4.

70. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is 23-13-A01 -sc02.

71. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is A10m3 or a fragment thereof.

72. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is DOM7r-31.

73. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is DOM7h-11-15.

74. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is Alb-1, Alb-8, or Alb-23.

75. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is 10G or 10GE.

76. The isolated polypeptide or polypeptide complex of claim 65, wherein the single domain antibody is SA21.

77. The isolated polypeptide or polypeptide complex of claim 1, wherein the polypeptide or polypeptide complex comprises a modified amino acid, a non-natural amino acid, a modified non-natural amino acid, or a combination thereof.

78. The isolated polypeptide or polypeptide complex of claim 77, wherein the modified amino acid or modified non-natural amino acid comprises a post-translational modification.

79. The isolated polypeptide or polypeptide complex of claim 51, wherein H_1 comprises a linking moiety (L_3) that connects H_1 to P_1.

80. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 is a peptide sequence having at least 5 to no more than 50 amino acids.

81. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 is a peptide sequence having at least 10 to no more than 30 amino acids.

82. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 is a peptide sequence having at least 10 amino acids.

83. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 is a peptide sequence having at least 18 amino acids.

84. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 is a peptide sequence having at least 26 amino acids.

85. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

86. The isolated polypeptide or polypeptide complex of claim 79, wherein L_3 comprises an amino acid sequence according to (GGGGSGGGS (SEQ ID NO: 921)).

87. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab light chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) of A_1.

88. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab heavy chain polypeptide of A_2 is bound to a C-terminus of the single chain variable fragment (scFv) A_1.

89. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab light chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) of A_1.

90. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab heavy chain polypeptide of A_2 is bound to a N-terminus of the single chain variable fragment (scFv) A_1.

91. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1.

92. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1.

93. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1.

94. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1.

95. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2.

96. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab light chain polypeptide of A_2 is bound to the scFv heavy chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2.

97. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab heavy chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab light chain polypeptide of A_2.

98. The isolated polypeptide or polypeptide complex of claim 48, wherein the Fab light chain polypeptide of A_2 is bound to the scFv light chain polypeptide of A_1 and L_2 is bound to the Fab heavy chain polypeptide of A_2.

99. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 impairs binding of A_2 to the tumor antigen.

100. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 is bound to A_2 through ionic interactions, electrostatic interactions, hydrophobic interactions, Pi-stacking interactions, or H-bonding interactions, or a combination thereof.

101. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 is bound to A_2 at or near an antigen binding site.

102. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 has less than 70% sequence homology to the tumor antigen.

103. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a peptide sequence of at least 10 amino acids in length.

104. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a peptide sequence of at least 10 amino acids in length and no more than 20 amino acids in length.

105. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a peptide sequence of at least 16 amino acids in length.

106. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a peptide sequence of no more than 40 amino acids in length.

107. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises at least two cysteine amino acid residues.

108. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a cyclic peptide or a linear peptide.

109. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a cyclic peptide.

110. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 comprises a linear peptide.

111. The isolated polypeptide or polypeptide complex of claim 16, wherein L_1 is bound to a N-terminus of A_1.

112. The isolated polypeptide or polypeptide complex of claim 16, wherein L_1 is bound to a C-terminus of A_1.

113. The isolated polypeptide or polypeptide complex of claim 21, wherein L_2 is bound to a N-terminus of A_2.

114. The isolated polypeptide or polypeptide complex of claim 21, wherein L_2 is bound to a C-terminus of A_2.

115. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 is a peptide sequence having at least 5 to no more than 50 amino acids.

116. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 is a peptide sequence having at least 10 to no more than 30 amino acids.

117. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 is a peptide sequence having at least 10 amino acids.

118. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 is a peptide sequence having at least 18 amino acids.

119. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 is a peptide sequence having at least 26 amino acids.

120. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 has a formula comprising $(G_2S)_n$ (SEQ ID NO: 922), wherein n is an integer from 1 to 3.

121. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 has a formula selected from the group consisting of $(G_2S)_n$, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO: 917), $(GGGS)_n$ (SEQ ID NO: 918), $(GGGGS)_n$ (SEQ ID NO: 919), and $(GSSGGS)_n$ (SEQ ID NO: 920), wherein n is an integer of at least 1.

122. The isolated polypeptide or polypeptide complex of claim 21, wherein P_1 becomes unbound from A_1 when L_1 is cleaved by the tumor specific protease thereby exposing A_1 to CD3.

123. The isolated polypeptide or polypeptide complex of claim 21, wherein P_2 becomes unbound from A_2 when L_2 is cleaved by the tumor specific protease thereby exposing A_2 to the tumor antigen.

124. The isolated polypeptide or polypeptide complex of claim 21, wherein the tumor specific protease is selected from the group consisting of metalloprotease, serine protease, cysteine protease, threonine protease, and aspartic protease.

125. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 comprises a urokinase cleavable amino acid sequence, a matriptase cleavable amino acid sequence, a matrix metalloprotease cleavable amino acid sequence, or a legumain cleavable amino acid sequence.

126. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 comprises an amino acid sequence selected from the group consisting of GGGGSLSGRSDNHGSSGT (SEQ ID NO: 923), GGGGSSGGSGGSGLSGRSDNHGSSGT (SEQ ID NO: 924), ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), ISSGLLAGRSDNH (SEQ ID NO: 928), LSGRSDNH (SEQ ID NO: 929), ISSGLLSGRSDNP (SEQ ID NO: 930), ISSGLLSGRSDNH (SEQ ID NO: 931), LSGRSDNHSPLGLAGS (SEQ ID NO: 932), SPLGLAGSLSGRSDNH (SEQ ID NO: 933), SPLGLSGRSDNH (SEQ ID NO: 934), LAGRSDNHSPLGLAGS (SEQ ID NO: 935), LSGRSDNHVPLSLKMG (SEQ ID NO: 936), and LSGRSDNHVPLSLSMG (SEQ ID NO: 937).

127. The isolated polypeptide or polypeptide complex of claim 21, wherein L_1 or L_2 comprises an amino acid sequence selected from the group consisting of ASGRSDNH (SEQ ID NO: 925), LAGRSDNH (SEQ ID NO: 926), ISSGLASGRSDNH (SEQ ID NO: 927), and ISSGLLAGRSDNH (SEQ ID NO: 928).

128. A pharmaceutical composition comprising: (i) the polypeptide or polypeptide complex of claim 1; and (ii) a pharmaceutically acceptable excipient.

129. An isolated recombinant nucleic acid molecule encoding the polypeptide or polypeptide complex of claim 1.

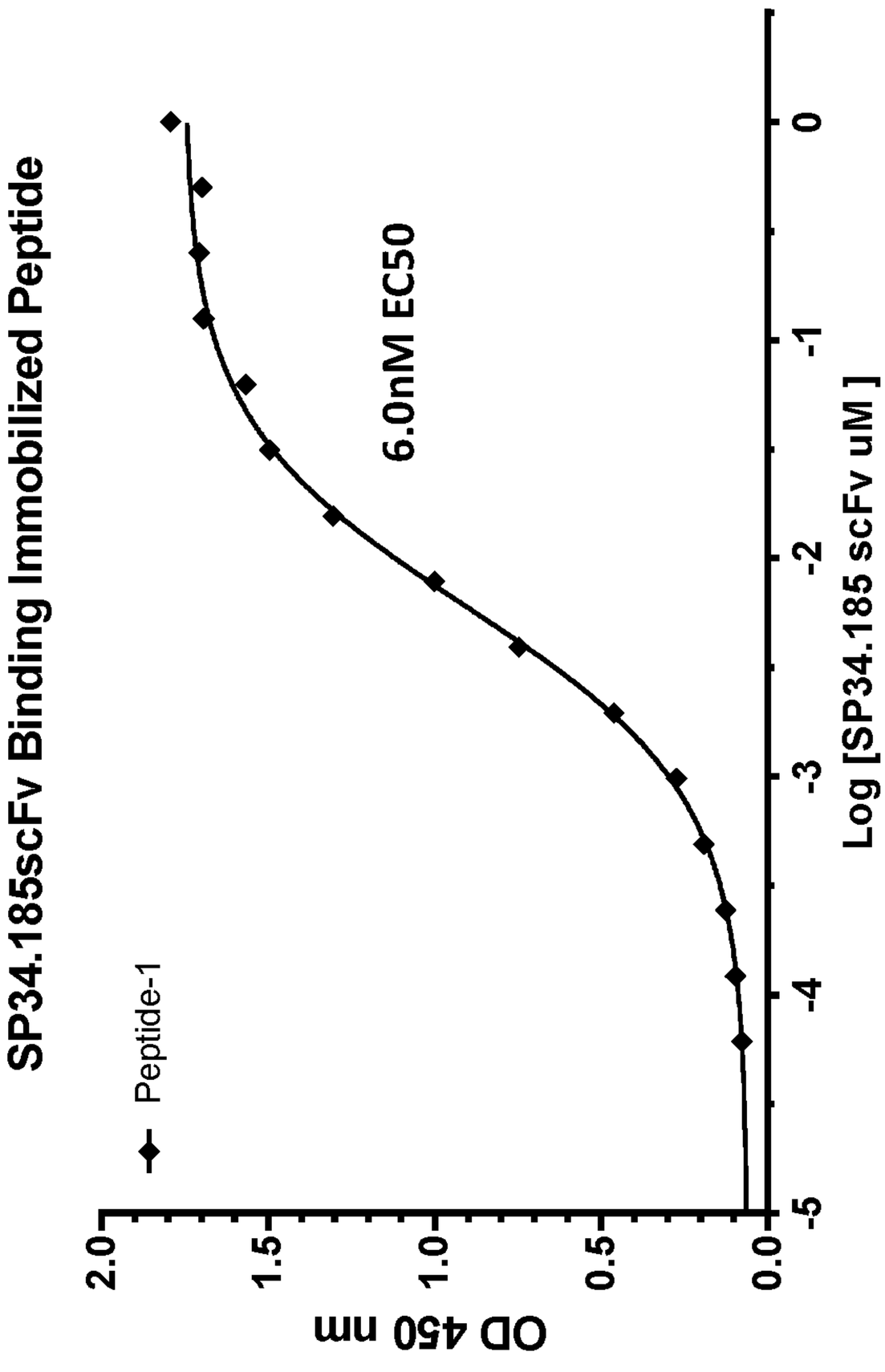

SP34.185scFv Binding Immobilized Peptide
Peptide-1
6.0nM EC50
OD 450 nm
2.0
1.5
1.0
0.5
0.0
-5
-4
-3
-2
-1
0
Log [SP34.185 scFv uM]

FIG. 1A

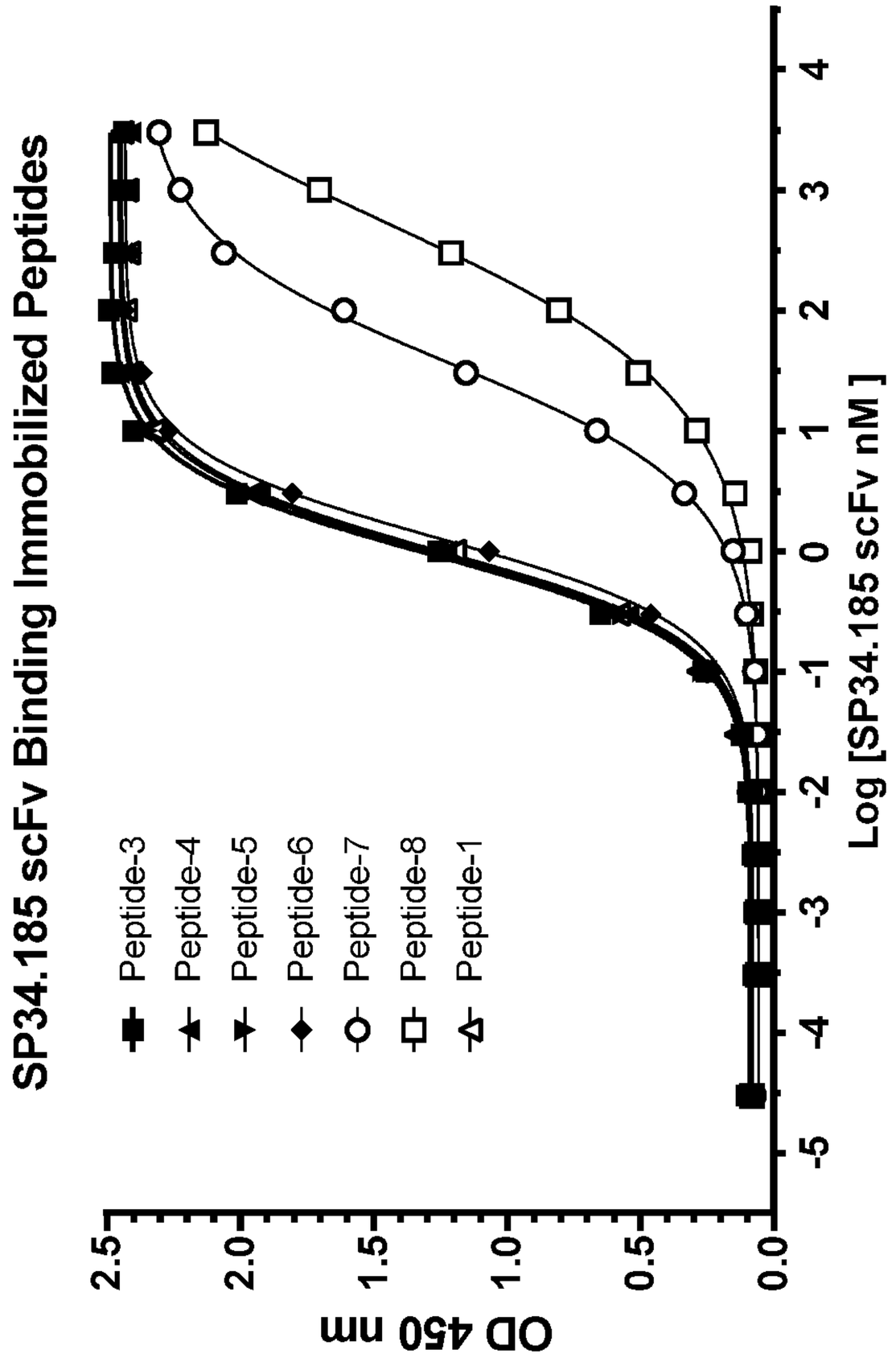

SP34.185 scFv Binding Immobilized Peptides
Peptide-3
Peptide-4
Peptide-5
Peptide-6
Peptide-7
Peptide-8
Peptide-1
OD 450 nm
2.5
2.0
1.5
1.0
0.5
0.0
-5
-4
-3
-2
-1
0
1
2
3
4
Log [SP34.185 scFv nM]

FIG. 1B

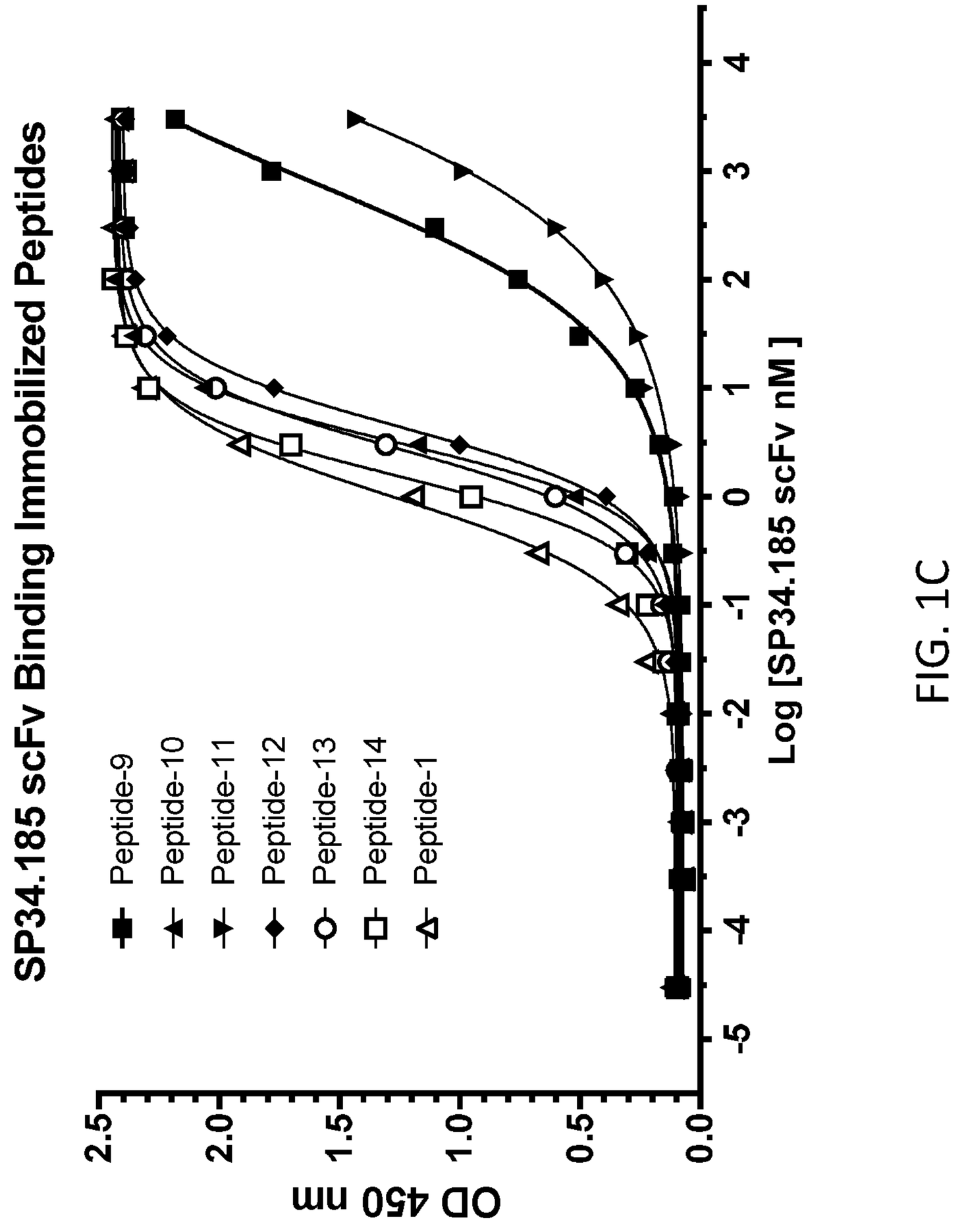

SP34.185 scFv Binding Immobilized Peptides
Peptide-9
Peptide-10
Peptide-11
Peptide-12
Peptide-13
Peptide-14
Peptide-1
OD 450 nm
2.5
2.0
1.5
1.0
0.5
0.0
-5
-4
-3
-2
-1
0
1
2
3
4
Log [SP34.185 scFv nM]

FIG. 1C

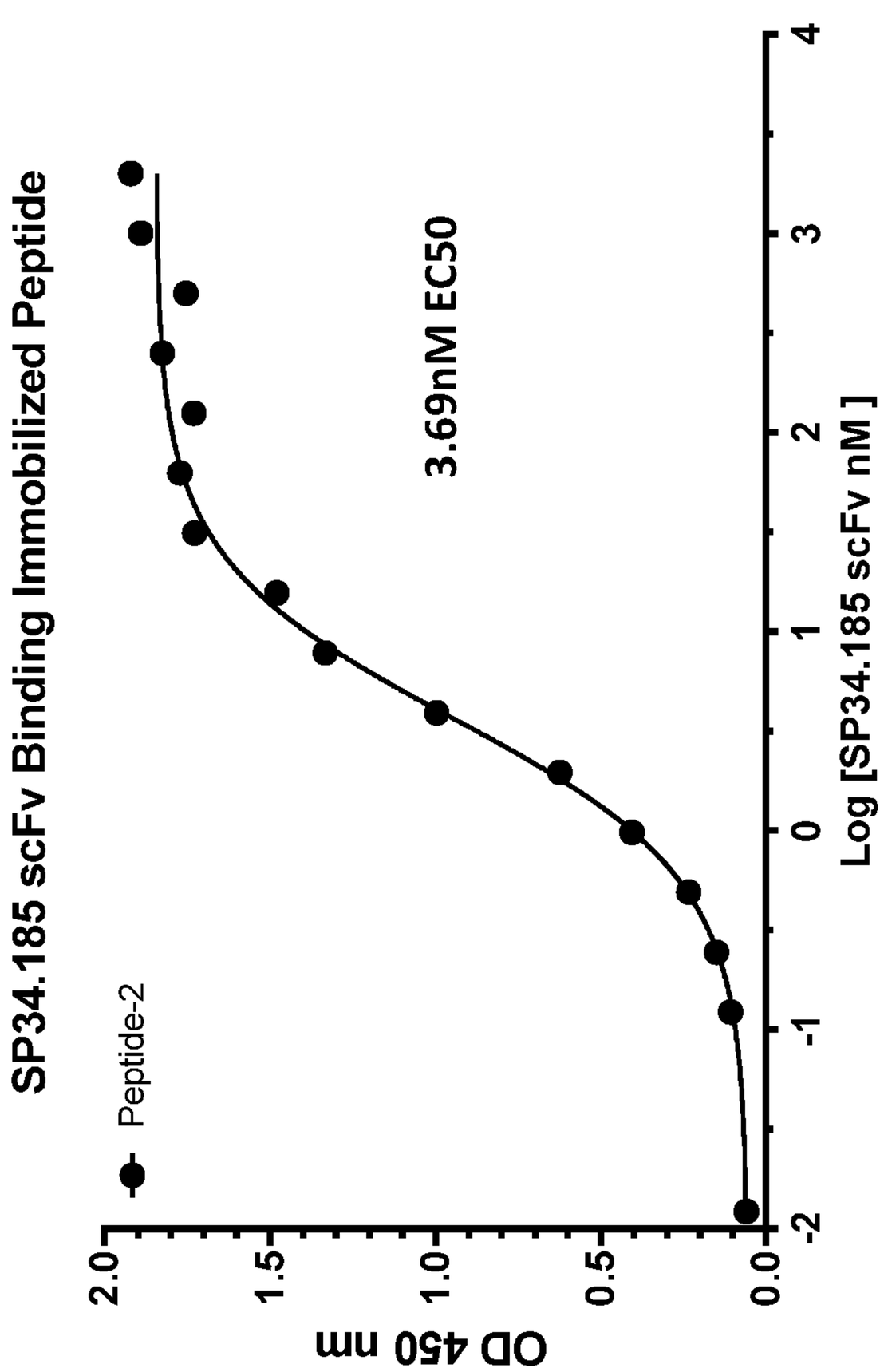

SP34.185 scFv Binding Immobilized Peptide
3.69nM EC50
Peptide-2
OD 450 nm
2.0
1.5
1.0
0.5
0.0
-2
-1
0
1
2
3
4
Log [SP34.185 scFv nM]

