US 20250255955A1

(19) United States
(12) Patent Application Publication
BURKOVITZ et al.

(10) Pub. No.: US 2025/0255955 A1
(43) Pub. Date: Aug. 14, 2025

(54) **DUAL FUNCTION ANTIGEN BINDING MOLECULES**

(71) Applicant: **TROJAN BIO LTD.**, Ganei Tikva (IL)

(72) Inventors: **Anat BURKOVITZ**, Ganei Tikva (IL); **Noam C. DIAMANT**, Ein Vered (IL); **Amir AHARONI**, Beit Kama (IL)

(21) Appl. No.: **18/702,391**

(22) PCT Filed: **Oct. 18, 2022**

(86) PCT No.: **PCT/IL2022/051102**

§ 371 (c)(1),
(2) Date: **Apr. 18, 2024**

(30) **Foreign Application Priority Data**

Oct. 18, 2021 (IL) 287372

Publication Classification

(51) **Int. Cl.**

A61K 39/385	(2006.01)
A61K 39/00	(2006.01)
A61K 39/12	(2006.01)
A61P 35/00	(2006.01)
C07K 14/005	(2006.01)
C07K 16/28	(2006.01)
C07K 16/46	(2006.01)
C12N 7/00	(2006.01)

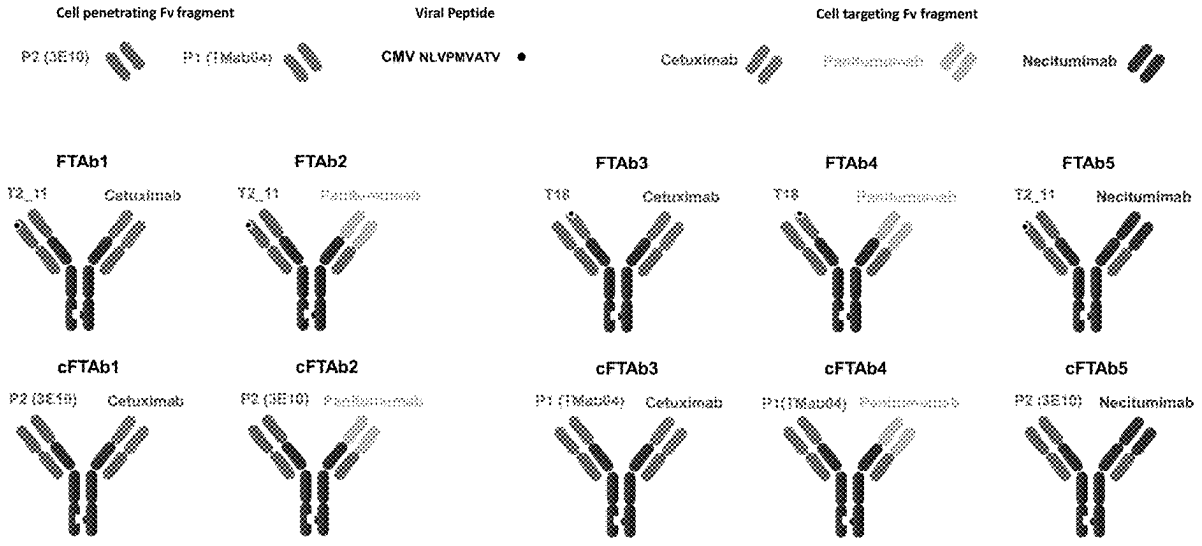
(52) **U.S. Cl.**

CPC ***A61K 39/385*** (2013.01); ***A61K 39/12*** (2013.01); ***A61P 35/00*** (2018.01); ***C07K 14/005*** (2013.01); ***C07K 16/2863*** (2013.01); ***C07K 16/46*** (2013.01); ***C12N 7/00*** (2013.01); *A61K 2039/6056* (2013.01); *C07K 2317/565* (2013.01); *C12N 2710/16122* (2013.01); *C12N 2710/16134* (2013.01); *C12N 2710/16222* (2013.01); *C12N 2710/16234* (2013.01); *C12N 2760/16121* (2013.01); *C12N 2760/16134* (2013.01); *C12N 2770/20011* (2013.01); *C12N 2770/20034* (2013.01)

(57) **ABSTRACT**

Antibodies or antigen binding fragments thereof comprising at least one immunogenic peptide inserted into a variable region of the antibody or antigen binding fragment thereof, wherein the insertion comprises removal of antibody or antigen binding fragment sequence are provided. Dual-function antigen binding molecules comprising an antibody or antigen binding fragment of the invention and a second antibody or antigen binding fragment thereof capable of binding an antigen overexpressed on a target cell are provided. Nucleic acid molecules encoding same, pharmaceutical compositions comprising same and methods of treating cancer by administrating same are also provided. Methods of producing antibodies or antigen binding fragments are also provided.