FIG. 1D

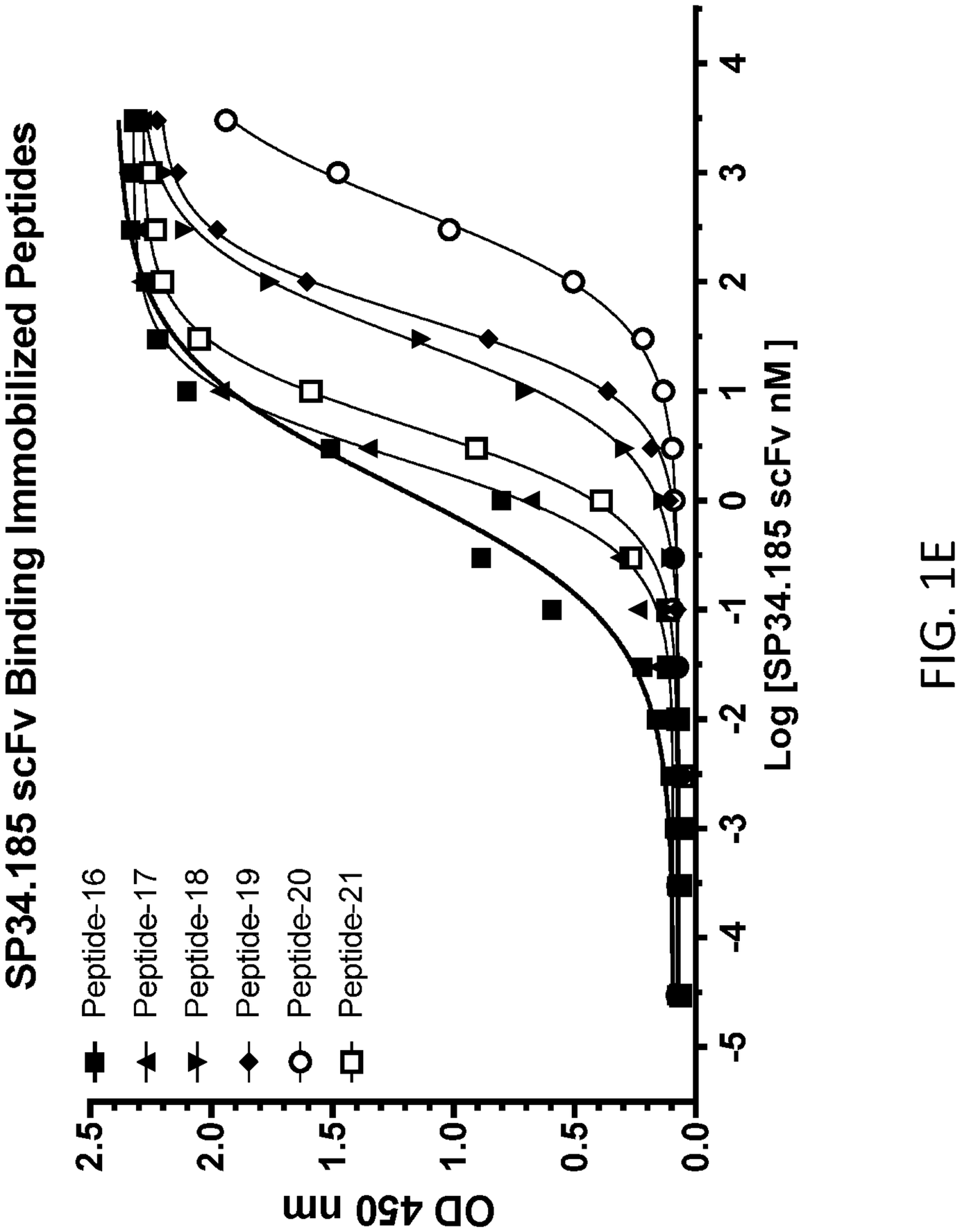

SP34.185 scFv Binding Immobilized Peptides
Peptide-16
Peptide-17
Peptide-18
Peptide-19
Peptide-20
Peptide-21
OD 450 nm
Log [SP34.185 scFv nM]

FIG. 1E

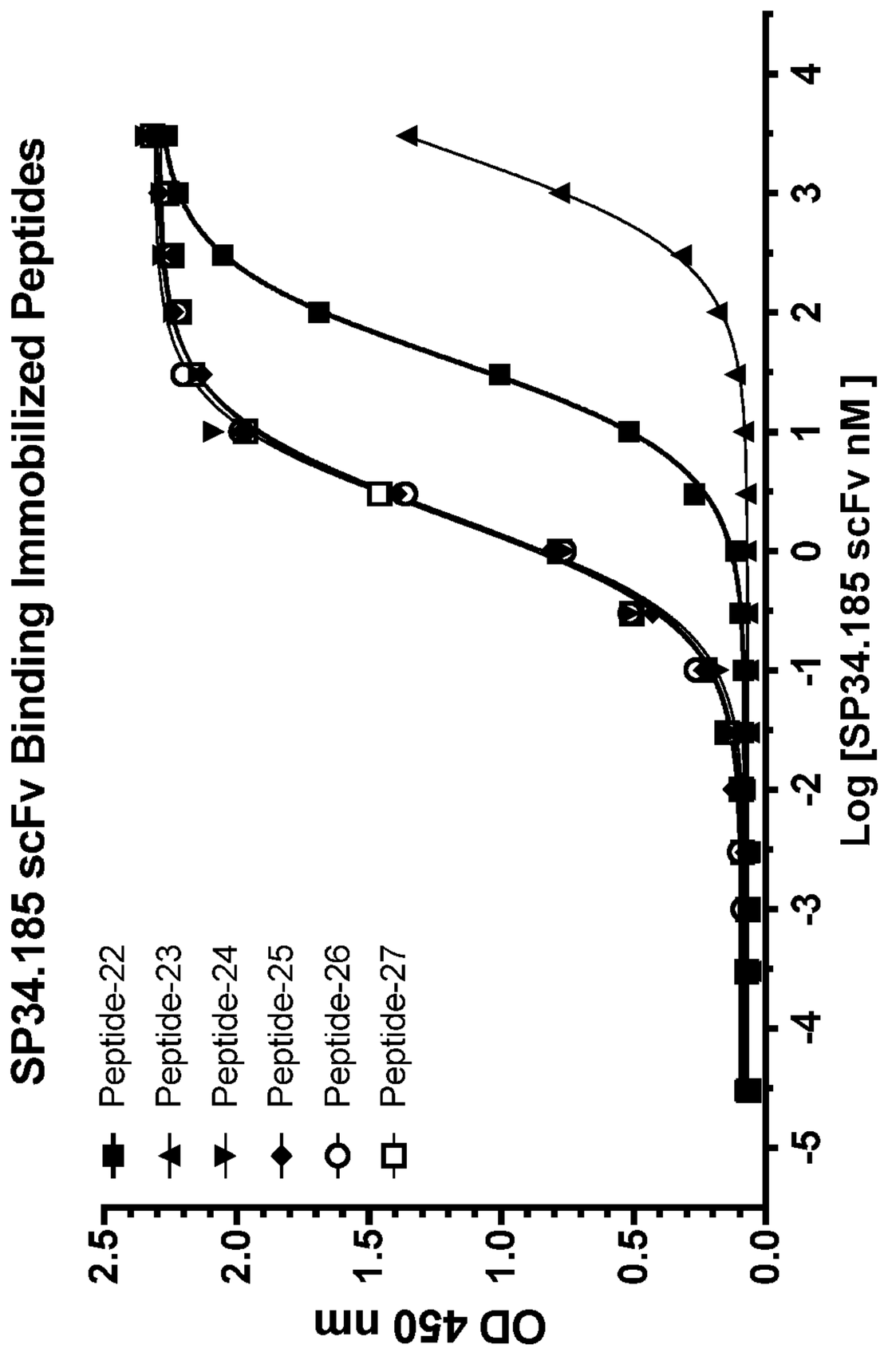

SP34.185 scFv Binding Immobilized Peptides
OD 450 nm
Log [SP34.185 scFv nM]
Peptide-22
Peptide-23
Peptide-24
Peptide-25
Peptide-26
Peptide-27
2.5
2.0
1.5
1.0
0.5
0.0
-5
-4
-3
-2
-1
0
1
2
3
4

FIG. 1F

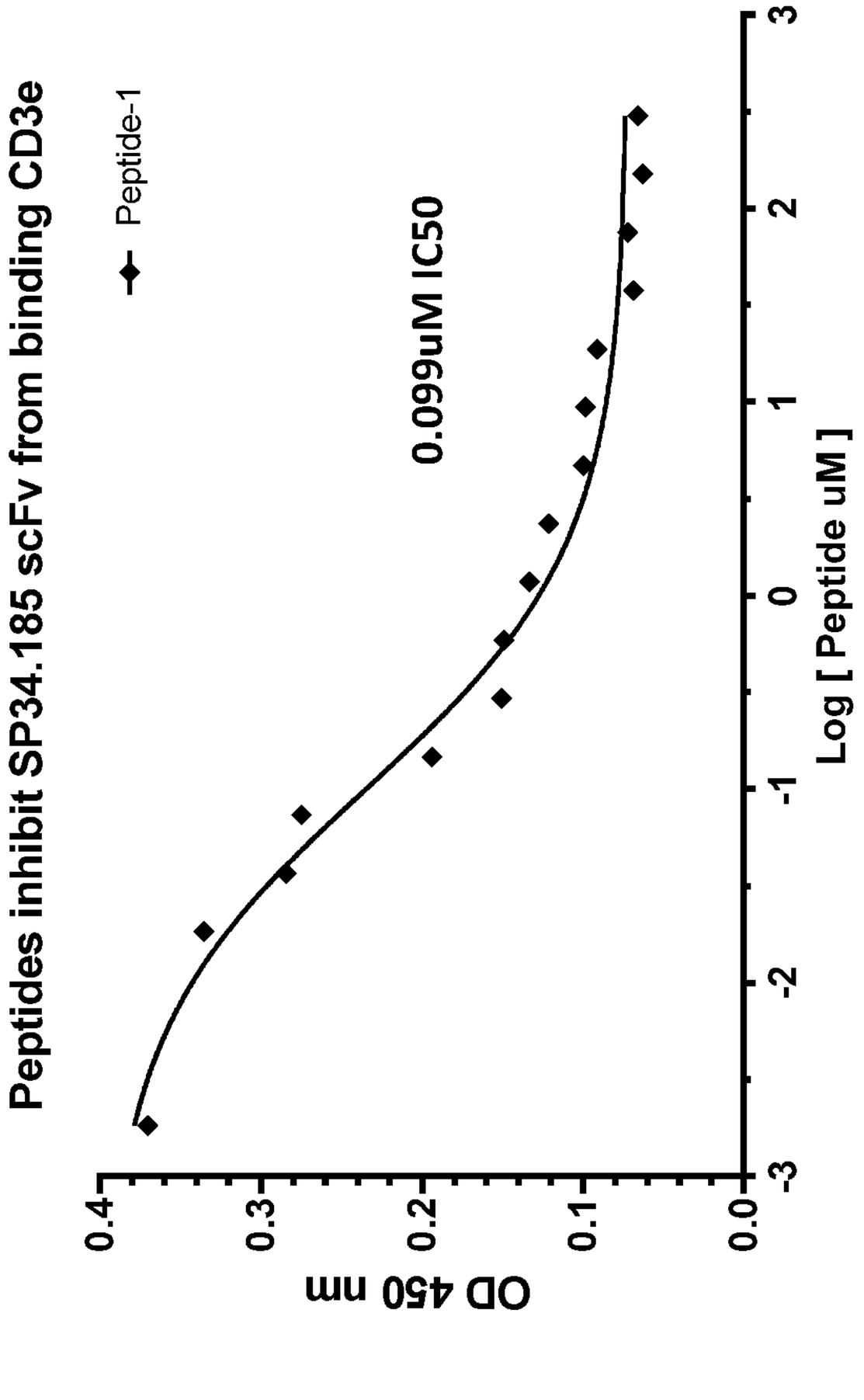

Peptides inhibit SP34.185 scFv from binding CD3e
Peptide-1
0.099uM IC50
OD 450 nm
0.0
0.1
0.2
0.3
0.4
-3
-2
-1
0
1
2
3
Log [Peptide uM]

FIG. 2A

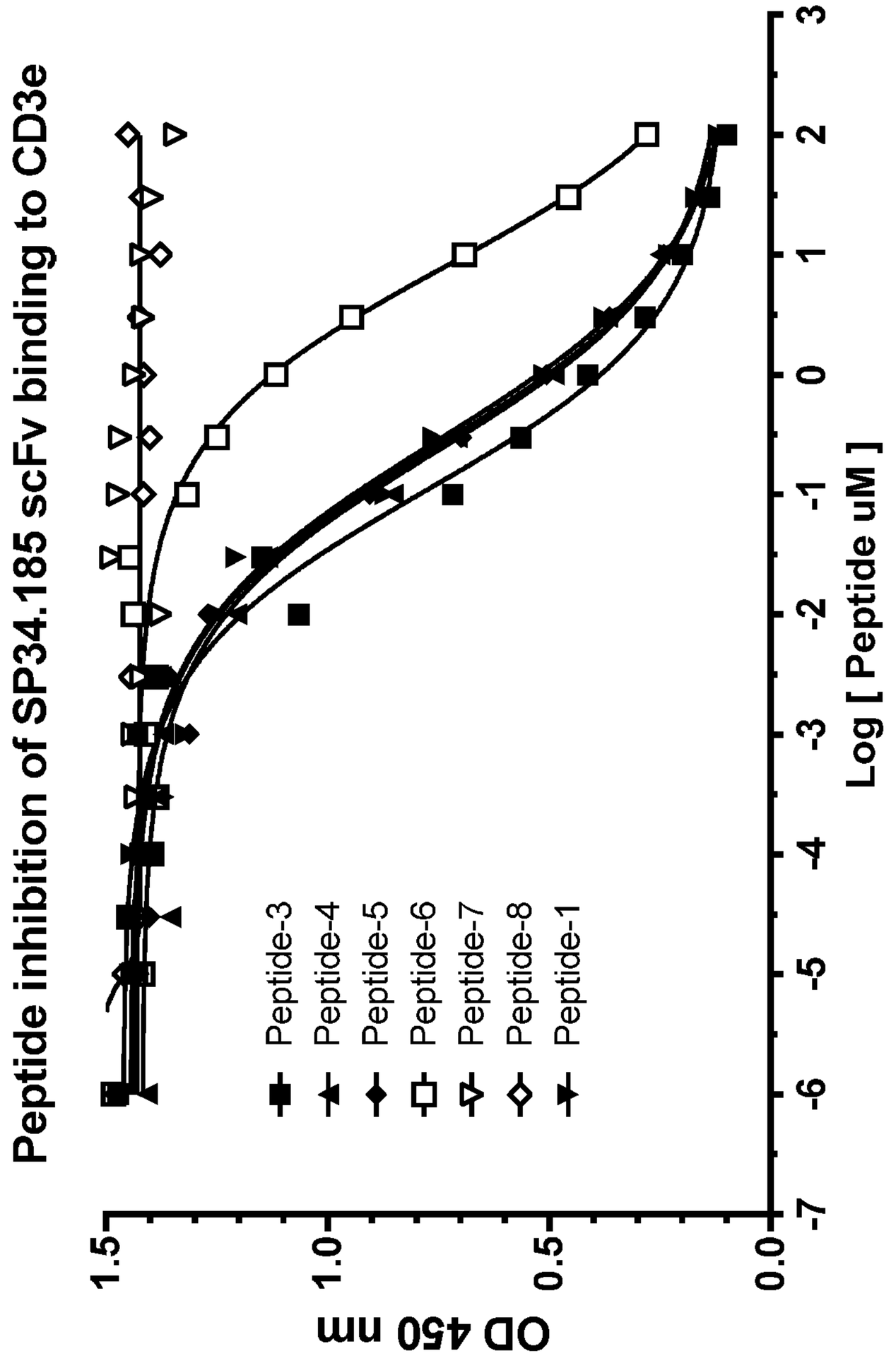

Peptide inhibition of SP34.185 scFv binding to CD3e
OD 450 nm
1.5
1.0
0.5
0.0
-7
-6
-5
-4
-3
-2
-1
0
1
2
3
Log [Peptide uM]
Peptide-3
Peptide-4
Peptide-5
Peptide-6
Peptide-7
Peptide-8
Peptide-1

FIG. 2B

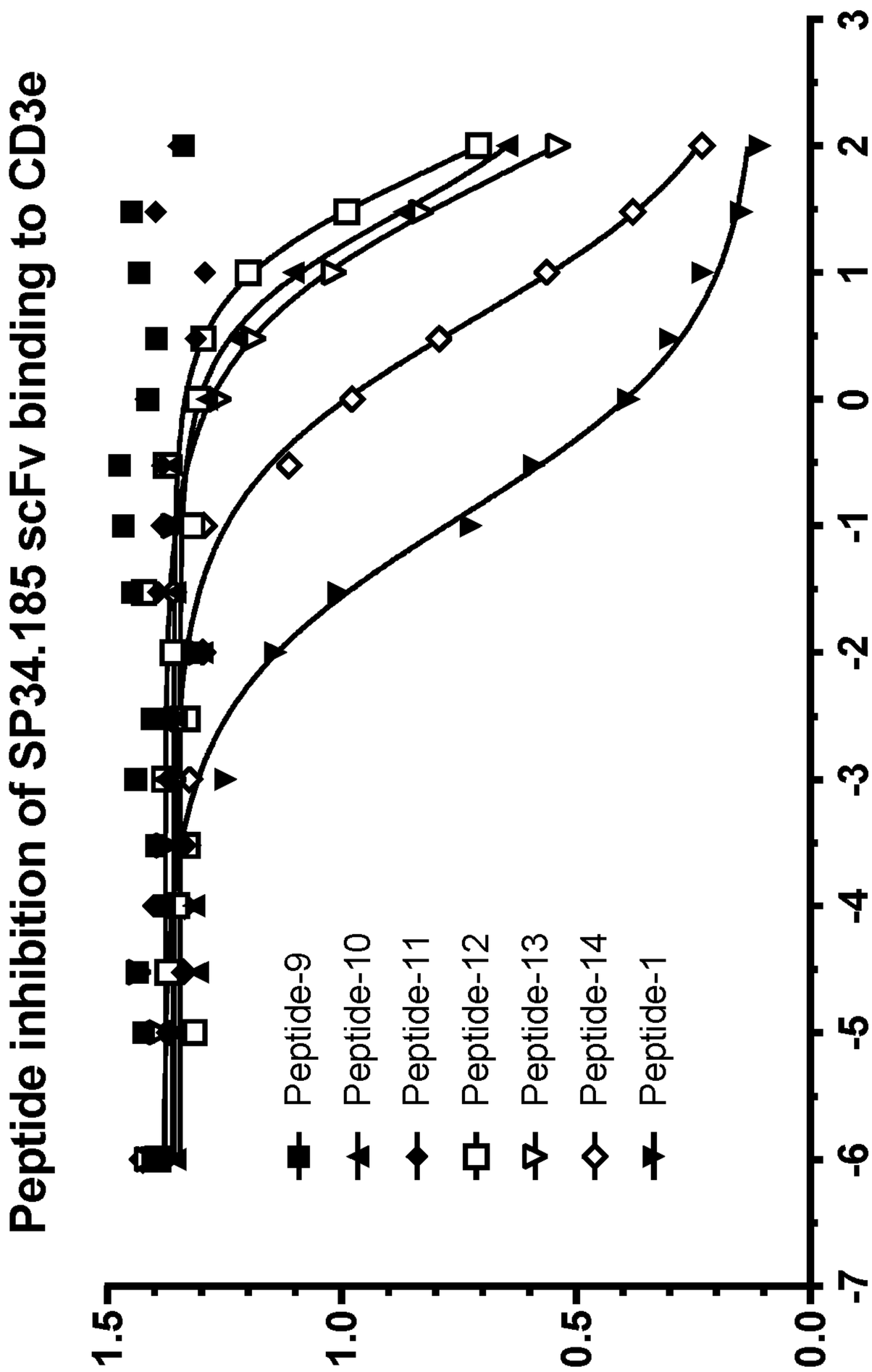

Peptide inhibition of SP34.185 scFv binding to CD3e
OD 450 nm
1.5
1.0
0.5
0.0
-7
-6
-5
-4
-3
-2
-1
0
1
2
3
Log [Peptide uM]
Peptide-9
Peptide-10
Peptide-11
Peptide-12
Peptide-13
Peptide-14
Peptide-1

FIG. 2C

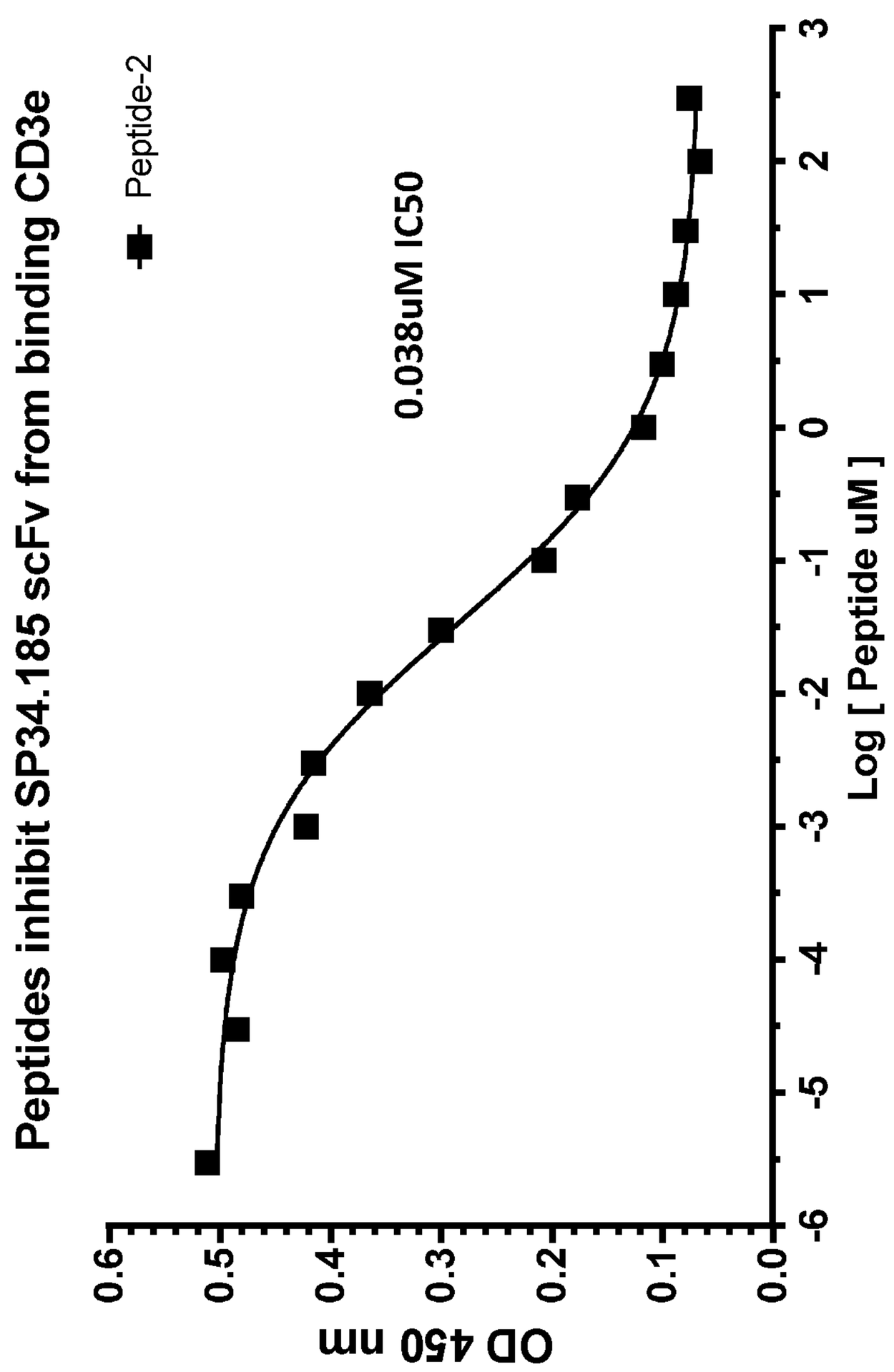

Peptides inhibit SP34.185 scFv from binding CD3e
Peptide-2
0.038uM IC50
OD 450 nm
0.6
0.5
0.4
0.3
0.2
0.1
0.0
-6
-5
-4
-3
-2
-1
0
1
2
3
Log [Peptide uM]

FIG. 2D

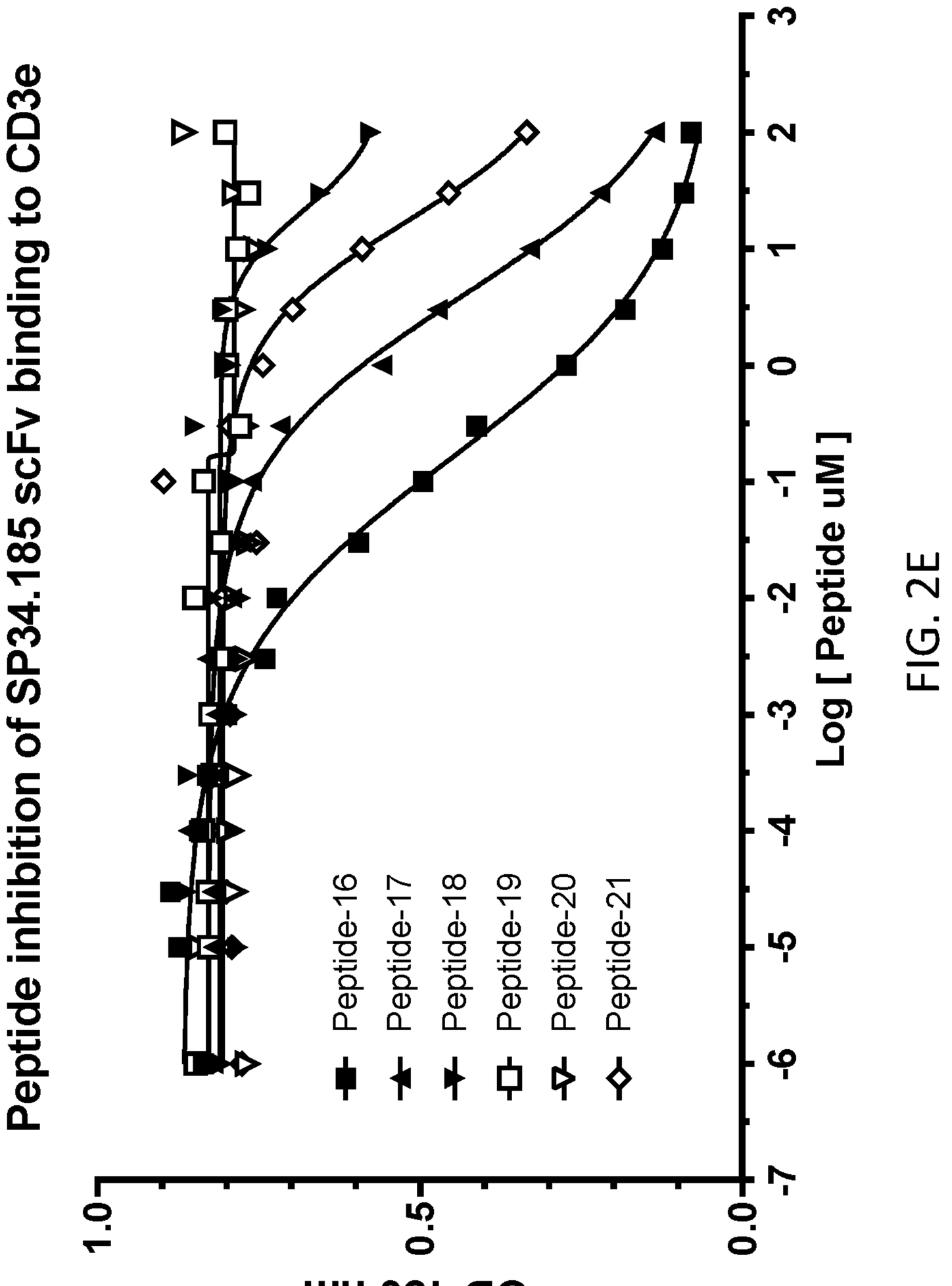

Peptide inhibition of SP34.185 scFv binding to CD3e
OD 450 nm
Log [Peptide uM]
Peptide-16
Peptide-17
Peptide-18
Peptide-19
Peptide-20
Peptide-21

FIG. 2E

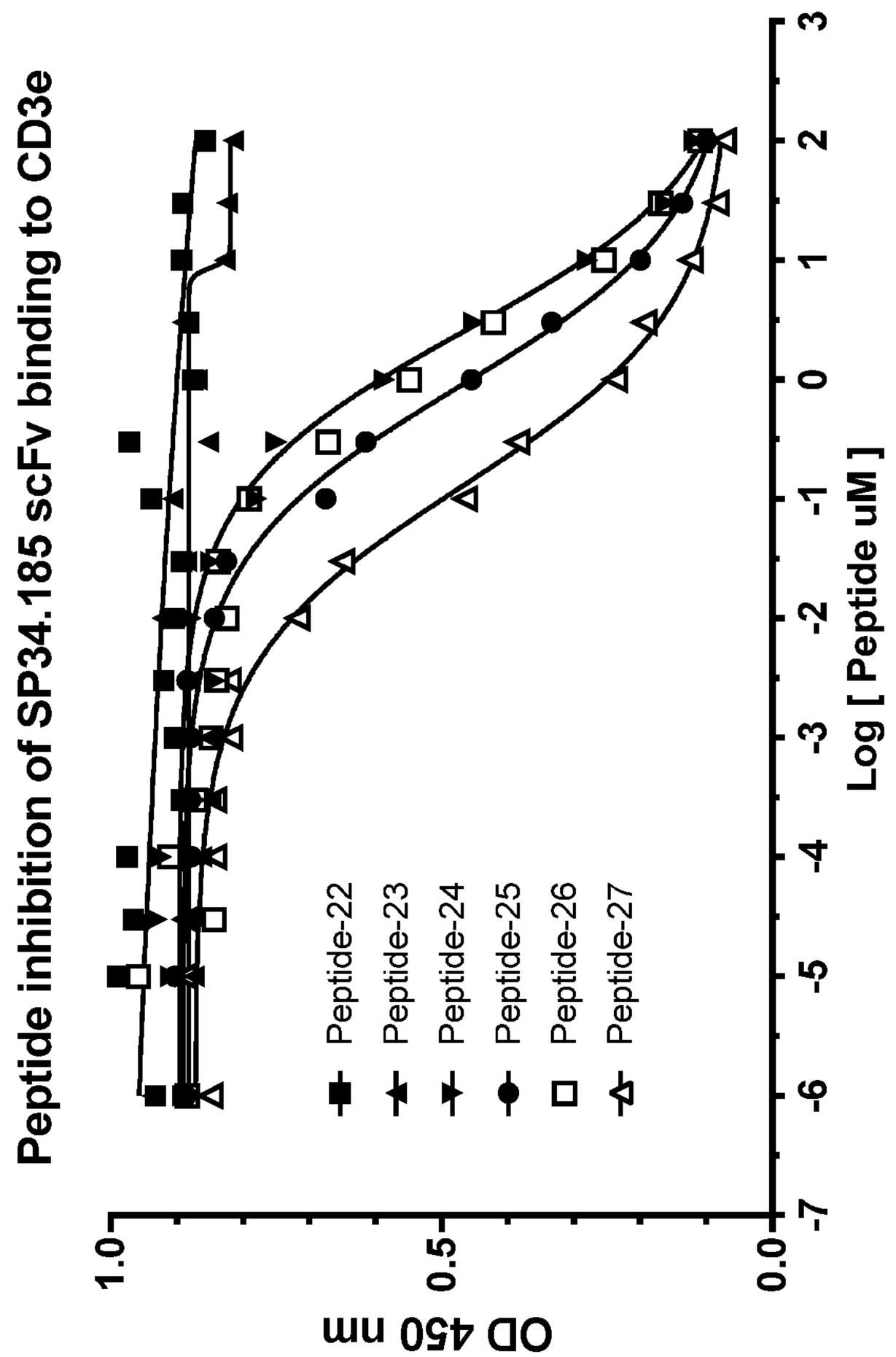

Peptide inhibition of SP34.185 scFv binding to CD3e
OD 450 nm
1.0
0.5
0.0
-7
-6
-5
-4
-3
-2
-1
0
1
2
3
Log [Peptide uM]
Peptide-22
Peptide-23
Peptide-24
Peptide-25
Peptide-26
Peptide-27

FIG. 2F

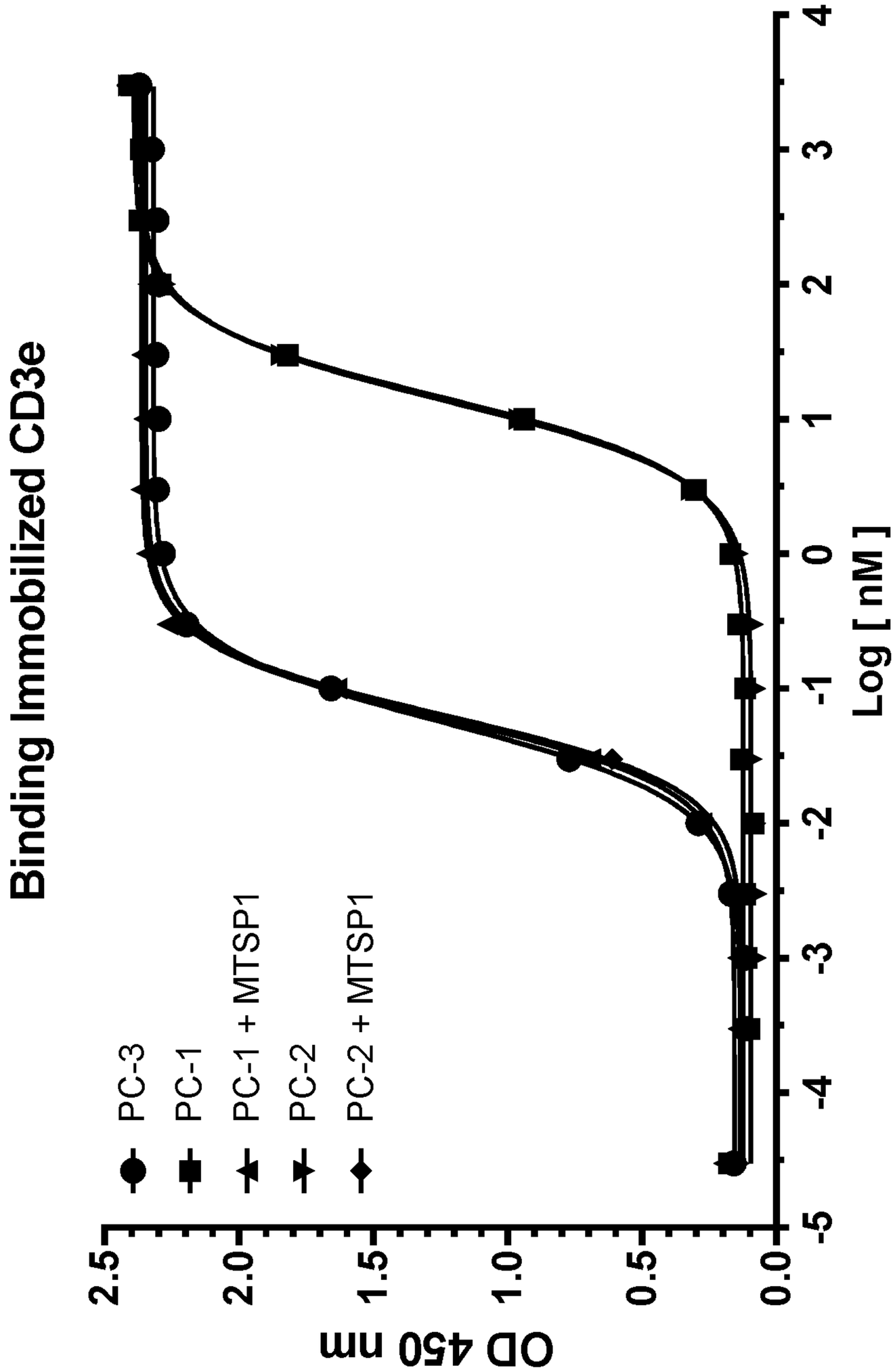

Binding Immobilized CD3e
PC-3
PC-1
PC-1 + MTSP1
PC-2
PC-2 + MTSP1
OD 450 nm
Log [nM]
2.5
2.0
1.5
1.0
0.5
0.0
4
3
2
1
0
-1
-2
-3
-4
-5

FIG. 3

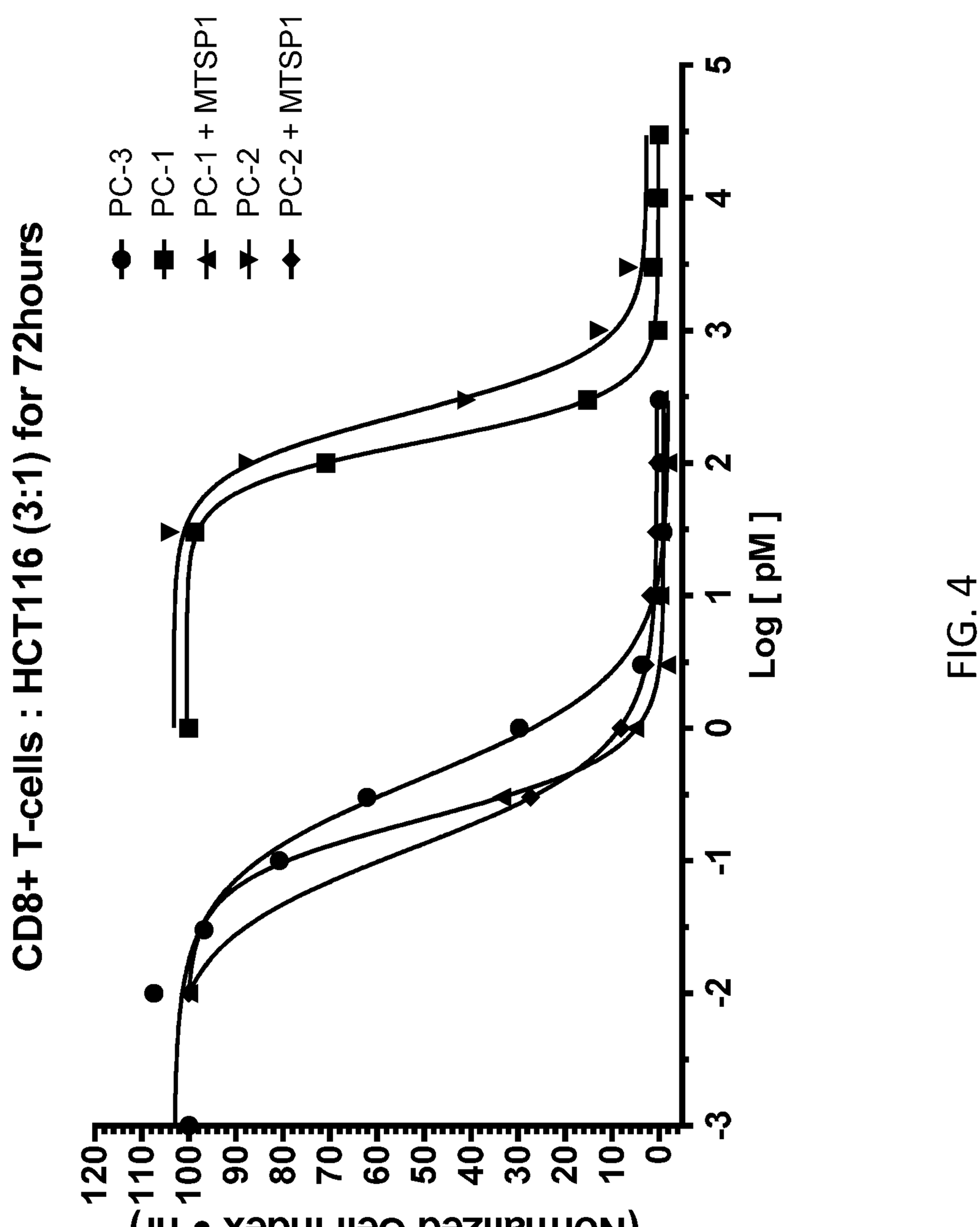

CD8+ T-cells : HCT116 (3:1) for 72hours
PC-3
PC-1
PC-1 + MTS
PC-2
PC-2 + MTS
Log [pM]
-3
-2
-1
0
1
2
3
4
5
Tumor cell viability
(Normalized Cell index • hr)
1
2
3
4
5
6
7
8
9
10
11
12

FIG. 4

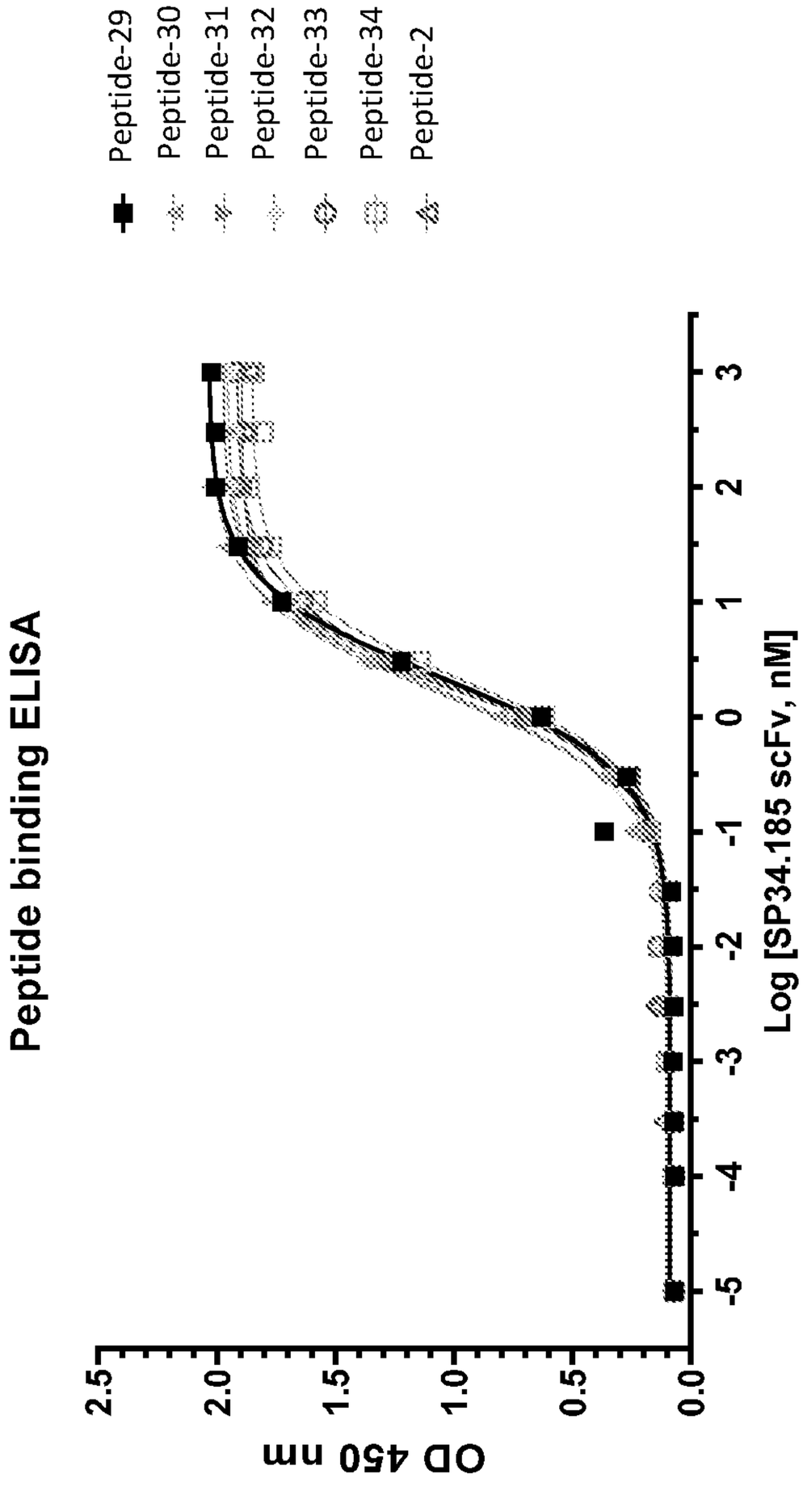

Peptide binding ELISA
OD 450 nm
2.5
2.0
1.5
1.0
0.5
0.0
-5
-4
-3
-2
-1
0
1
2
3
Log [SP34.185 scFv, nM]
Peptide-29
Peptide-30
Peptide-31
Peptide-32
Peptide-33
Peptide-34
Peptide-2