Specification includes a Sequence Listing.



continued

Figure 1

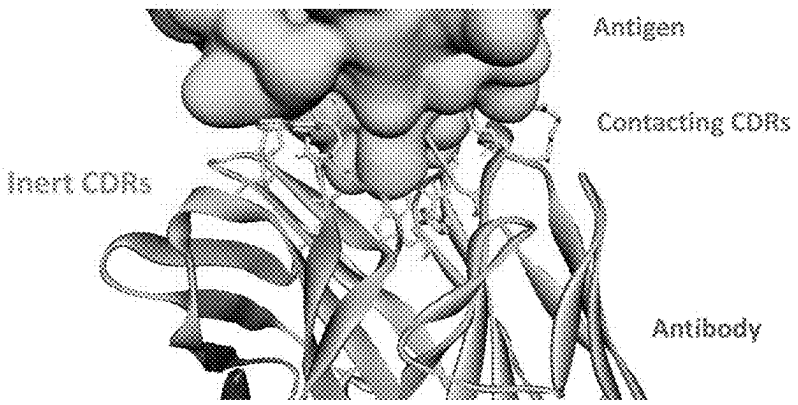
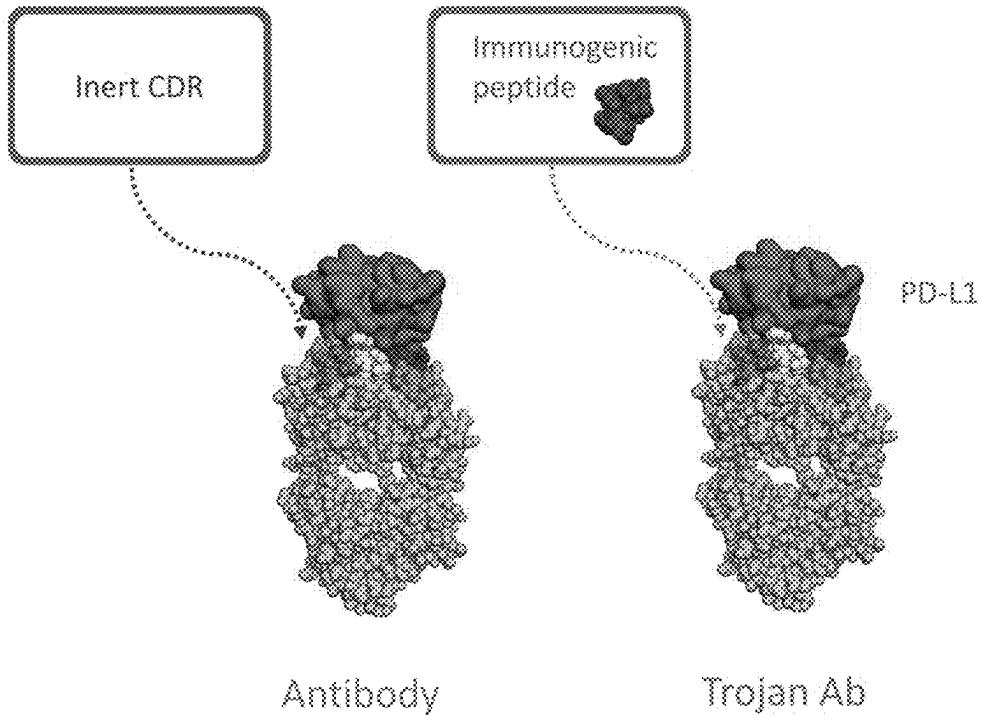