FIG. 5A

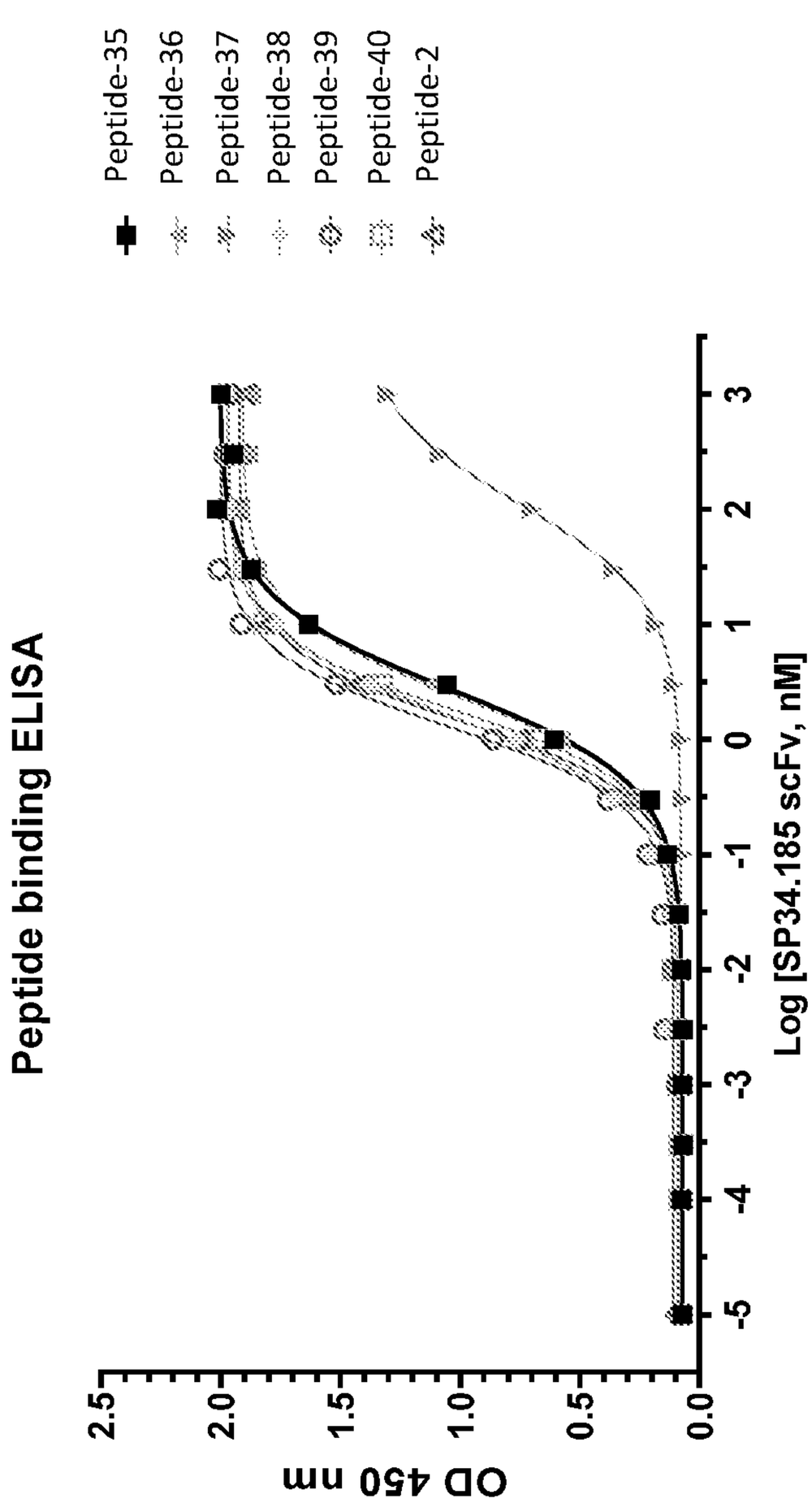

Peptide binding ELISA
OD 450 nm
Log [SP34.185 scFv, nM]
-5
-4
-3
-2
-1
0
1
2
3
0.0
0.5
1.0
1.5
2.0
2.5
Peptide-35
Peptide-36
Peptide-37
Peptide-38
Peptide-39
Peptide-40
Peptide-2

FIG. 5B

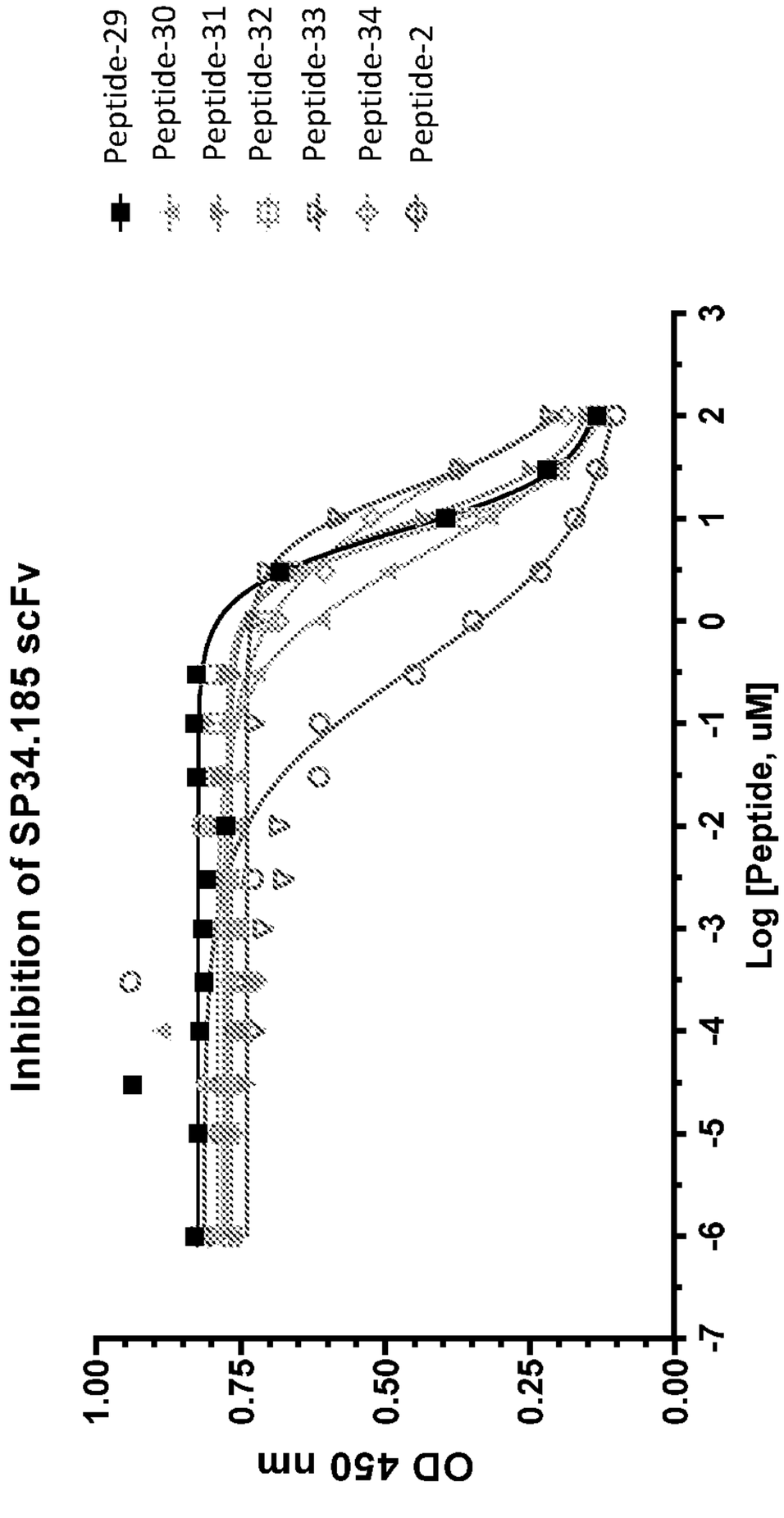

Inhibition of SP34.185 scFv
OD 450 nm
1.00
0.75
0.50
0.25
0.00
-7
-6
-5
-4
-3
-2
-1
0
1
2
3
Log [Peptide, uM]
Peptide-29
Peptide-30
Peptide-31
Peptide-32
Peptide-33
Peptide-34
Peptide-2

FIG. 6A

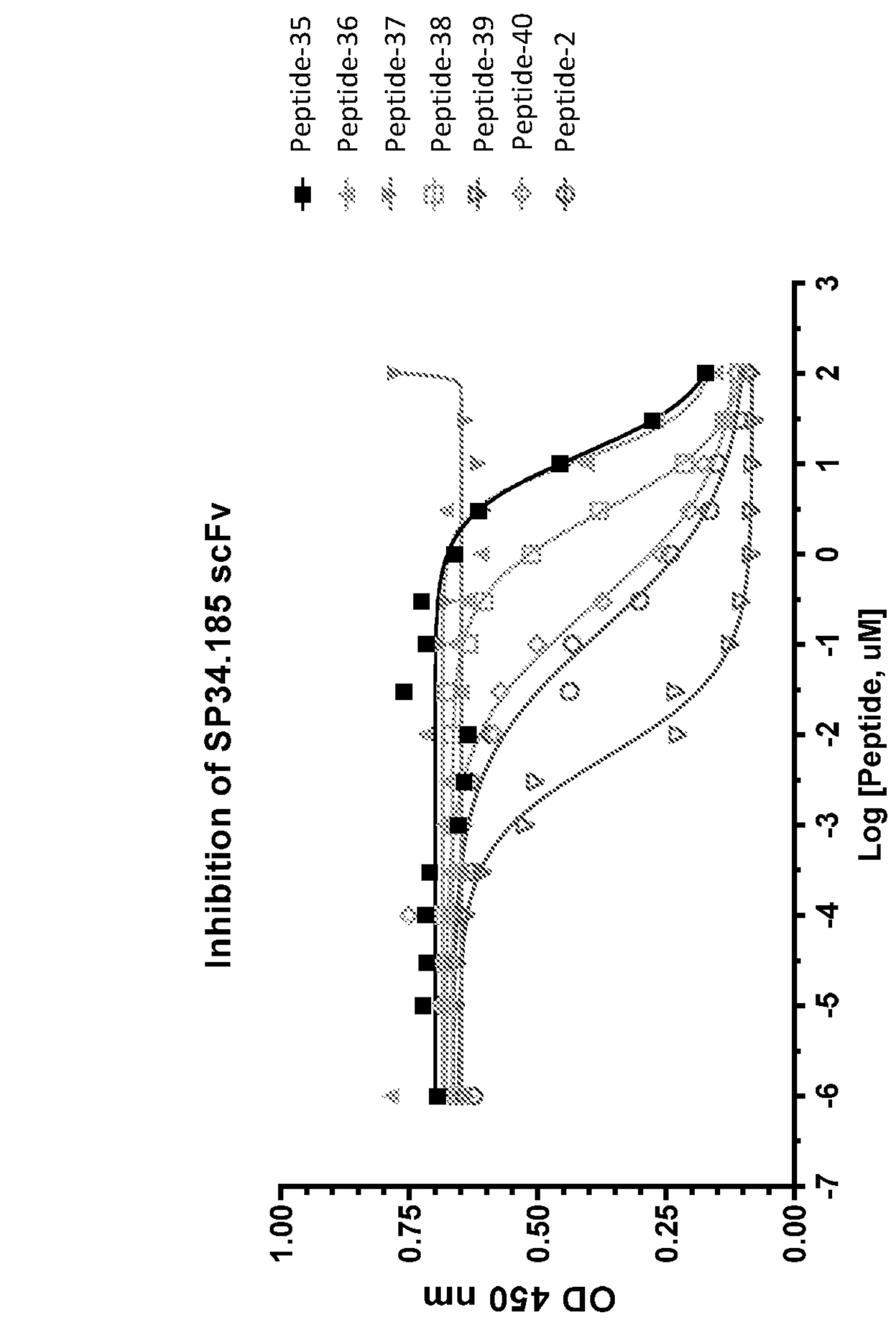

Inhibition of SP34.185 scFv
OD 450 nm
1.00
0.75
0.50
0.25
0.00
Log [Peptide, uM]
3
2
1
0
-1
-2
-3
-4
-5
-6
-7
Peptide-35
Peptide-36
Peptide-37
Peptide-38
Peptide-39
Peptide-40
Peptide-2

FIG. 6B

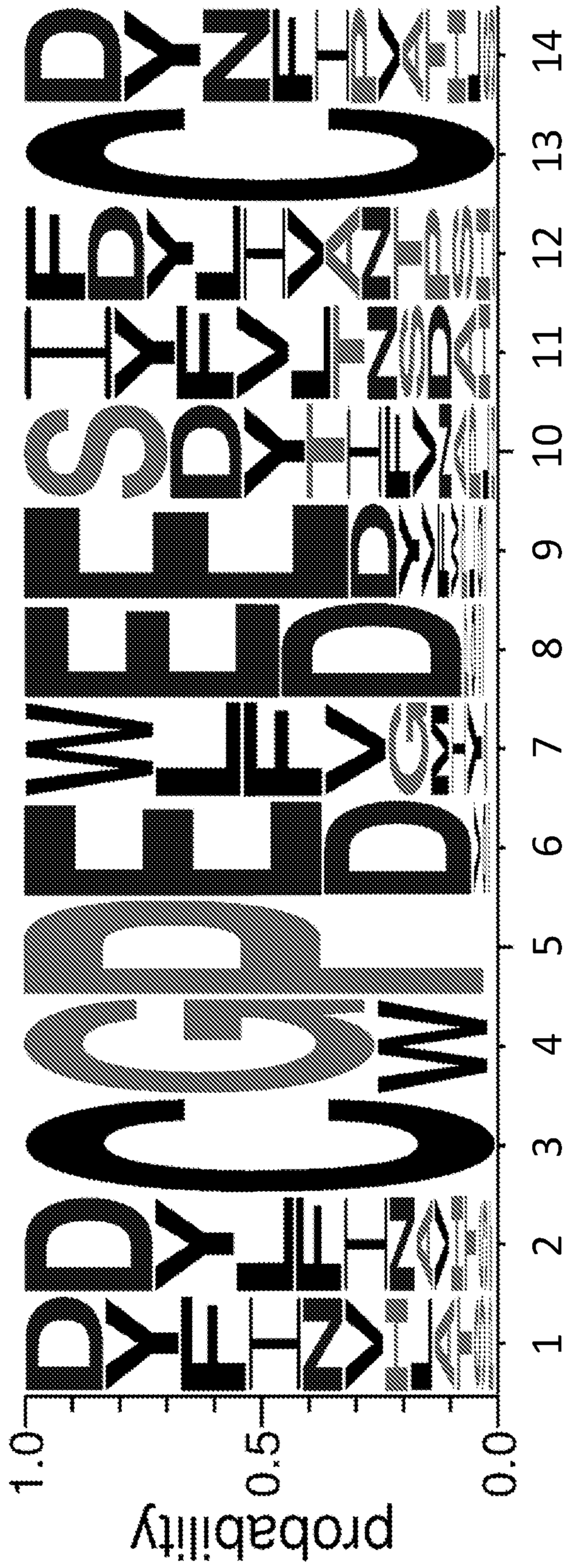


FIG. 7

SEQUENCE LISTING

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<120> PEPTIDE COMPOSITIONS AND METHODS FOR ANTI-CD3 BINDING DOMAINS

<130> 52426-732.601

<140>
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<150> 63/122,820
<151> 2020-12-08

<160> 943

<170> PatentIn version 3.5

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<220>
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peptide

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Gly Ser Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Tyr
1 5 10

<210> 2
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<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2
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1 5 10

<210> 3
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 3
Gly Phe Thr Phe Asn Lys Tyr Ala
1 5

<210> 4
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 4
Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr
1 5 10

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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peptide

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1 5 10 15

<210> 6
<211> 9
<212> PRT
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<220>
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peptide

<400> 6
Thr Gly Ala Val Thr Ser Gly Asn Tyr
1 5

<210> 7
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 7
Gly Thr Lys
1

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 8
Val Leu Trp Tyr Ser Asn Arg Trp Val
1 5

<210> 9
<211> 249
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 9
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
    50                  55                  60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65                  70                  75                  80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
            100                 105                 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
    130                 135                 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
145                 150                 155                 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
                165                 170                 175

Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
            180                 185                 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
        195                 200                 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
    210                 215                 220

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
225                 230                 235                 240
```

Gly Gly Gly Thr Lys Leu Thr Val Leu
245

<210> 10
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
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<400> 10
Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

```
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160


Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175


Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190


Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205


Phe Asn Arg Gly Glu Cys
    210


<210> 11
<211> 222
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 11
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
1               5                   10                  15


Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr
    50                  55                  60


Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe
65                  70                  75                  80
```

```
Lys Met Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala
                85                  90                  95


Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125


Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
    130                 135                 140


Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160


Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175


Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190


Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205


Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
    210                 215                 220


<210> 12
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 12
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1               5                   10                  15
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
            20   25   30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
            100   105   110

Val Ser Ser
        115

<210> 13
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 13
Gln Gly Gln Ser Gly Gln Leu Ser Cys Glu Gly Trp Ala Met Asn Arg
1   5   10   15

Glu Gln Cys Arg Ala Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
            20   25   30

Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly
        35   40   45

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Ser Ser Gly Thr Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser
    50                  55                  60

Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser
65                  70                  75                  80

Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro
                85                  90                  95

Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser
            100                 105                 110

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
        115                 120                 125

Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn
    130                 135                 140

Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
145                 150                 155                 160

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                165                 170                 175

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            180                 185                 190

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        195                 200                 205

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    210                 215                 220

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
225                 230                 235                 240

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                245                 250                 255
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Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
260 265

<210> 14
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
115 120 125

Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Tyr Gly Gly Gly Gly
130 135 140

```
Ser Gly Gly Gly Ser Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg
145                 150                 155                 160

Ser Asp Asn His Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
                165                 170                 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
            180                 185                 190

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
        195                 200                 205

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
    210                 215                 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225                 230                 235                 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
                245                 250                 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
            260                 265                 270

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
        275                 280                 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
305                 310                 315                 320

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
                325                 330                 335
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```
Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
            340                 345                 350

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
        355                 360                 365

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
    370                 375                 380

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
385                 390                 395                 400

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
                405                 410                 415

Leu Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly
            420                 425                 430

Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
        435                 440                 445

Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
    450                 455                 460

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp
465                 470                 475                 480

Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser
                485                 490                 495

Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr
            500                 505                 510

Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe
        515                 520                 525

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
    530                 535                 540
```

```
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
545                 550                 555                 560


Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                565                 570                 575


Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            580                 585                 590


Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        595                 600                 605


Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    610                 615                 620


Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
625                 630                 635                 640


Pro Lys Ser Cys
```

<210> 15
<211> 266
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 15

```
Gln Gly Gln Ser Gly Gln Leu Ser Cys Glu Gly Trp Ala Met Asn Arg
1               5                   10                  15


Glu Gln Cys Arg Ala Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Gly
            20                  25                  30


Ser Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His Gly
        35                  40                  45
```

```
Ser Ser Gly Thr Asp Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser
    50                  55                  60

Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser
65                  70                  75                  80

Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro
                85                  90                  95

Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser
            100                 105                 110

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
        115                 120                 125

Ser Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn
    130                 135                 140

Asn Trp Pro Thr Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
145                 150                 155                 160

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
                165                 170                 175

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
            180                 185                 190

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
        195                 200                 205

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
    210                 215                 220

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
225                 230                 235                 240
```

```
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
                245                 250                 255


Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            260                 265


<210> 16
<211> 644
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 16
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Asn
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Phe
            20                  25                  30


Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ser Ile Ser Gly Ser Gly Arg Asp Thr Leu Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Thr Ile Gly Gly Ser Leu Ser Val Ser Ser Gln Gly Thr Leu Val Thr
            100                 105                 110


Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Val Tyr
        115                 120                 125
```

```
Cys Gly Pro Glu Phe Asp Glu Ser Val Gly Cys Met Gly Gly Gly Gly
    130                 135                 140

Ser Gly Gly Gly Ser Gly Gly Ile Ser Ser Gly Leu Leu Ser Gly Arg
145                 150                 155                 160

Ser Asp Asn His Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly
                165                 170                 175

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala
            180                 185                 190

Ser Gly Phe Thr Phe Asn Lys Tyr Ala Met Asn Trp Val Arg Gln Ala
        195                 200                 205

Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Arg Ser Lys Tyr Asn
    210                 215                 220

Asn Tyr Ala Thr Tyr Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile
225                 230                 235                 240

Ser Arg Asp Asp Ser Lys Asn Thr Ala Tyr Leu Gln Met Asn Asn Leu
                245                 250                 255

Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys Val Arg His Gly Asn Phe
            260                 265                 270

Gly Asn Ser Tyr Ile Ser Tyr Trp Ala Tyr Trp Gly Gln Gly Thr Leu
        275                 280                 285

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    290                 295                 300

Gly Gly Gly Ser Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val
305                 310                 315                 320

Ser Pro Gly Gly Thr Val Thr Leu Thr Cys Gly Ser Ser Thr Gly Ala
                325                 330                 335
```

```
Val Thr Ser Gly Asn Tyr Pro Asn Trp Val Gln Gln Lys Pro Gly Gln
            340                 345                 350

Ala Pro Arg Gly Leu Ile Gly Gly Thr Lys Phe Leu Ala Pro Gly Thr
        355                 360                 365

Pro Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr
    370                 375                 380

Leu Ser Gly Val Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Val Leu
385                 390                 395                 400

Trp Tyr Ser Asn Arg Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val
                405                 410                 415

Leu Gly Gly Gly Gly Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly
            420                 425                 430

Leu Val Gln Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly
        435                 440                 445

Phe Ser Leu Thr Asn Tyr Gly Val His Trp Val Arg Gln Ser Pro Gly
    450                 455                 460

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Asn Thr Asp
465                 470                 475                 480

Tyr Asn Thr Pro Phe Thr Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser
                485                 490                 495

Lys Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Ser Gln Asp Thr
            500                 505                 510

Ala Ile Tyr Tyr Cys Ala Arg Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe
        515                 520                 525
```

```
Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr
    530                 535                 540

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
545                 550                 555                 560

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
                565                 570                 575

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
            580                 585                 590

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
        595                 600                 605

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
    610                 615                 620

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
625                 630                 635                 640

Pro Lys Ser Cys
```

<210> 17
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 17

```
Gln Ile Leu Leu Thr Gln Ser Pro Val Ile Leu Ser Val Ser Pro Gly
1               5                   10                  15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
            20                  25                  30
```

```
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
        35                  40                  45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Ser
65                  70                  75                  80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
                85                  90                  95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 18
<211> 476

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 18
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Lys Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Asp
50 55 60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr
65 70 75 80

Ala Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Ile Ser Tyr Trp
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Thr Val Val
130 135 140

Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly Thr Val Thr Leu
145 150 155 160

Thr Cys Gly Ser Ser Thr Gly Ala Val Thr Ser Gly Asn Tyr Pro Asn
165 170 175

```
Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly Leu Ile Gly Gly
            180                 185                 190

Thr Lys Phe Leu Ala Pro Gly Thr Pro Ala Arg Phe Ser Gly Ser Leu
        195                 200                 205

Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val Gln Pro Glu Asp
    210                 215                 220

Glu Ala Glu Tyr Tyr Cys Val Leu Trp Tyr Ser Asn Arg Trp Val Phe
225                 230                 235                 240

Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gln Val
                245                 250                 255

Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Pro Ser Gln Ser Leu
            260                 265                 270

Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr Gly Val
        275                 280                 285

His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu Gly Val
    290                 295                 300

Ile Trp Ser Gly Gly Asn Thr Asp Tyr Asn Thr Pro Phe Thr Ser Arg
305                 310                 315                 320

Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln Val Phe Phe Lys Met
                325                 330                 335

Asn Ser Leu Gln Ser Gln Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Ala
            340                 345                 350

Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365
```

```
Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
    370                 375                 380

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
385                 390                 395                 400

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
                405                 410                 415

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
            420                 425                 430

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
        435                 440                 445

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
    450                 455                 460