Figure 2



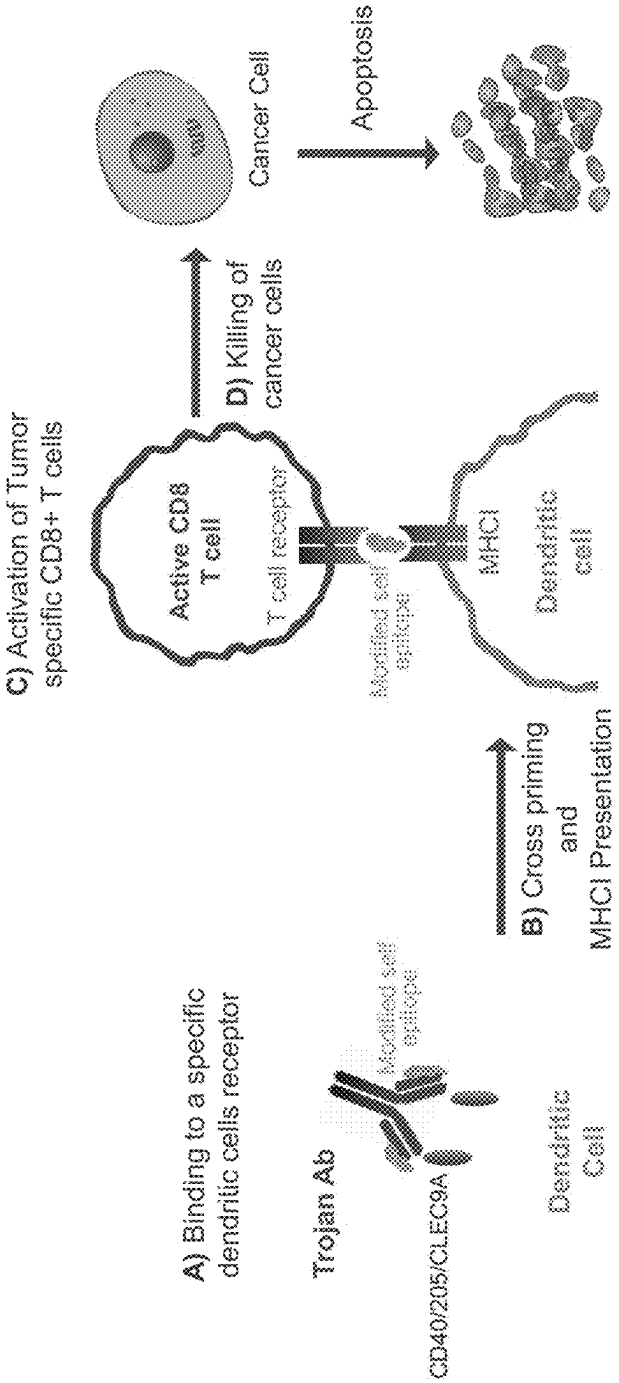

A) Binding to a specific dendritic cells receptor
Trojan Ab
Modified self epitope
CD40/205/CLEC9A
Dendritic Cell
B) Cross priming and MHCI Presentation
Modified self epitope
MHCI
Dendritic cell
C) Activation of Tumor specific CD8+ T cells
Active CD8 T cell
T cell receptor
D) Killing of cancer cells
Cancer Cell
Apoptosis