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
465                 470                 475
```

<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 19
```
Ala Ser Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Tyr
1               5                   10
```

<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 20
Gly Ala Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Tyr
1   5   10

<210> 21
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 21
Gly Ser Ala Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Tyr
1   5   10

<210> 22
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 22
Gly Ser Gln Cys Ala Gly Pro Glu Trp Glu Val Cys Pro Tyr
1   5   10

<210> 23
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 23
Gly Ser Gln Cys Leu Ala Pro Glu Trp Glu Val Cys Pro Tyr
1   5   10

<210> 24
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 24
Gly Ser Gln Cys Leu Gly Ala Glu Trp Glu Val Cys Pro Tyr
1 5 10

<210> 25
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 25
Gly Ser Gln Cys Leu Gly Pro Ala Trp Glu Val Cys Pro Tyr
1 5 10

<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 26
Gly Ser Gln Cys Leu Gly Pro Glu Ala Glu Val Cys Pro Tyr
1 5 10

<210> 27
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 27

Gly Ser Gln Cys Leu Gly Pro Glu Trp Ala Val Cys Pro Tyr
1   5   10

<210> 28
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 28
Gly Ser Gln Cys Leu Gly Pro Glu Trp Glu Ala Cys Pro Tyr
1   5   10

<210> 29
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 29
Gly Ser Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Ala Tyr
1   5   10

<210> 30
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 30
Gly Ser Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Ala
1   5   10

<210> 31
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 31
Gly Ser Gln Cys Leu Gly Pro Glu Trp Glu Val Cys Pro Tyr
1 5 10

<210> 32
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 32
Ala Tyr Cys Gly Pro Glu Phe Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 33
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 33
Val Ala Cys Gly Pro Glu Phe Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 34
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 34
Val Tyr Cys Ala Pro Glu Phe Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 35
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 35
Val Tyr Cys Gly Ala Glu Phe Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 36
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 36
Val Tyr Cys Gly Pro Ala Phe Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 37
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 37
Val Tyr Cys Gly Pro Glu Ala Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 38
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 38
Val Tyr Cys Gly Pro Glu Phe Ala Glu Ser Val Gly Cys Met
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 39
Val Tyr Cys Gly Pro Glu Phe Asp Ala Ser Val Gly Cys Met
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 40
Val Tyr Cys Gly Pro Glu Phe Asp Glu Ala Val Gly Cys Met
1 5 10

<210> 41
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 41
Val Tyr Cys Gly Pro Glu Phe Asp Glu Ser Ala Gly Cys Met
1 5 10

<210> 42
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 42
Val Tyr Cys Gly Pro Glu Phe Asp Glu Ser Val Ala Cys Met
1 5 10

<210> 43
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 43
Val Tyr Cys Gly Pro Glu Phe Asp Glu Ser Val Gly Cys Ala
1 5 10

<210> 44
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 44
Asp Asp Cys Trp Pro Asp Trp Glu Phe Asp Phe Ala Cys Ala
1 5 10

<210> 45
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 45
Tyr Ile Cys Gly Leu Asp Phe Pro Asp Phe Leu Tyr Cys Asp
1   5   10

<210> 46
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 46
Phe Asp Cys Trp Pro Asp Trp Glu Glu Tyr Phe Val Cys Asp
1   5   10

<210> 47
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 47
Tyr Ile Cys Trp Pro Asp Trp Glu Glu Tyr Phe Asp Cys Asp
1   5   10

<210> 48
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 48
Asn Ile Cys Trp Pro Asp Trp Glu Asp Asp Tyr Phe Cys Phe
1   5   10

<210> 49
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 49
Asn Phe Cys Trp Pro Asp Trp Glu Tyr Ile Tyr Pro Cys Ile
1 5 10

<210> 50
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 50
Val Asp Cys Trp Pro Asp Trp Glu Glu Asp Phe Leu Cys Ile
1 5 10

<210> 51
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 51
His Ala Cys Trp Pro Asp Trp Glu Glu Tyr Phe Pro Cys Asn
1 5 10

<210> 52
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 52

Tyr Asp Cys Gly Pro Asp Val Asp Glu Ser Tyr Val Cys Val
1 5 10

<210> 53
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 53
Ile Asp Cys Trp Pro Asp Trp Glu Asp Asp Thr Phe Cys Tyr
1 5 10

<210> 54
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 54
Tyr Leu Cys Gly Pro Asp Gly Asp Glu Thr Leu Ala Cys Tyr
1 5 10

<210> 55
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 55
Val Asp Cys Gly Pro Asp Gly Asp Glu Ser Ile Leu Cys Tyr
1 5 10

<210> 56
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 56
Val Tyr Cys Gly Pro Glu Phe Asp Glu Ser Val Gly Cys Met
1 5 10

<210> 57
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 57
Asp Asp Cys Trp Pro Asp Trp Glu Phe Asp Phe Ala Cys Ala
1 5 10

<210> 58
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 58
Tyr Ile Cys Gly Leu Asp Phe Pro Asp Phe Leu Tyr Cys Asp
1 5 10

<210> 59
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 59
Phe Asp Cys Trp Pro Asp Trp Glu Glu Tyr Phe Val Cys Asp
1 5 10

<210> 60
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 60
Tyr Ile Cys Trp Pro Asp Trp Glu Glu Tyr Phe Asp Cys Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 61
Asn Ile Cys Trp Pro Asp Trp Glu Asp Asp Tyr Phe Cys Phe
1 5 10

<210> 62
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 62
Asn Phe Cys Trp Pro Asp Trp Glu Tyr Ile Tyr Pro Cys Ile
1 5 10

<210> 63
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 63
Val Asp Cys Trp Pro Asp Trp Glu Glu Asp Phe Leu Cys Ile
1 5 10

<210> 64
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 64
His Ala Cys Trp Pro Asp Trp Glu Glu Tyr Phe Pro Cys Asn
1 5 10

<210> 65
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 65
Tyr Asp Cys Gly Pro Asp Val Asp Glu Ser Tyr Val Cys Val
1 5 10

<210> 66
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 66
Ile Asp Cys Trp Pro Asp Trp Glu Asp Asp Thr Phe Cys Tyr
1 5 10

<210> 67
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 67
Tyr Leu Cys Gly Pro Asp Gly Asp Glu Thr Leu Ala Cys Tyr
1 5 10

<210> 68
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 68
Val Asp Cys Gly Pro Asp Gly Asp Glu Ser Ile Leu Cys Tyr
1 5 10

<210> 69
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 69
Phe Ile Cys Trp Pro Asp Trp Glu Glu Asp Tyr Phe Cys Ala
1 5 10

<210> 70
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 70
Gly Asp Cys Trp Pro Asp Trp Glu Trp Asp Phe Tyr Cys Asp
1   5   10

<210> 71
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 71
Tyr Leu Cys Trp Pro Asp Trp Glu Tyr Ile Asp Leu Cys Asp
1   5   10

<210> 72
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 72
Ser Phe Cys Trp Pro Asp Trp Glu Glu Tyr Phe Asp Cys Asp
1   5   10

<210> 73
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 73
Asp Asp Cys Trp Pro Asp Trp Glu Glu Tyr Ala Ser Cys Asp
1   5   10

<210> 74
<211> 14

<212> PRT
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<220>
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<400> 74
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1 5 10

<210> 75
<211> 14
<212> PRT
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<220>
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peptide

<400> 75
Phe Asp Cys Trp Pro Asp Trp Glu Glu Ser Phe Val Cys Asp
1 5 10

<210> 76
<211> 14
<212> PRT
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<220>
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peptide

<400> 76
Asp Ile Cys Gly Pro Asp Gly Asp Glu Thr Ile Ile Cys Asp
1 5 10

<210> 77
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 77

Asp Asp Cys Trp Pro Asp Trp Glu Tyr Tyr Ala Val Cys Asp
1   5   10

<210> 78
<211> 14
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<220>
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      peptide

<400> 78
Tyr Asp Cys Trp Pro Asp Trp Glu Glu Tyr Ser Asn Cys Asp
1   5   10

<210> 79
<211> 14
<212> PRT
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<220>
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      peptide

<400> 79
Ile Asn Cys Trp Pro Asp Trp Glu Asp Tyr Phe Phe Cys Asp
1   5   10

<210> 80
<211> 14
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<220>
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<400> 80
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1   5   10

<210> 81
<211> 14
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<220>
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peptide

<400> 81
Asn Ile Cys Trp Pro Asp Trp Glu Pro Asn Ser Phe Cys Phe
1 5 10

<210> 82
<211> 14
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<220>
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peptide

<400> 82
Tyr Asp Cys Gly Pro Glu Met Asp Glu Ser Ile Asp Cys Phe
1 5 10

<210> 83
<211> 14
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<220>
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peptide

<400> 83
Asp Phe Cys Trp Pro Asp Trp Glu Phe Pro Phe Ile Cys His
1 5 10

<210> 84
<211> 14
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<220>
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peptide

<400> 84
Asp Phe Cys Gly Pro Glu Met Asp Glu Ser Ile Thr Cys Ile
1 5 10

<210> 85
<211> 14
<212> PRT
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<220>
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peptide

<400> 85
Tyr Asp Cys Gly Pro Glu Phe Asp Glu Ser Thr Val Cys Ile
1 5 10

<210> 86
<211> 14
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<220>
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peptide

<400> 86
His Asp Cys Trp Pro Asp Trp Glu Trp Asp Ile Phe Cys Ile
1 5 10

<210> 87
<211> 14
<212> PRT
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<220>
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peptide

<400> 87
His Ala Cys Trp Pro Asp Trp Glu Glu Tyr Asn Pro Cys Asn
1 5 10

<210> 88
<211> 14
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<220>

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peptide

<400> 88
Asp Val Cys Trp Pro Asp Trp Glu Trp Asp Phe Phe Cys Asn
1 5 10

<210> 89
<211> 14
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<220>
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peptide

<400> 89
Asn Tyr Cys Trp Pro Asp Trp Glu Tyr Tyr Ile Pro Cys Asn
1 5 10

<210> 90
<211> 14
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<220>
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peptide

<400> 90
Ile Ile Cys Trp Pro Asp Trp Glu Phe Ile Asp Tyr Cys Asn
1 5 10

<210> 91
<211> 14
<212> PRT
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<220>
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peptide

<400> 91
Ser Leu Cys Trp Pro Asp Trp Glu Tyr Asp Ile Ala Cys Pro
1 5 10

<210> 92
<211> 14
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<220>
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peptide

<400> 92
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1 5 10

<210> 93
<211> 14
<212> PRT
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<220>
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peptide

<400> 93
Thr Asn Cys Trp Pro Asp Trp Glu Trp Val Leu Pro Cys Pro
1 5 10

<210> 94
<211> 14
<212> PRT
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<220>
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peptide

<400> 94
Ile Glu Cys Trp Pro Asp Trp Glu Pro Asn Tyr Phe Cys Pro
1 5 10

<210> 95
<211> 14
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<220>
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peptide

<400> 95
Ile Phe Cys Trp Pro Asp Trp Glu Asp Tyr Val Asp Cys Pro
1   5   10

<210> 96
<211> 14
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<220>
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      peptide

<400> 96
Ile Asp Cys Trp Pro Asp Trp Glu Tyr Asp Phe Phe Cys Pro
1   5   10

<210> 97
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      peptide

<400> 97
Leu Phe Cys Trp Pro Asp Trp Glu Asp Ser Phe Phe Cys Pro
1   5   10

<210> 98
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      peptide

<400> 98
Val Asp Cys Trp Pro Asp Trp Glu Asp Tyr Ala Asp Cys Thr
1   5   10

<210> 99
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<212> PRT
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<220>
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peptide

<400> 99
Val Ile Cys Trp Pro Asp Trp Glu Gln Tyr Phe Pro Cys Val
1 5 10

<210> 100
<211> 14
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<220>
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peptide

<400> 100
Ile Glu Cys Trp Pro Asp Trp Glu Pro Ile Tyr Pro Cys Tyr
1 5 10

<210> 101
<211> 14
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<220>
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peptide

<400> 101
Ile Thr Cys Trp Pro Asp Trp Glu Val Tyr Phe Pro Cys Tyr
1 5 10

<210> 102
<211> 14
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<220>
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peptide

<400> 102

Ile Asp Cys Trp Pro Asp Trp Glu Tyr Ile His Pro Cys Tyr
1   5   10

<210> 103
<211> 14
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<220>
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      peptide

<400> 103
Ile Asp Cys Trp Pro Asp Trp Glu Tyr Ile Asn Pro Cys Tyr
1   5   10

<210> 104
<211> 14
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<220>
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      peptide

<400> 104
Ala Asp Cys Trp Pro Asp Trp Glu Glu Ala Phe Pro Cys Tyr
1   5   10

<210> 105
<211> 14
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<220>
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      peptide

<400> 105
Ile Asp Cys Trp Pro Asp Trp Glu Tyr Ile Tyr Pro Cys Tyr
1   5   10

<210> 106
<211> 14
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<220>
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peptide

<400> 106
Asn Ile Cys Trp Pro Asp Trp Glu Asp Asp Asn Phe Cys Phe
1 5 10

<210> 107
<211> 14
<212> PRT
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<220>
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peptide

<400> 107
Tyr Asp Cys Trp Pro Asp Trp Glu Tyr Val Asp Ala Cys Tyr
1 5 10

<210> 108
<211> 14
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<220>
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peptide

<400> 108
Phe Tyr Cys Gly Pro Asp Gly Asp Glu Ser Tyr Val Cys Asp
1 5 10

<210> 109
<211> 14
<212> PRT
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<220>
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peptide

<400> 109
Asp Ile Cys Trp Pro Asp Trp Glu Tyr Ile Asn Ile Cys Ser
1 5 10

<210> 110
<211> 14
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<220>
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peptide

<400> 110
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1 5 10

<210> 111
<211> 14
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peptide

<400> 111
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1 5 10

<210> 112
<211> 14
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<220>
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peptide

<400> 112
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1 5 10

<210> 113
<211> 14
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<220>

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peptide

<400> 113
Tyr Asp Cys Trp Pro Asp Trp Glu Glu Tyr Asn Asp Cys Ala
1 5 10

<210> 114
<211> 14
<212> PRT
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<220>
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peptide

<400> 114
Asp Asp Cys Gly Pro Asp Gly Asp Glu Thr Ile Ile Cys Val
1 5 10

<210> 115
<211> 14
<212> PRT
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<220>
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peptide

<400> 115
Phe Pro Cys Trp Pro Asp Trp Glu Glu Tyr Ala Ile Cys Asp
1 5 10

<210> 116
<211> 14
<212> PRT
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<220>
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peptide

<400> 116
Pro Asp Cys Gly Pro Asp Gly Asp Glu Ser Leu Phe Cys Thr
1 5 10

<210> 117
<211> 14
<212> PRT
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<220>
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peptide

<400> 117
Asp Asn Cys Trp Pro Asp Trp Glu Tyr Asp Tyr Phe Cys Val
1 5 10

<210> 118
<211> 14
<212> PRT
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<220>
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peptide

<400> 118
Ile Phe Cys Trp Pro Asp Trp Glu Glu Phe Tyr Asp Cys Tyr
1 5 10

<210> 119
<211> 14
<212> PRT
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<220>
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peptide

<400> 119
Ala Asp Cys Trp Pro Asp Trp Glu Glu Tyr Phe Pro Cys Asn
1 5 10

<210> 120
<211> 14
<212> PRT
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<220>
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peptide

<400> 120
His Thr Cys Trp Pro Asp Trp Glu Asp Asp Ile Phe Cys Asn
1   5   10

<210> 121
<211> 14
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<220>
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      peptide

<400> 121
Phe Ala Cys Trp Pro Asp Trp Glu Glu Ala Phe Leu Cys Leu
1   5   10

<210> 122
<211> 14
<212> PRT
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<220>
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      peptide

<400> 122
Tyr Asp Cys Gly Pro Glu Leu Asp Glu Ser Ile Ala Cys Asp
1   5   10

<210> 123
<211> 14
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<220>
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      peptide

<400> 123
Asn Ser Cys Trp Pro Asp Trp Glu Tyr Asp Ile Ile Cys Asp
1   5   10

<210> 124
<211> 14

<212> PRT
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<220>
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peptide

<400> 124
Phe Ala Cys Trp Pro Asp Trp Glu Glu Val Ala Pro Cys Tyr
1 5 10

<210> 125
<211> 14
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<220>
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peptide

<400> 125
Leu Asp Cys Gly Pro Asp Gly Asp Glu Thr Leu Thr Cys Tyr
1 5 10

<210> 126
<211> 14
<212> PRT
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<220>
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peptide

<400> 126
Val Leu Cys Trp Pro Asp Trp Glu Glu Phe Tyr Asp Cys Pro
1 5 10

<210> 127
<211> 14
<212> PRT
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<220>
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peptide

<400> 127

His Ala Cys Trp Pro Val Trp Glu Glu Tyr Phe Pro Cys Asn
1 5 10

<210> 128
<211> 14
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<220>
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<400> 128
Asn Glu Cys Trp Pro Asn Gly Glu Pro Thr Phe Pro Cys Thr
1 5 10

<210> 129
<211> 14
<212> PRT
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<220>
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<400> 129
Leu Thr Cys Gly Pro Asp Gly Asp Glu Thr Leu Tyr Cys Asp
1 5 10

<210> 130
<211> 14
<212> PRT
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<220>
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<400> 130
Tyr Asp Cys Gly Pro Glu Tyr Asp Glu Ser Val Pro Cys Ile
1 5 10

<210> 131
<211> 14
<212> PRT
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<220>
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peptide

<400> 131
Ile Glu Cys Trp Pro Asp Trp Glu Pro Asn Ser Phe Cys Asp
1 5 10

<210> 132
<211> 14
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<220>
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peptide

<400> 132
Tyr Asp Cys Gly Pro Glu Leu Asp Glu Ser Ile His Cys Tyr
1 5 10

<210> 133
<211> 14
<212> PRT
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peptide

<400> 133
Ile Tyr Cys Gly Pro Glu Phe Asp Glu Ser Thr Ile Cys Asn
1 5 10

<210> 134
<211> 14
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<220>
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peptide

<400> 134
Ile Tyr Cys Gly Pro Glu Val Glu Glu Ala Tyr Leu Cys Tyr
1 5 10

<210> 135
<211> 14
<212> PRT
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peptide

<400> 135
Phe Asp Cys Gly Pro Asp Gly Asp Glu Thr Val Tyr Cys Asp
1 5 10

<210> 136
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 136
Ile Asp Cys Gly Pro Asp Gly Asp Glu Thr Ile Ser Cys Tyr
1 5 10

<210> 137
<211> 14
<212> PRT
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<220>
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peptide

<400> 137
Asn Tyr Cys Gly Pro Glu Phe Asp Glu Ser Ser Thr Cys Leu
1 5 10

<210> 138
<211> 14
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<220>

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peptide

<400> 138
Tyr Asp Cys Gly Pro Asp Gly Asp Glu Ser Tyr Phe Cys Asp
1 5 10

<210> 139
<211> 14
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<220>
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peptide

<400> 139
Asn Phe Cys Trp Pro Asp Trp Glu Tyr Phe Asn Asp Cys Asn
1 5 10

<210> 140
<211> 14
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<220>
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peptide

<400> 140
Val Leu Cys Trp Pro Asp Trp Glu Ala Phe Phe Asp Cys Asp
1 5 10

<210> 141
<211> 14
<212> PRT
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<220>
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peptide

<400> 141
Ile Tyr Cys Gly Pro Glu Trp Glu Trp Pro Val Ala Cys Asn
1 5 10

<210> 142
<211> 14
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<220>
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peptide

<400> 142
Val Phe Cys Trp Pro Asp Trp Glu Asp Asn Phe Phe Cys Asn
1 5 10

<210> 143
<211> 14
<212> PRT
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<220>
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peptide

<400> 143
Val Val Cys Trp Pro Asp Trp Glu Thr Phe Phe Pro Cys Asp
1 5 10

<210> 144
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<220>
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peptide

<400> 144
Asp Asn Cys Gly Pro Asp Gly Asp Glu Thr Tyr Ile Cys Asn
1 5 10

<210> 145
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<220>
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peptide

<400> 145
Asp Asn Cys Trp Pro Asp Trp Glu Tyr Asn Phe Phe Cys Val
1   5   10

<210> 146
<211> 14
<212> PRT
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<220>
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      peptide

<400> 146
Phe Tyr Cys Gly Pro Glu Val Glu Glu Asp Tyr Leu Cys Ile
1   5   10

<210> 147
<211> 14
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<220>
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      peptide

<400> 147
Asp Asn Cys Trp Pro Asp Trp Glu Tyr Asp Ile Phe Cys Val
1   5   10

<210> 148
<211> 14
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<220>
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      peptide

<400> 148
Ile Asp Cys Gly Pro Glu Phe Asp Glu Ser Ile Ala Cys Pro
1   5   10

<210> 149
<211> 14

<212> PRT
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<220>
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peptide

<400> 149
Tyr Phe Cys Gly Pro Glu Val Glu Glu Tyr Thr Leu Cys Phe
1 5 10

<210> 150
<211> 14
<212> PRT
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peptide

<400> 150
Phe Tyr Cys Gly Pro Glu Phe Asp Glu Ser Ala Pro Cys Asn
1 5 10

<210> 151
<211> 14
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peptide

<400> 151
Phe Asp Cys Gly Pro Glu Val Glu Glu Tyr Phe Tyr Cys Ala
1 5 10

<210> 152
<211> 14
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<220>
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peptide

<400> 152

Asp Phe Cys Trp Pro Asp Trp Glu Asp Phe Phe Phe Cys Ala
1 5 10

<210> 153
<211> 14
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<220>
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<400> 153
Phe Phe Cys Gly Pro Asp Gly Asp Glu Thr Leu Ser Cys Asn
1 5 10

<210> 154
<211> 14
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<220>
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<400> 154
Phe Ile Cys Gly Pro Glu Phe Asp Glu Ser Val Ala Cys Leu
1 5 10

<210> 155
<211> 14
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<220>
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<400> 155
Tyr Asp Cys Gly Pro Glu Phe Asp Glu Ala Ile Gly Cys Tyr
1 5 10

<210> 156
<211> 14
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peptide

<400> 156
Tyr Ile Cys Trp Pro Asp Trp Glu Glu Tyr Leu Tyr Cys Pro
1 5 10

<210> 157
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<220>
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peptide

<400> 157
Phe Asp Cys Trp Pro Asp Trp Glu Glu Pro Thr Thr Cys His
1 5 10

<210> 158
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peptide

<400> 158
Tyr Asp Cys Trp Pro Asp Trp Glu Asp Phe Pro Ile Cys Asp
1 5 10

<210> 159
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<220>
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peptide

<400> 159
Val Val Cys Trp Pro Asp Trp Glu Tyr Ile Asp Asp Cys Ser
1 5 10

<210> 160
<211> 14
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<220>
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peptide

<400> 160
Ile Asn Cys Trp Pro Asp Trp Glu Val Ile Ser Phe Cys Asp
1 5 10

<210> 161
<211> 14
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peptide

<400> 161
Leu Ser Cys Trp Pro Asp Trp Glu Glu Val Thr Pro Cys Leu
1 5 10

<210> 162
<211> 14
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<220>
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peptide

<400> 162
Phe Ala Cys Trp Pro Asp Trp Glu Glu Val Asp Ile Cys Tyr
1 5 10

<210> 163
<211> 14
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<220>

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peptide

<400> 163
Tyr Asp Cys Gly Pro Glu Met Asp Glu Ser Ile Val Cys Asp
1 5 10

<210> 164
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peptide

<400> 164
Tyr Asp Cys Trp Pro Asp Trp Glu Val Phe Ile Val Cys Asp
1 5 10

<210> 165
<211> 14
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<220>
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peptide

<400> 165
Asp Asn Cys Trp Pro Asp Trp Glu His Asn Phe Phe Cys Val
1 5 10

<210> 166
<211> 14
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<220>
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peptide

<400> 166
Tyr Asp Cys Gly Pro Asp Gly Asp Glu Ser Ile Tyr Cys Pro
1 5 10

<210> 167
<211> 14
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<220>
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peptide

<400> 167
Tyr Asp Cys Gly Pro Glu Phe Glu Phe Pro Tyr Tyr Cys Phe
1 5 10

<210> 168
<211> 14
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peptide

<400> 168
Ala Asp Cys Gly Pro Glu Tyr Asp Glu Ser Val Pro Cys Val
1 5 10

<210> 169
<211> 14
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<220>
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peptide

<400> 169
Phe Leu Cys Gly Pro Glu Val Glu Glu Val His Tyr Cys Ser
1 5 10

<210> 170
<211> 14
<212> PRT
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<220>
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peptide

<400> 170
Thr Asp Cys Trp Pro Asp Trp Glu Tyr Ile Thr Ser Cys Ser
1   5   10

<210> 171
<211> 14
<212> PRT
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<220>
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      peptide

<400> 171
Ala Phe Cys Gly Pro Glu Leu Asp Glu Ser Ile Thr Cys Asp
1   5   10

<210> 172
<211> 14
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<220>
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      peptide

<400> 172
Asn Asp Cys Trp Pro Asp Trp Glu Glu Tyr Phe Ser Cys Tyr
1   5   10

<210> 173
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<220>
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      peptide

<400> 173
Phe Asp Cys Gly Pro Glu Trp Glu Ile Val Thr Asp Cys Tyr
1   5   10

<210> 174
<211> 14

<212> PRT
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<220>
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peptide

<400> 174
Asn Leu Cys Gly Pro Glu Met Asp Glu Ser Ile Ile Cys Pro
1 5 10

<210> 175
<211> 14
<212> PRT
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peptide

<400> 175
Asp Leu Cys Gly Pro Glu Met Asp Glu Ser Ile Tyr Cys Asp
1 5 10

<210> 176
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<220>
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peptide

<400> 176
Phe Asp Cys Gly Pro Asp Gly Val Glu Asp Tyr Ile Cys Asp
1 5 10

<210> 177
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1 5 10

<210> 178
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1 5 10

<210> 179
<211> 14
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<400> 179
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<210> 180
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1 5 10

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peptide

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1 5 10

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1 5 10

<210> 193
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1 5 10

<210> 194
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1   5   10

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1   5   10

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1   5   10

<210> 199
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1 5 10

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1 5 10

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1 5 10

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1   5   10

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1   5   10

<210> 204
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1   5   10

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1   5   10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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peptide

<400> 213
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1 5 10

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peptide

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1 5 10

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peptide

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1 5 10

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peptide

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1 5 10

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peptide

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1 5 10

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peptide

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1 5 10

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peptide

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1 5 10

<210> 220
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<220>
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peptide

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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peptide

<400> 226
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1 5 10

<210> 227
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peptide

<400> 227

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1   5   10

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1   5   10

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1 5 10

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peptide

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1 5 10

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1 5 10

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1 5 10

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peptide

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1 5 10

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peptide

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peptide

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peptide

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1 5 10

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1 5 10

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1   5   10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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peptide

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1   5   10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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peptide

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1 5 10

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1 5 10

<210> 484
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peptide

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1   5   10

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1   5   10

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1   5   10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1   5   10

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1   5   10

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1   5   10

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1 5 10

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peptide

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1 5 10

<210> 577
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peptide

<400> 577

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1 5 10

<210> 578
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1 5 10

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peptide

<400> 581
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1 5 10

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peptide

<400> 582
Val Tyr Cys Gly Pro Glu Val Glu Glu Asn Ile Leu Cys His
1 5 10

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peptide

<400> 583
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1 5 10

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peptide

<400> 584
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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peptide

<400> 589
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1 5 10

<210> 590
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peptide

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1 5 10

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<400> 591
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1 5 10

<210> 592
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<220>
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peptide

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Asp His Cys Gly Pro Glu Val Glu Leu Ile Phe Tyr Cys His
1 5 10

<210> 593
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<220>
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peptide

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1 5 10

<210> 594
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1 5 10

<210> 595
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1   5   10

<210> 597
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1   5   10

<210> 598
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1   5   10

<210> 599
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Phe Phe Cys Gly Pro Glu Phe Glu Glu Ile Phe Leu Cys Tyr
1 5 10

<210> 600
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Tyr Asn Cys Gly Pro Asp Gly Asp Glu Ser Tyr Asp Cys His
1 5 10

<210> 601
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<220>
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peptide

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Asp Asn Cys Gly Pro Glu Leu Asp Glu Thr Ile Thr Cys Phe
1 5 10

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<400> 602

His Asn Cys Gly Pro Asp Gly Asp Glu Ala Phe Ile Cys Asn
1   5   10

<210> 603
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1   5   10

<210> 604
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<400> 604
Asp Tyr Cys Gly Pro Glu Leu Asp Glu Ser Leu Asn Cys Phe
1   5   10

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<400> 605
Asp Tyr Cys Gly Pro Glu Phe Gln Glu Asp Phe His Cys His
1   5   10

<210> 606
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peptide

<400> 606
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1 5 10

<210> 607
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peptide

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1 5 10

<210> 608
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peptide

<400> 608
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1 5 10

<210> 609
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peptide

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1 5 10

<210> 610
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peptide

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1 5 10

<210> 611
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1 5 10

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peptide

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1 5 10

<210> 613
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1 5 10

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peptide

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1 5 10

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peptide

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1 5 10

<210> 616
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peptide

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Asn Leu Cys Gly Pro Glu Phe Asp Glu Ser Ile Phe Cys Tyr
1 5 10

<210> 617
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peptide

<400> 617
Ile Asp Cys Trp Pro Asp Trp Glu Glu Tyr Ile Pro Cys Thr
1 5 10

<210> 618
<211> 14
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peptide

<400> 618
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1 5 10

<210> 619
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<220>
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peptide

<400> 619
Asp Tyr Cys Gly Pro Glu Phe Asp Glu Ser Val Val Cys Tyr
1 5 10

<210> 620
<211> 14
<212> PRT
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<220>
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peptide

<400> 620
Val Phe Cys Gly Pro Glu Trp Glu Asp Ile Thr Asp Cys Asp
1   5   10

<210> 621
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<220>
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<400> 621
Leu Asp Cys Gly Pro Glu Val Asp Glu Thr Phe Thr Cys His
1   5   10

<210> 622
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<220>
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      peptide

<400> 622
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1   5   10

<210> 623
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<220>
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      peptide

<400> 623
Ile Tyr Cys Gly Pro Glu Tyr Gln Glu Asp Leu Pro Cys Asn
1   5   10

<210> 624
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<212> PRT
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peptide

<400> 624
Leu Asp Cys Gly Pro Glu Val Glu Glu Tyr Asn Tyr Cys Val
1 5 10

<210> 625
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<212> PRT
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peptide

<400> 625
Tyr Val Cys Gly Pro Glu Phe Asp Glu Ser Ser Ala Cys Asn
1 5 10

<210> 626
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<212> PRT
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peptide

<400> 626
Thr Pro Cys Gly Pro Glu Leu Glu Glu Ala Ile Gly Cys Tyr
1 5 10

<210> 627
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<220>
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peptide

<400> 627

Tyr Phe Cys Gly Pro Glu Phe Asp Glu Ser Ala Asp Cys Asn
1 5 10

<210> 628
<211> 14
<212> PRT
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<220>
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<400> 628
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1 5 10

<210> 629
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<220>
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<400> 629
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1 5 10

<210> 630
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Val Ile Cys Gly Pro Asp Gly Glu Glu Leu Ile Ala Cys Ala
1 5 10

<210> 631
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peptide

<400> 631
Phe Ala Cys Trp Pro Asp Trp Gln Glu Thr Tyr Val Cys Asn
1 5 10

<210> 632
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<220>
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peptide

<400> 632
Tyr Ile Cys Gly Pro Glu Val Glu Phe Leu Phe Phe Cys Asn
1 5 10

<210> 633
<211> 14
<212> PRT
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<220>
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peptide

<400> 633
Thr Gln Cys Gly Pro Lys Gly Glu Pro Thr Tyr His Cys Tyr
1 5 10

<210> 634
<211> 14
<212> PRT
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<220>
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peptide

<400> 634
Asn Tyr Cys Gly Pro Glu Val Glu Glu Tyr His Asn Cys Asp
1 5 10

<210> 635
<211> 14
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<220>
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peptide

<400> 635
Val Tyr Cys Gly Pro Glu Trp Glu Phe Phe Ser Asp Cys Ala
1 5 10

<210> 636
<211> 14
<212> PRT
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<220>
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peptide

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Phe Tyr Cys Gly Pro Glu Leu Glu Glu Ser Phe Phe Cys Tyr
1 5 10

<210> 637
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<220>
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peptide

<400> 637
Asp Tyr Cys Gly Pro Glu Ile Glu Glu Asn Phe Tyr Cys Tyr
1 5 10

<210> 638
<211> 14
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<220>

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peptide

<400> 638
Tyr Ala Cys Gly Pro Glu Val Glu Glu Tyr Val Tyr Cys Ala
1 5 10

<210> 639
<211> 14
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<220>
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peptide

<400> 639
Val Asp Cys Gly Pro Glu Leu Asp Glu Ser Ile Ile Cys Asp
1 5 10

<210> 640
<211> 14
<212> PRT
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<220>
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peptide

<400> 640
Asn Asp Cys Gly Pro Glu Met Asp Glu Ser Ile Ala Cys Tyr
1 5 10

<210> 641
<211> 14
<212> PRT
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<220>
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peptide

<400> 641
Val Tyr Cys Gly Pro Glu Phe Asp Glu Tyr Leu Ala Cys Ala
1 5 10

<210> 642
<211> 14
<212> PRT
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<220>
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peptide

<400> 642
Val Ile Cys Gly Pro Glu Phe Asp Glu Ser Ala Asn Cys Asp
1 5 10

<210> 643
<211> 14
<212> PRT
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<220>
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peptide

<400> 643
Leu Thr Cys Trp Pro Asp Trp Glu Glu Asp Phe Phe Cys Asn
1 5 10

<210> 644
<211> 14
<212> PRT
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<220>
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peptide

<400> 644
Phe Tyr Cys Gly Pro Glu Gln Glu Glu Ile Asn Tyr Cys Tyr
1 5 10

<210> 645
<211> 14
<212> PRT
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<220>
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peptide

<400> 645
Thr Tyr Cys Gly Pro Glu Leu Glu Glu Phe Phe Leu Cys Tyr
1   5   10

<210> 646
<211> 14
<212> PRT
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<220>
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      peptide

<400> 646
Pro Asp Cys Gly Pro Glu Leu Asp Glu Ser Val Ala Cys His
1   5   10

<210> 647
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 647
Asn Asp Cys Gly Pro Glu Phe Glu Glu Ile Ile Phe Cys Val
1   5   10

<210> 648
<211> 14
<212> PRT
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<220>
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      peptide

<400> 648
Tyr Ile Cys Gly Pro Glu Phe Asp Glu Ser Phe Tyr Cys Asn
1   5   10

<210> 649
<211> 14

<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 649
His Ala Cys Gly Pro Glu Leu Asp Glu Ser Leu Leu Cys Asn
1 5 10

<210> 650
<211> 14
<212> PRT
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<220>
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peptide

<400> 650
Tyr Tyr Cys Gly Pro Glu Trp Glu Glu Ala Val Leu Cys Ala
1 5 10

<210> 651
<211> 14
<212> PRT
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<220>
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peptide

<400> 651
Ala Phe Cys Gly Pro Glu Val Glu Glu Tyr Asp Leu Cys Asn
1 5 10

<210> 652
<211> 14
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<220>
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peptide

<400> 652

Tyr Asn Cys Gly Pro Glu Phe Asp Glu Ser Val Ala Cys Ser
1 5 10

<210> 653
<211> 14
<212> PRT
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<220>
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<400> 653
Tyr Leu Cys Gly Pro Glu Val Glu Asp Asp Thr Leu Cys Ala
1 5 10

<210> 654
<211> 14
<212> PRT
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<220>
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<400> 654
Ala Val Cys Gly Pro Glu Phe Asp Glu Ser Val Asn Cys Asp
1 5 10

<210> 655
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 655
Asn Tyr Cys Gly Pro Glu Trp Glu Val Tyr Ser Leu Cys Pro
1 5 10

<210> 656
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<220>
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peptide

<400> 656
Asp Phe Cys Gly Pro Glu Val Glu Glu Asp Thr Tyr Cys His
1 5 10

<210> 657
<211> 14
<212> PRT
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<220>
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peptide

<400> 657
Ile Ser Cys Gly Pro Glu Tyr Glu Trp Asp Tyr Ala Cys Asn
1 5 10

<210> 658
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<220>
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peptide

<400> 658
Val Asn Cys Gly Pro Glu Leu Asp Glu Ser Ile Ile Cys Tyr
1 5 10

<210> 659
<211> 14
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<220>
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peptide

<400> 659
Tyr Asp Cys Gly Pro Glu Phe Asp Glu Thr Ala Pro Cys Tyr
1 5 10

<210> 660
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 660
Tyr Leu Cys Gly Pro Glu Phe Glu Glu Asn Phe Leu Cys Thr
1 5 10

<210> 661
<211> 14
<212> PRT
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<220>
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peptide

<400> 661
Phe Asp Cys Gly Pro Glu Val Asp Glu Ser Val Asp Cys Ala
1 5 10

<210> 662
<211> 14
<212> PRT
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<220>
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peptide

<400> 662
Tyr Asp Cys Gly Pro Glu Gln Glu Glu Ile Ser Phe Cys Asn
1 5 10

<210> 663
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<220>

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peptide

<400> 663
Ile Asp Cys Gly Pro Glu Ile Glu Leu Tyr Asp Asp Cys Phe
1 5 10

<210> 664
<211> 14
<212> PRT
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<220>
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peptide

<400> 664
Thr Phe Cys Gly Pro Glu Leu Asp Glu Ser Val Tyr Cys Tyr
1 5 10

<210> 665
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<220>
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peptide

<400> 665
Phe Phe Cys Gly Pro Glu Ile Asp Glu Ser Asn Ala Cys Val
1 5 10

<210> 666
<211> 14
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<220>
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peptide

<400> 666
Tyr His Cys Trp Pro Asp Trp Glu Pro Ile Tyr Ile Cys Ile
1 5 10

<210> 667
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 667
Ala Ile Cys Gly Pro Glu Tyr Glu Glu Asp His Tyr Cys Tyr
1 5 10

<210> 668
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 668
Pro Leu Cys Gly Pro Asp Gly Phe Glu Asn Tyr Asn Cys Phe
1 5 10

<210> 669
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<220>
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peptide

<400> 669
Phe Pro Cys Trp Pro Asp Trp Glu Trp Asp Asn Asn Cys His
1 5 10

<210> 670
<211> 14
<212> PRT
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<220>
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peptide

<400> 670
Val Asp Cys Gly Pro Asp Gly Asp Glu Leu Ala Ala Cys His
1   5   10

<210> 671
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<220>
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      peptide

<400> 671
Val Asp Cys Trp Pro Asp Trp Glu Glu Tyr Tyr Ser Cys Asp
1   5   10

<210> 672
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<220>
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      peptide

<400> 672
Val Tyr Cys Gly Pro Glu Tyr Asp Glu Ser Tyr Asp Cys Thr
1   5   10

<210> 673
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<220>
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      peptide

<400> 673
Asn Leu Cys Gly Pro Glu Trp Glu Asn Phe Ala Asp Cys Phe
1   5   10

<210> 674
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<212> PRT
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<220>
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peptide

<400> 674
Tyr Leu Cys Gly Pro Glu Leu Glu Val Phe Phe Val Cys Asp
1 5 10

<210> 675
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<220>
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peptide

<400> 675
Ile Phe Cys Gly Pro Glu Leu Glu Asp Tyr Ser Ile Cys Phe
1 5 10

<210> 676
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<220>
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peptide

<400> 676
Asp Tyr Cys Gly Pro Glu Leu Glu Gln Tyr Asp Leu Cys Phe
1 5 10

<210> 677
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<220>
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peptide

<400> 677

Leu Leu Cys Gly Pro Val Asn Glu Asp Pro Leu Asp Cys Tyr
1 5 10

<210> 678
<211> 14
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<220>
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<400> 678
Ile Asp Cys Gly Pro Glu Phe Asp Glu Ser Val Phe Cys Tyr
1 5 10

<210> 679
<211> 14
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<220>
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<400> 679
Ile Ile Cys Gly Pro Glu Val Glu Glu Ile Asp Ile Cys Ser
1 5 10

<210> 680
<211> 14
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<220>
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<400> 680
Ile Ala Cys Trp Pro Asp Trp Glu Asp Tyr Ser Ser Cys Pro
1 5 10

<210> 681
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peptide

<400> 681
Tyr Tyr Cys Gly Pro Glu Val Glu Asp Ile Asn Asp Cys Ile
1 5 10

<210> 682
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<220>
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peptide

<400> 682
Asn Ile Cys Gly Pro Glu Met Asp Glu Ser Ile Asp Cys Ile
1 5 10

<210> 683
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<220>
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peptide

<400> 683
Phe Asp Cys Trp Pro Asp Trp Glu Glu Leu Val Ser Cys Tyr
1 5 10

<210> 684
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<220>
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peptide

<400> 684
Tyr Phe Cys Gly Pro Glu Trp Glu Asp His Phe Phe Cys Asp
1 5 10

<210> 685
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peptide

<400> 685
Thr Tyr Cys Gly Pro Glu Phe Glu Glu Asp Ser Tyr Cys Asp
1 5 10

<210> 686
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peptide

<400> 686
Asn Leu Cys Gly Pro Glu Val Glu Leu Ile Asp Ile Cys Ser
1 5 10

<210> 687
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peptide

<400> 687
Asp Asn Cys Gly Pro Glu Trp Glu Glu Val Tyr Leu Cys Asn
1 5 10

<210> 688
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peptide

<400> 688
Phe Leu Cys Gly Pro Glu Phe Asp Glu Ser Asp Leu Cys Phe
1 5 10

<210> 689
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peptide

<400> 689
His Ile Cys Gly Pro Glu Gln Asp Glu Ser Ile Gly Cys Thr
1 5 10

<210> 690
<211> 14
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peptide

<400> 690
Phe Asp Cys Trp Pro Asp Trp Glu Asp Asn Ser Tyr Cys Asp
1 5 10

<210> 691
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<220>
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peptide

<400> 691
Thr Ala Cys Gly Pro Glu Trp Glu Phe Asp Phe Asn Cys Asp
1 5 10

<210> 692
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<220>
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peptide

<400> 692
His His Cys Trp Pro Asp Trp Glu Asp Tyr Ser Thr Cys Pro
1 5 10

<210> 693
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peptide

<400> 693
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1 5 10

<210> 694
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<220>
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peptide

<400> 694
Leu His Cys Trp Pro Asp Trp Glu Glu Ile Asp Ile Cys Asp
1 5 10

<210> 695
<211> 14
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<220>
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<400> 695
Asp Ile Cys Gly Pro Asp Gly Gln Glu Asp Phe Val Cys Ser
1   5   10

<210> 696
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<220>
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1   5   10

<210> 697
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<220>
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<400> 697
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1   5   10

<210> 698
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<220>
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1   5   10

<210> 699
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<220>
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peptide

<400> 699
Asp Leu Cys Gly Pro Glu Phe Glu Glu Val His Asn Cys Asn
1 5 10

<210> 700
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peptide

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Val Asn Cys Gly Pro Glu Phe Asp Glu Ser Ser Tyr Cys Phe
1 5 10

<210> 701
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<220>
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<400> 701
Asn Ile Cys Trp Pro Asp Trp Glu Glu Asp Asn Phe Cys Ser
1 5 10

<210> 702
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<220>
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peptide

<400> 702

Phe Val Cys Gly Pro Glu Trp Glu Val Tyr Asp Asp Cys Asp
1 5 10

<210> 703
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<220>
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<400> 703
Ala Tyr Cys Gly Pro Glu Leu Glu Val Val His Leu Cys Val
1 5 10

<210> 704
<211> 14
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<220>
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<400> 704
Pro Phe Cys Gly Pro Glu Met Asp Glu Thr Ile Asp Cys Tyr
1 5 10

<210> 705
<211> 14
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<220>
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<400> 705
Leu Leu Cys Gly Pro Val Met Glu Asp Val Phe Ala Cys Tyr
1 5 10

<210> 706
<211> 14
<212> PRT
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<220>
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peptide

<400> 706
Asp Leu Cys Gly Pro Glu Phe Asp Glu Ser Thr Asn Cys Tyr
1 5 10

<210> 707
<211> 14
<212> PRT
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<220>
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peptide

<400> 707
His Asp Cys Gly Pro Glu Met Glu Glu Tyr Tyr Leu Cys Pro
1 5 10

<210> 708
<211> 14
<212> PRT
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<220>
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peptide

<400> 708
Thr Asp Cys Gly Pro Glu Tyr Asp Glu Ser Ile Ile Cys Pro
1 5 10

<210> 709
<211> 14
<212> PRT
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<220>
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peptide

<400> 709
Val Leu Cys Trp Pro Asp Trp Glu Asp Tyr Ala Asp Cys Asn
1 5 10

<210> 710
<211> 14
<212> PRT
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<220>
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peptide

<400> 710
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1 5 10

<210> 711
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<220>
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peptide

<400> 711
Ile Tyr Cys Gly Pro Glu Leu Asp Glu Ser Ile Ala Cys Tyr
1 5 10

<210> 712
<211> 14
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<220>
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peptide

<400> 712
Asn Tyr Cys Gly Pro Glu Val Glu Glu Phe Asn Phe Cys His
1 5 10

<210> 713
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<220>

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peptide

<400> 713
Asp Val Cys Gly Pro Glu Ile Glu Glu Tyr Ser Phe Cys Ile
1 5 10

<210> 714
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<212> PRT
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<220>
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peptide

<400> 714
Asp Leu Cys Gly Pro Glu Val Glu Glu Ile Thr Asp Cys Ala
1 5 10

<210> 715
<211> 14
<212> PRT
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<220>
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peptide

<400> 715
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1 5 10

<210> 716
<211> 14
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<220>
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peptide

<400> 716
Pro Leu Cys Gly Pro Val Leu Glu Glu Asp Ile Tyr Cys Tyr
1 5 10

<210> 717
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peptide

<400> 717
Asp Leu Cys Gly Pro Glu Phe Glu Asp Ile Ile Asp Cys Asn
1 5 10

<210> 718
<211> 14
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peptide

<400> 718
Asp Tyr Cys Gly Pro Glu Val Glu Val Pro Ser Asn Cys Asn
1 5 10

<210> 719
<211> 14
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<220>
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peptide

<400> 719
Ile Ile Cys Gly Pro Glu Leu Asp Glu Ser Thr Ala Cys Asp
1 5 10

<210> 720
<211> 14
<212> PRT
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<220>
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peptide

<400> 720
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1   5   10

<210> 721
<211> 14
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<220>
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      peptide

<400> 721
Phe Asp Cys Gly Pro Glu Phe Asp Glu Ser Leu Tyr Cys Ser
1   5   10

<210> 722
<211> 14
<212> PRT
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<220>
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      peptide

<400> 722
Phe Ala Cys Trp Pro Asp Trp Glu Glu Val Tyr Ile Cys Tyr
1   5   10

<210> 723
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 723
Leu Tyr Cys Gly Pro Glu Phe Asp Glu Ser Leu Asp Cys Ser
1   5   10

<210> 724
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<212> PRT
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<220>
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peptide

<400> 724
Asp Leu Cys Gly Pro Glu Leu Glu Glu Ala Phe Leu Cys Ala
1 5 10

<210> 725
<211> 14
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<220>
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peptide

<400> 725
Phe Ala Cys Gly Pro Glu Leu Asp Glu Thr Leu Thr Cys Leu
1 5 10

<210> 726
<211> 14
<212> PRT
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<220>
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peptide

<400> 726
Phe Asp Cys Gly Pro Glu Val Glu Glu Ile Ser Asn Cys Asp
1 5 10

<210> 727
<211> 14
<212> PRT
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<220>
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peptide

<400> 727

Val His Cys Gly Pro Glu Leu Glu Tyr Pro Phe Asp Cys Asn
1 5 10

<210> 728
<211> 14
<212> PRT
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<220>
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<400> 728
Ala Tyr Cys Gly Pro Glu Phe Glu Glu His Thr Thr Cys Asn
1 5 10

<210> 729
<211> 14
<212> PRT
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<220>
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<400> 729
Leu Tyr Cys Gly Pro Val Ser Glu Gln Phe Thr Phe Cys Ile
1 5 10

<210> 730
<211> 14
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<400> 730
Asp Tyr Cys Gly Pro Glu Leu Asp Glu Ser Tyr Asp Cys Asn
1 5 10

<210> 731
<211> 14
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<220>
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peptide

<400> 731
Phe Tyr Cys Gly Pro Glu Trp Glu Glu Phe Asp Val Cys Ile
1 5 10

<210> 732
<211> 14
<212> PRT
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<220>
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peptide

<400> 732
Phe Thr Cys Gly Pro Glu Val Glu Glu Tyr Asp His Cys Ile
1 5 10

<210> 733
<211> 14
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<220>
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peptide

<400> 733
Tyr Asn Cys Gly Pro Glu Phe Asp Glu Ser Val Thr Cys Phe
1 5 10

<210> 734
<211> 14
<212> PRT
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<220>
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peptide

<400> 734
Ala Val Cys Gly Pro Glu Asn Asp Glu Ser Asn Ser Cys Ala
1 5 10

<210> 735
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 735
Ile Tyr Cys Trp Pro Asp Trp Glu Val Pro Asn Asp Cys Ala
1 5 10

<210> 736
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 736
Tyr Phe Cys Gly Pro Glu Phe Glu Glu Phe Phe His Cys Tyr
1 5 10

<210> 737
<211> 14
<212> PRT
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<220>
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<400> 737
Tyr Val Cys Gly Pro Asp Gly Asp Glu Ser Ser Phe Cys Asp
1 5 10

<210> 738
<211> 14
<212> PRT
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<220>

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peptide

<400> 738
Ile Ser Cys Gly Pro Glu Val Glu Glu Phe Phe Tyr Cys Tyr
1 5 10

<210> 739
<211> 14
<212> PRT
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<220>
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peptide

<400> 739
Leu Ile Cys Gly Pro Val Phe Glu Glu Asp Val Tyr Cys Asp
1 5 10

<210> 740
<211> 14
<212> PRT
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<220>
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peptide

<400> 740
Val Tyr Cys Gly Pro Glu Val Glu Asp His Asn Tyr Cys Ala
1 5 10

<210> 741
<211> 14
<212> PRT
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<220>
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peptide

<400> 741
Leu Asp Cys Gly Pro Glu Phe Glu Phe Val Tyr Ile Cys Ala
1 5 10

<210> 742
<211> 14
<212> PRT
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<220>
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peptide

<400> 742
Tyr Asp Cys Gly Pro Glu Phe Glu Glu Asp Leu Pro Cys Ile
1 5 10

<210> 743
<211> 14
<212> PRT
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<220>
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peptide

<400> 743
Asp Val Cys Gly Pro Glu Val Glu Glu Asp Tyr Tyr Cys Asp
1 5 10

<210> 744
<211> 14
<212> PRT
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<220>
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peptide

<400> 744
Asn Asp Cys Trp Pro Asp Trp Glu Tyr Asp Asn Val Cys Val
1 5 10

<210> 745
<211> 14
<212> PRT
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<220>
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peptide

<400> 745
Asp Leu Cys Gly Pro Glu Phe Glu Val Ala Asn Asp Cys Asn
1   5   10

<210> 746
<211> 14
<212> PRT
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<220>
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      peptide

<400> 746
His Asp Cys Gly Pro Glu Leu Asp Glu Ser Ile Ser Cys Asn
1   5   10

<210> 747
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 747
Leu Asp Cys Trp Pro Asp Trp Glu Glu Thr Thr His Cys Asp
1   5   10

<210> 748
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 748
Ile Ile Cys Gly Pro Glu Val Glu Glu Asp Asp Tyr Cys Leu
1   5   10

<210> 749
<211> 14

<212> PRT
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<220>
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peptide

<400> 749
Tyr Tyr Cys Trp Pro Asp Trp Glu Glu Val Ile Ile Cys Asp
1 5 10

<210> 750
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 750
Phe Asp Cys Gly Pro Glu Ile Asp Glu Tyr Thr Asn Cys Asn
1 5 10

<210> 751
<211> 14
<212> PRT
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<220>
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peptide

<400> 751
Ile Thr Cys Gly Pro Glu Leu Asp Glu Thr Ile Asn Cys Asp
1 5 10

<210> 752
<211> 14
<212> PRT
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<220>
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peptide

<400> 752

Asp Ser Cys Gly Pro Glu Val Glu Glu Asp Ile Tyr Cys Ile
1   5   10

<210> 753
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 753
Tyr Leu Cys Gly Pro Glu Phe Asp Glu Ser Gly Asn Cys His
1   5   10

<210> 754
<211> 14
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<220>
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      peptide

<400> 754
Asp Asn Cys Gly Pro Glu Leu Pro Glu Asp Tyr Phe Cys Asp
1   5   10

<210> 755
<211> 14
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<220>
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      peptide

<400> 755
Val Leu Cys Gly Pro Glu Phe Glu Glu Val Ser Asn Cys Asn
1   5   10

<210> 756
<211> 14
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<220>
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peptide

<400> 756
Val Asp Cys Trp Pro Asp Trp Glu Glu Asp Ile Val Cys Asp
1 5 10

<210> 757
<211> 14
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<220>
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peptide

<400> 757
Val Tyr Cys Trp Pro Asp Trp Glu Asp Asn Phe Pro Cys Tyr
1 5 10

<210> 758
<211> 14
<212> PRT
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<220>
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peptide

<400> 758
Asp Tyr Cys Gly Pro Glu Val Glu Glu His Phe Asn Cys His
1 5 10

<210> 759
<211> 14
<212> PRT
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<220>
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peptide

<400> 759
Ala Asp Cys Gly Pro Glu Ile Glu Glu Asp Ala Tyr Cys Tyr
1 5 10

<210> 760
<211> 14
<212> PRT
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<220>
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peptide

<400> 760
Ile Leu Cys Trp Pro Asp Trp Glu Asp Ala Thr Phe Cys Tyr
1 5 10

<210> 761
<211> 14
<212> PRT
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<220>
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peptide

<400> 761
Ile His Cys Trp Pro Asp Trp Glu Asp Phe Asn Ile Cys Pro
1 5 10

<210> 762
<211> 14
<212> PRT
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<220>
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peptide

<400> 762
Thr Ile Cys Gly Pro Glu Val Glu Asp Tyr Asn Asp Cys Ile
1 5 10

<210> 763
<211> 14
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<220>

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peptide

<400> 763
Asp Asp Cys Gly Pro Glu Leu Asp Glu Ser Val Ala Cys Ile
1 5 10

<210> 764
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 764
Asp Asp Cys Trp Pro Asp Trp Glu Asp His Ile Phe Cys Phe
1 5 10

<210> 765
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 765
Val Asn Cys Gly Pro Glu Val Glu Glu Ile Ile Phe Cys Asp
1 5 10

<210> 766
<211> 14
<212> PRT
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<220>
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peptide

<400> 766
Ile Phe Cys Trp Pro Asp Trp Glu Asp Asp Thr Val Cys Ile
1 5 10

<210> 767
<211> 14
<212> PRT
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<220>
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peptide

<400> 767
Ile Ile Cys Gly Pro Glu Phe Glu Glu Ile Ser Asp Cys Leu
1 5 10

<210> 768
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 768
Phe Asp Cys Gly Pro Glu Val Glu Glu Tyr Asn Asp Cys Asp
1 5 10

<210> 769
<211> 14
<212> PRT
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<220>
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peptide

<400> 769
Asn Asp Cys Gly Pro Glu Leu Asp Glu Thr Leu Tyr Cys Ile
1 5 10

<210> 770
<211> 14
<212> PRT
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<220>
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peptide

<400> 770
Ala Ile Cys Gly Pro Glu Leu Glu Glu Asp Ile Ser Cys Asn
1   5   10

<210> 771
<211> 14
<212> PRT
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<220>
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      peptide

<400> 771
His Leu Cys Gly Pro Glu Phe Asp Glu Ser Thr Asn Cys Tyr
1   5   10

<210> 772
<211> 14
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<220>
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      peptide

<400> 772
Ser Tyr Cys Gly Pro Glu Leu Asp Glu Ser Val Ala Cys Ile
1   5   10

<210> 773
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<220>
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      peptide

<400> 773
Leu Tyr Cys Gly Pro Glu Phe Glu Gln Leu Ala Asp Cys Thr
1   5   10

<210> 774
<211> 14

<212> PRT
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<220>
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peptide

<400> 774
Ile Asp Cys Gly Pro Glu Leu Asp Glu Ser Ile Ala Cys Asn
1 5 10

<210> 775
<211> 14
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<220>
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peptide

<400> 775
Phe Asp Cys Gly Pro Asp Gly Gln Glu Asp Leu Val Cys Asn
1 5 10

<210> 776
<211> 14
<212> PRT
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<220>
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peptide

<400> 776
Asn Leu Cys Gly Pro Glu Phe Glu Glu Phe Phe Asp Cys Tyr
1 5 10

<210> 777
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 777

Ser Ile Cys Gly Pro Glu Leu Gln Glu Asp Ile Val Cys Pro
1   5   10

<210> 778
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 778
Asn Pro Cys Gly Pro Glu Tyr Asp Glu Ser Ala His Cys Asp
1   5   10

<210> 779
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 779
Tyr Asp Cys Gly Pro Glu Leu Asp Glu Tyr Tyr Asn Cys Asn
1   5   10

<210> 780
<211> 14
<212> PRT
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<220>
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      peptide

<400> 780
Val Asp Cys Gly Pro Glu Leu Asp Glu Thr Ile Phe Cys Asp
1   5   10

<210> 781
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<220>
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peptide

<400> 781
Asp Asn Cys Gly Pro Glu Leu Asp Glu Ser Val Thr Cys Thr
1 5 10

<210> 782
<211> 14
<212> PRT
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<220>
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peptide

<400> 782
Val Asp Cys Gly Pro Glu Leu Asp Glu Ser Ser Tyr Cys Asp
1 5 10

<210> 783
<211> 14
<212> PRT
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<220>
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peptide

<400> 783
Tyr Tyr Cys Gly Pro Glu Phe Glu Phe Ile Asp Phe Cys Phe
1 5 10

<210> 784
<211> 14
<212> PRT
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<220>
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peptide

<400> 784
Tyr Asp Cys Trp Pro Asp Trp Glu Val Ile Thr Tyr Cys Asn
1 5 10

<210> 785
<211> 14
<212> PRT
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<220>
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peptide

<400> 785
Phe Asp Cys Gly Pro Glu Ile Glu Glu Asp Phe Phe Cys Val
1 5 10

<210> 786
<211> 14
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<220>
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peptide

<400> 786
Ile Phe Cys Trp Pro Asp Trp Asp Asp Ile Asn Phe Cys Asp
1 5 10

<210> 787
<211> 14
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<220>
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peptide

<400> 787
Asn Phe Cys Gly Pro Glu Leu Pro Glu Asp Ile Thr Cys Tyr
1 5 10

<210> 788
<211> 14
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<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 788
Ser Leu Cys Gly Pro Glu Phe Glu Glu Tyr Tyr His Cys Leu
1 5 10

<210> 789
<211> 14
<212> PRT
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<220>
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peptide

<400> 789
Ala Ser Cys Gly Pro Glu Leu Asp Glu Ser Leu Asp Cys Leu
1 5 10

<210> 790
<211> 14
<212> PRT
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<220>
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peptide

<400> 790
Ser Phe Cys Gly Pro Glu Arg Glu Trp Asp Leu Ala Cys Tyr
1 5 10

<210> 791
<211> 14
<212> PRT
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<220>
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peptide

<400> 791
His Leu Cys Gly Pro Glu Phe Glu Asp Val Leu Asp Cys Ile
1 5 10

<210> 792
<211> 14
<212> PRT
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<220>
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peptide

<400> 792
Leu Asp Cys Gly Pro Asp Gly Asp Glu Phe Tyr Tyr Cys Leu
1 5 10

<210> 793
<211> 14
<212> PRT
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<220>
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peptide

<400> 793
Asp Asn Cys Trp Pro Asp Trp Glu Glu Asp Ile Ala Cys Thr
1 5 10

<210> 794
<211> 14
<212> PRT
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<220>
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peptide

<400> 794
Ser Asp Cys Gly Pro Glu Leu Asp Glu Thr Ile His Cys Ile
1 5 10

<210> 795
<211> 14
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<220>
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peptide

<400> 795
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1   5   10

<210> 796
<211> 14
<212> PRT
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<220>
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      peptide

<400> 796
Asp Leu Cys Gly Pro Glu Leu Asp Glu Ser Thr Leu Cys Ile
1   5   10

<210> 797
<211> 14
<212> PRT
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<220>
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      peptide

<400> 797
Phe Asp Cys Gly Pro Glu Ser Asp Glu Ser Phe Asn Cys Tyr
1   5   10

<210> 798
<211> 14
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<220>
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      peptide

<400> 798
Asp Leu Cys Gly Pro Glu Phe Glu Glu Asp Asp Ile Cys Tyr
1   5   10

<210> 799
<211> 14

<212> PRT
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<220>
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peptide

<400> 799
His Ala Cys Gly Pro Glu Phe Glu Glu Asp Thr Tyr Cys Phe
1 5 10

<210> 800
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 800
Ser Asp Cys Gly Pro Glu Leu Asp Glu Ser Val Ala Cys Ile
1 5 10

<210> 801
<211> 14
<212> PRT
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<220>
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peptide

<400> 801
Ile Val Cys Gly Pro Glu Leu Pro Glu Asp Tyr Asn Cys Tyr
1 5 10

<210> 802
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 802

Asp Leu Cys Gly Pro Glu Phe Asp Glu Ser Phe Ile Cys Phe
1 5 10

<210> 803
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 803
Tyr Asp Cys Gly Pro Glu Phe Asp Glu Thr Leu Thr Cys Asn
1 5 10

<210> 804
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 804
Tyr Asp Cys Gly Pro Glu Val Glu Glu Ile Val Asn Cys Asp
1 5 10

<210> 805
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 805
Val Phe Cys Gly Pro Glu Ile Glu Asp Asp His Val Cys Ile
1 5 10

<210> 806
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 806
Phe Ile Cys Gly Pro Glu Trp Glu Asp Asp Tyr Ala Cys Ser
1 5 10

<210> 807
<211> 14
<212> PRT
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<220>
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peptide

<400> 807
Asn Phe Cys Gly Pro Glu Phe Asp Glu Ser Val Gly Cys Asn
1 5 10

<210> 808
<211> 14
<212> PRT
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<220>
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peptide

<400> 808
Asn Leu Cys Gly Pro Glu Val Glu Glu Ile Leu Ile Cys Asp
1 5 10

<210> 809
<211> 14
<212> PRT
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<220>
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peptide

<400> 809
Asp Ser Cys Gly Pro Glu Val Glu Glu Tyr Asp Leu Cys Asn
1 5 10

<210> 810
<211> 14
<212> PRT
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<220>
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peptide

<400> 810
Thr Leu Cys Gly Pro Glu Phe Glu Glu Ile Thr Asp Cys Asn
1 5 10

<210> 811
<211> 14
<212> PRT
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<220>
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peptide

<400> 811
Thr Val Cys Gly Pro Lys Met Glu Met Asn Ser Thr Cys Asp
1 5 10

<210> 812
<211> 14
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<220>
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peptide

<400> 812
Val His Cys Trp Pro Asp Trp Glu Asp Ala Val Ser Cys Asn
1 5 10

<210> 813
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<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 813
Asp Leu Cys Gly Pro Asp Gly Asn Glu Leu Asp Phe Cys Phe
1 5 10

<210> 814
<211> 14
<212> PRT
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<220>
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peptide

<400> 814
Asp Leu Cys Gly Pro Asp Gly Glu Glu His Tyr Tyr Cys Asp
1 5 10

<210> 815
<211> 14
<212> PRT
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<220>
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peptide

<400> 815
Phe Asn Cys Gly Pro Glu Val Glu Glu Ile Leu Leu Cys Thr
1 5 10

<210> 816
<211> 14
<212> PRT
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<220>
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peptide

<400> 816
His Tyr Cys Gly Pro Glu Val Glu Asn Ile Asn Asp Cys Ile
1 5 10

<210> 817
<211> 14
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<220>
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peptide

<400> 817
Ile Asp Cys Gly Pro Glu Leu Asp Glu Ser Val Ile Cys Asp
1 5 10

<210> 818
<211> 14
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<220>
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peptide

<400> 818
Ile Phe Cys Gly Pro Glu Ile Glu Gln Pro Ala Leu Cys Tyr
1 5 10

<210> 819
<211> 14
<212> PRT
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<220>
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peptide

<400> 819
Tyr Asp Cys Gly Pro Glu Phe Gln Glu Asp Leu Val Cys Pro
1 5 10

<210> 820
<211> 14
<212> PRT
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<220>
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peptide

<400> 820
His Ala Cys Trp Pro Asp Trp Glu Glu Pro Asn Tyr Cys Asp
1   5   10

<210> 821
<211> 14
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<220>
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      peptide

<400> 821
Asn Val Cys Trp Pro Asp Trp Glu Glu Asp Tyr Asn Cys Tyr
1   5   10

<210> 822
<211> 14
<212> PRT
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<220>
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      peptide

<400> 822
Ser Phe Cys Gly Gln Glu Leu Gly Asp Asn Tyr Asp Cys Ile
1   5   10

<210> 823
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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      peptide

<400> 823
Asp Asp Cys Gly Pro Glu Leu Asp Glu Thr Thr Val Cys Tyr
1   5   10

<210> 824
<211> 14

<212> PRT
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<220>
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peptide

<400> 824
Asn Phe Cys Gly Pro Glu Trp Glu Val Ala Thr Leu Cys Leu
1 5 10

<210> 825
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 825
Asp Leu Cys Gly Pro Glu Val Glu Glu Asp Thr Tyr Cys Asn
1 5 10

<210> 826
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 826
Ala Leu Cys Gly Pro Glu Val Glu Gln Val Asp Leu Cys Thr
1 5 10

<210> 827
<211> 14
<212> PRT
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<220>
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peptide

<400> 827

Asp Asp Cys Gly Pro Glu Leu Asp Glu Ser Val Asn Cys Asn
1 5 10

<210> 828
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 828
Ile Phe Cys Gly Pro Glu Phe Glu Gln Ile Ile Tyr Cys Asp
1 5 10

<210> 829
<211> 14
<212> PRT
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<220>
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<400> 829
Ser Asp Cys Trp Pro Asp Trp Glu Glu Val Tyr Tyr Cys Ser
1 5 10

<210> 830
<211> 14
<212> PRT
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<220>
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<400> 830
Phe Phe Cys Gly Pro Asp Gly Asp Glu Val Ala Ile Cys Asp
1 5 10

<210> 831
<211> 14
<212> PRT
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<220>
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peptide

<400> 831
Asp Asp Cys Trp Pro Asp Trp Glu Asp Asp Val Tyr Cys Tyr
1 5 10

<210> 832
<211> 14
<212> PRT
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<220>
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peptide

<400> 832
Tyr Asp Cys Gly Pro Glu Phe Asp Glu Thr Val Val Cys Pro
1 5 10

<210> 833
<211> 14
<212> PRT
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<220>
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peptide

<400> 833
Ser Tyr Cys Gly Pro Glu Leu Asp Glu Ser Val Asn Cys Val
1 5 10

<210> 834
<211> 14
<212> PRT
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<220>
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peptide

<400> 834
Ala Phe Cys Val Ser Phe Gln Gln Ser Leu Pro His Cys Asp
1 5 10

<210> 835
<211> 14
<212> PRT
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<220>
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peptide

<400> 835
Val Asn Cys Gly Pro Glu Val Glu Glu Tyr Phe Val Cys Phe
1 5 10

<210> 836
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 836
Thr Asn Cys Trp Pro Asp Trp Glu Glu Asp Phe Ala Cys Val
1 5 10

<210> 837
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 837
Asp Asp Cys Gly Pro Glu Phe Glu Glu Ile Ile Leu Cys Phe
1 5 10

<210> 838
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 838
Asn Ser Cys Gly Pro Glu Leu Glu Asp Tyr His Leu Cys Pro
1 5 10

<210> 839
<211> 14
<212> PRT
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<220>
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peptide

<400> 839
Ile His Cys Gly Pro Asp Ser Asp Gly Phe Asp Phe Cys Asp
1 5 10

<210> 840
<211> 14
<212> PRT
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<220>
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peptide

<400> 840
Phe Asp Cys Gly Pro Glu Leu Glu Glu Asp His Leu Cys Phe
1 5 10

<210> 841
<211> 14
<212> PRT
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<220>
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peptide

<400> 841
Thr Val Cys Trp Pro Asp Phe Glu Glu Tyr Ala Asp Cys Asp
1 5 10

<210> 842
<211> 14
<212> PRT
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<220>
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peptide

<400> 842
Tyr Phe Cys Trp Pro Asp Trp Glu Glu Ala Ala Asp Cys Leu
1 5 10

<210> 843
<211> 14
<212> PRT
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<220>
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peptide

<400> 843
Val Ser Cys Gly Pro Glu Phe Asp Glu Ser Val Asp Cys Ile
1 5 10

<210> 844
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 844
Ala Val Cys Gly Pro Glu Leu Pro Glu Asp Ile Val Cys Tyr
1 5 10

<210> 845
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 845
Val Leu Cys Gly Pro Glu Val Glu Glu Tyr His Leu Cys Ala
1   5   10

<210> 846
<211> 14
<212> PRT
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<220>
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      peptide

<400> 846
Ser Leu Cys Trp Pro Asp Trp Glu Glu Val Asp Asn Cys Phe
1   5   10

<210> 847
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 847
Thr Ile Cys Gly Pro Asp Gly Gln Glu Asp Tyr Asn Cys His
1   5   10

<210> 848
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 848
Phe Leu Cys Gly Pro Glu Gly Glu Pro Thr Tyr Leu Cys Thr
1   5   10

<210> 849
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 849
Asp Asp Cys Trp Leu Glu Gln His Asp Ile Tyr Val Cys Ala
1 5 10

<210> 850
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 850
Ile Phe Cys Gly Pro Glu Val Glu Glu Val Ala Phe Cys Phe
1 5 10

<210> 851
<211> 14
<212> PRT
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<220>
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peptide

<400> 851
Ala Leu Cys Gly Pro Glu Val Glu Asp Asp Tyr Asp Cys Leu
1 5 10

<210> 852
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 852

Asp Asp Cys Gly Pro Glu Ile Glu Leu Tyr Leu Thr Cys Ala
1   5   10

<210> 853
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 853
Thr Asp Cys Trp Pro Asp Trp Glu Asp Asp Ser Ile Cys Asp
1   5   10

<210> 854
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 854
Ser Ile Cys Gly Pro Glu Leu Glu Glu Ile Phe Leu Cys Asn
1   5   10

<210> 855
<211> 14
<212> PRT
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<220>
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      peptide

<400> 855
Asn Asp Cys Gly Pro Glu Leu Glu Glu Asp Ile Leu Cys Phe
1   5   10

<210> 856
<211> 14
<212> PRT
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<220>
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peptide

<400> 856
Asp Asp Cys Gly Pro Glu Leu Asp Glu Thr Tyr Ser Cys Tyr
1 5 10

<210> 857
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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peptide

<400> 857
Phe Val Cys Gly Pro Glu Trp Glu Glu Ile Asp Leu Cys Ile
1 5 10

<210> 858
<211> 14
<212> PRT
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<220>
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peptide

<400> 858
Tyr Asp Cys Gly Pro Glu Leu Asp Glu Ser Leu Ser Cys Pro
1 5 10

<210> 859
<211> 14
<212> PRT
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<220>
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peptide

<400> 859
Asn Leu Cys Gly Pro Glu Leu Asp Glu Ser Ile Ile Cys Pro
1 5 10

<210> 860
<211> 14
<212> PRT
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<220>
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peptide

<400> 860
Ile Asp Cys Trp Pro Asp Trp Glu Glu Phe Asn Asn Cys Phe
1 5 10

<210> 861
<211> 14
<212> PRT
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<220>
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peptide

<400> 861
Ala Tyr Cys Gly Pro Glu Leu Glu Glu His Asp Tyr Cys Tyr
1 5 10

<210> 862
<211> 14
<212> PRT
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<220>
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peptide

<400> 862
Asp Asp Cys Ser Pro Gln Phe Asp Gln Ile Asp Leu Cys Asp
1 5 10

<210> 863
<211> 14
<212> PRT
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<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 863
Ser Tyr Cys Gly Pro Glu Ser Asp Glu Ser Ile Tyr Cys Tyr
1 5 10

<210> 864
<211> 14
<212> PRT
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<220>
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peptide

<400> 864
Ser Leu Cys Gly Pro Glu Phe Gln Glu Asp Ala Pro Cys Asn
1 5 10

<210> 865
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 865
Asp Ala Cys Gly Pro Glu Leu Asp Glu Thr Thr His Cys Asp
1 5 10

<210> 866
<211> 14
<212> PRT
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<220>
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peptide

<400> 866
Asn Asp Cys Gly Pro Glu Val Glu Glu Val Ala Asp Cys Phe
1 5 10

<210> 867
<211> 14
<212> PRT
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<220>
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peptide

<400> 867
Tyr Ile Cys Gly Pro Glu Phe Glu Gln Asp Tyr Phe Cys Phe
1 5 10

<210> 868
<211> 14
<212> PRT
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<220>
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peptide

<400> 868
Thr Asp Cys Gly Pro Asp Gly Asp Glu Thr Asn Tyr Cys Phe
1 5 10

<210> 869
<211> 14
<212> PRT
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<220>
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peptide

<400> 869
Tyr Asp Cys Gly Pro Glu Val Asp Glu Ser Val Leu Cys Pro
1 5 10

<210> 870
<211> 14
<212> PRT
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<220>
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peptide

<400> 870
Ile Asp Cys Gly Pro Glu Phe Asp Glu Ser Ala Tyr Cys Thr
1   5   10

<210> 871
<211> 14
<212> PRT
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<220>
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      peptide

<400> 871
Phe Asp Cys Gly Pro Glu Phe Glu Glu Phe Phe His Cys Tyr
1   5   10

<210> 872
<211> 14
<212> PRT
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<220>
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      peptide

<400> 872
Phe Pro Cys Gly Pro Glu Ile Glu Glu Tyr Asp Tyr Cys Val
1   5   10

<210> 873
<211> 14
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<220>
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      peptide

<400> 873
Ala Asp Cys Gly Pro Ile Phe Glu Ser Ile Asp Ile Cys Val
1   5   10

<210> 874
<211> 14

<212> PRT
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<220>
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peptide

<400> 874
Ile Ser Cys Gly Pro Asp Leu Trp Pro Thr Asp Ile Cys Thr
1 5 10

<210> 875
<211> 14
<212> PRT
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<220>
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peptide

<400> 875
Asp Asp Cys Gly Pro Asp Gly Asp Glu Val His Thr Cys Asn
1 5 10

<210> 876
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 876
Ile Asp Cys Trp Pro Asp Trp Glu Gly Ser Phe Ala Cys Asn
1 5 10

<210> 877
<211> 14
<212> PRT
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<220>
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peptide

<400> 877

Leu Asn Cys Gly Pro Asp Gly Asp Glu Thr Phe Tyr Cys Asp
1   5   10

<210> 878
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 878
Ile His Cys Gly Pro Glu Leu Gly Ala Tyr Ile Ser Cys Ser
1   5   10

<210> 879
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 879
Thr Ile Cys Trp Pro Asp Trp Glu Glu Asp Tyr Phe Cys Tyr
1   5   10

<210> 880
<211> 14
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<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 880
His Ser Cys Leu Ala Gln Phe Asp Gln Asp Leu Val Cys Ile
1   5   10

<210> 881
<211> 14
<212> PRT
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<220>
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peptide

<400> 881
Asn Asn Cys Ala Ser Asp Leu Ser Glu Asp Asn Ser Cys Ile
1 5 10

<210> 882
<211> 14
<212> PRT
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<220>
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peptide

<400> 882
Val Asn Cys Trp Pro Asp Trp Glu Glu Asp Val Ala Cys Asn
1 5 10

<210> 883
<211> 14
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<220>
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peptide

<400> 883
Val Tyr Cys Gly Pro Glu Leu Asp Glu Ser Phe Tyr Cys Phe
1 5 10

<210> 884
<211> 14
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<220>
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peptide

<400> 884
Leu Phe Cys Gly Thr Val Leu Asp Glu Phe Phe Asp Cys Asp
1 5 10

<210> 885
<211> 14
<212> PRT
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<220>
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peptide

<400> 885
Phe Asp Cys Gly Pro Glu Leu Asp Glu Ser Val Ser Cys Ala
1 5 10

<210> 886
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 886
Tyr Tyr Cys Gly Pro Glu Val Glu Glu Asn Val Tyr Cys Ile
1 5 10

<210> 887
<211> 14
<212> PRT
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<220>
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peptide

<400> 887
Asp Tyr Cys Gly Pro Glu Leu Asp Asp Ser Thr Ile Cys His
1 5 10

<210> 888
<211> 14
<212> PRT
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<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 888
Val Phe Cys Gly Pro Gln Trp Ala Glu Ala Asn Ala Cys Phe
1 5 10

<210> 889
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<220>
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peptide

<400> 889
Phe Thr Cys Gly Pro Glu Tyr Asp Glu Ser Ile Thr Cys Pro
1 5 10

<210> 890
<211> 14
<212> PRT
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<220>
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peptide

<400> 890
Leu Asn Cys Gly Pro Val Asn Asp Glu Ser Ser Val Cys Ile
1 5 10

<210> 891
<211> 14
<212> PRT
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<220>
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peptide

<400> 891
Ala Ile Cys Trp Pro Asp Trp Glu Glu Phe Ser Asp Cys His
1 5 10

<210> 892
<211> 14
<212> PRT
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<220>
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peptide

<400> 892
Tyr Tyr Cys Gly Val Asp Leu Gly Ala Asn Val Tyr Cys Tyr
1 5 10

<210> 893
<211> 14
<212> PRT
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<220>
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peptide

<400> 893
His Tyr Cys Gly Pro Glu Val Glu Glu Asp Tyr His Cys Asp
1 5 10

<210> 894
<211> 14
<212> PRT
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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 894
Asn Asp Cys Gly Ser Leu Gln Tyr Asp Ile Pro Thr Cys Val
1 5 10

<210> 895
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 895
Tyr Val Cys Arg Pro Gln Leu Asp Val Tyr His Tyr Cys Asn
1   5   10

<210> 896
<211> 14
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 896
His Asp Cys Gly Pro Asp Gly Asp Glu Ser Ile Ile Cys Ser
1   5   10

<210> 897
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 897
Phe Asp Cys Gly Pro Glu Leu Asp Glu Thr Ile Ile Cys Pro
1   5   10

<210> 898
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 898
Val Asp Cys Gly Ser Asp Arg Gly Glu Asn Ala Ala Cys His
1   5   10

<210> 899
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 899
Asn Ile Cys Leu Ala Gln Phe Asn Glu Asp Pro Thr Cys Asn
1 5 10

<210> 900
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 900
Thr Asn Cys Gly Ser Lys Ser Gln Val Ser Asp His Cys Ile
1 5 10

<210> 901
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 901
Asn His Cys His Pro Gln Phe Trp Glu Leu Thr Asn Cys Asn
1 5 10

<210> 902
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 902

Leu Leu Cys His Pro Gln Gly Asp Leu Tyr His Leu Cys His
1 5 10

<210> 903
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 903
Thr Asn Cys Asp Ser Lys Leu Glu Gly Asp Asp Asn Cys Phe
1 5 10

<210> 904
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 904
Asn Asp Cys Gly Pro Glu Met Asp Glu Ser Leu Leu Cys Asp
1 5 10

<210> 905
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 905
Phe His Cys Gly Pro Glu Val Asp Glu Ser Ile Asn Cys Asn
1 5 10

<210> 906
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 906
Asp Phe Cys Gly Pro Asp Gly Asp Glu Thr Tyr Val Cys Ser
1 5 10

<210> 907
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 907
Val Ser Cys Gly Pro Gln Phe Asp Glu Asn Asn Thr Cys Asn
1 5 10

<210> 908
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 908
Val Tyr Cys His Leu Glu Ser Glu Gln Phe Asp Ile Cys Ile
1 5 10

<210> 909
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 909
Asp Asp Cys Gly Pro Glu Trp Glu Phe Val Phe Phe Cys Asp
1 5 10

<210> 910
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 910
Tyr Asn Cys Glu Gln Gln Gln Asp Glu Asp Pro Ser Cys Ile
1 5 10

<210> 911
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 911
Asn Thr Cys Gly Thr Glu Gln His Glu Phe Asn Gly Cys Leu
1 5 10

<210> 912
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 912
His Pro Cys Gln Pro Gly Phe Glu Glu Val Asp Tyr Cys Val
1 5 10

<210> 913
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 913
Val Ala Cys Ser Arg Gln Leu Gly Glu Asp Ala Tyr Cys Asn
1 5 10

<210> 914
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 914
Asp Ile Cys Gly Ala Gln Glu Val His Val Tyr Thr Cys Pro
1 5 10

<210> 915
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 915
Phe Phe Cys Glu Gly Asn Leu Asp Ala Tyr Leu Leu Cys Leu
1 5 10

<210> 916
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 916
Tyr Tyr Cys Gly Pro Asp Gly Glu Glu Asn Ile Val Cys Asp
1 5 10

<210> 917
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 917
Gly Ser Gly Gly Ser
1 5

<210> 918
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 918
Gly Gly Gly Ser
1

<210> 919
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 919
Gly Gly Gly Gly Ser
1 5

<210> 920
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 920
Gly Ser Ser Gly Gly Ser
1   5

<210> 921
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 921
Gly Gly Gly Gly Ser Gly Gly Gly Ser
1   5

<210> 922
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> SITE
<222> (1)..(9)
<223> This sequence may encompass 1-3 "Gly Gly Ser"
      repeating units

<400> 922
Gly Gly Ser Gly Gly Ser Gly Gly Ser
1   5

<210> 923
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 923
Gly Gly Gly Gly Ser Leu Ser Gly Arg Ser Asp Asn His Gly Ser Ser
1   5   10   15

Gly Thr

<210> 924
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 924
Gly Gly Gly Gly Ser Ser Gly Gly Ser Gly Gly Ser Gly Leu Ser Gly
1   5   10   15

Arg Ser Asp Asn His Gly Ser Ser Gly Thr
            20   25

<210> 925
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 925
Ala Ser Gly Arg Ser Asp Asn His
1   5

<210> 926
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 926
Leu Ala Gly Arg Ser Asp Asn His
1   5

<210> 927
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 927
Ile Ser Ser Gly Leu Ala Ser Gly Arg Ser Asp Asn His
1   5   10

<210> 928
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 928
Ile Ser Ser Gly Leu Leu Ala Gly Arg Ser Asp Asn His
1   5   10

<210> 929
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 929
Leu Ser Gly Arg Ser Asp Asn His
1   5

<210> 930
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 930
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn Pro
1 5 10

<210> 931
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 931
Ile Ser Ser Gly Leu Leu Ser Gly Arg Ser Asp Asn His
1 5 10

<210> 932
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 932
Leu Ser Gly Arg Ser Asp Asn His Ser Pro Leu Gly Leu Ala Gly Ser
1 5 10 15

<210> 933
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 933
Ser Pro Leu Gly Leu Ala Gly Ser Leu Ser Gly Arg Ser Asp Asn His

1 5 10 15

<210> 934
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 934
Ser Pro Leu Gly Leu Ser Gly Arg Ser Asp Asn His
1 5 10

<210> 935
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 935
Leu Ala Gly Arg Ser Asp Asn His Ser Pro Leu Gly Leu Ala Gly Ser
1 5 10 15

<210> 936
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 936
Leu Ser Gly Arg Ser Asp Asn His Val Pro Leu Ser Leu Lys Met Gly
1 5 10 15

<210> 937
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 937
Leu Ser Gly Arg Ser Asp Asn His Val Pro Leu Ser Leu Ser Met Gly
1 5 10 15

<210> 938
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(6)
<223> This sequence may encompass 1-3 "Gly Ser"
repeating units

<400> 938
Gly Ser Gly Ser Gly Ser
1 5

<210> 939
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(15)
<223> This sequence may encompass 1-3 "Gly Ser Gly Gly Ser"
repeating units

<400> 939
Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser
1 5 10 15

<210> 940
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(12)
<223> This sequence may encompass 1-3 "Gly Gly Gly Ser"
repeating units

<400> 940
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10

<210> 941
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> SITE
<222> (1)..(15)
<223> This sequence may encompass 1-3 "Gly Gly Gly Gly Ser"
repeating units

<400> 941
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 942
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<220>
<221> SITE
<222> (1)..(18)
<223> This sequence may encompass 1-3 "Gly Ser Ser Gly Gly Ser" repeating units

<400> 942
Gly Ser Ser Gly Gly Ser Gly Ser Ser Gly Gly Ser Gly Ser Ser Gly
1 5 10 15

Gly Ser

<210> 943
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 943
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ile Ser Ser Gly Leu
1 5 10 15

Leu Ser Gly Arg Ser Asp Asn His Gly Gly Gly Ser
20 25