Figure 3

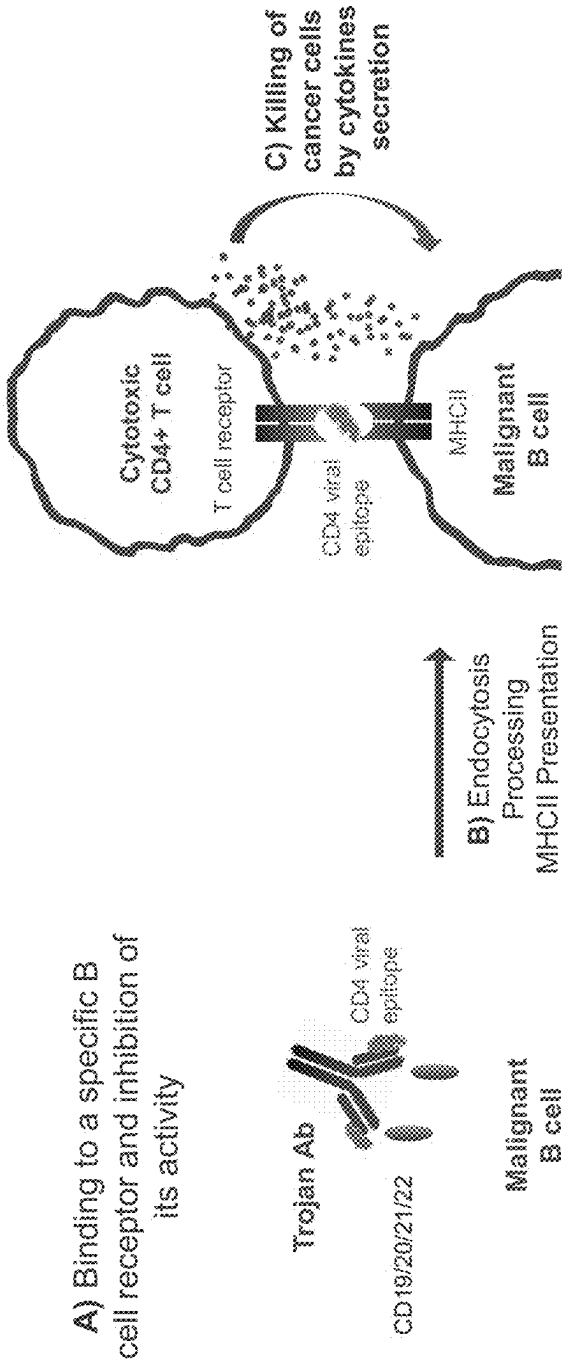

A) Binding to a specific B cell receptor and inhibition of its activity
Trojan Ab
CD19/20/21/22
CD4 viral epitope
Malignant B cell
B) Endocytosis Processing MHCII Presentation
Cytotoxic CD4+ T cell
T cell receptor
CD4 viral epitope
MHCII
Malignant B cell
C) Killing of cancer cells by cytokines secretion

Figure 4

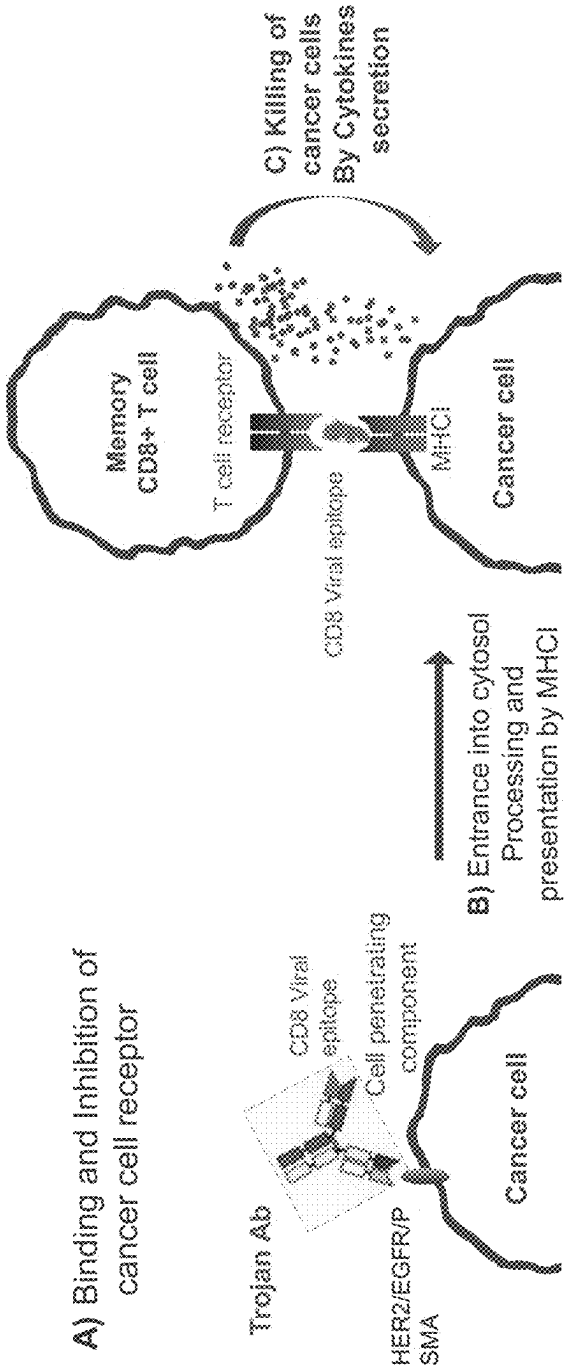

A) Binding and Inhibition of cancer cell receptor
Trojan Ab
CD8 Viral epitope
Cell penetrating component
HER2/EGFR/P SMA
Cancer cell
B) Entrance into cytosol Processing and presentation by MHCI
Memory CD8+ T cell
T cell receptor
CD8 Viral epitope
MHCI
Cancer cell
C) Killing of cancer cells By Cytokines secretion

Figure 5

Figure 6

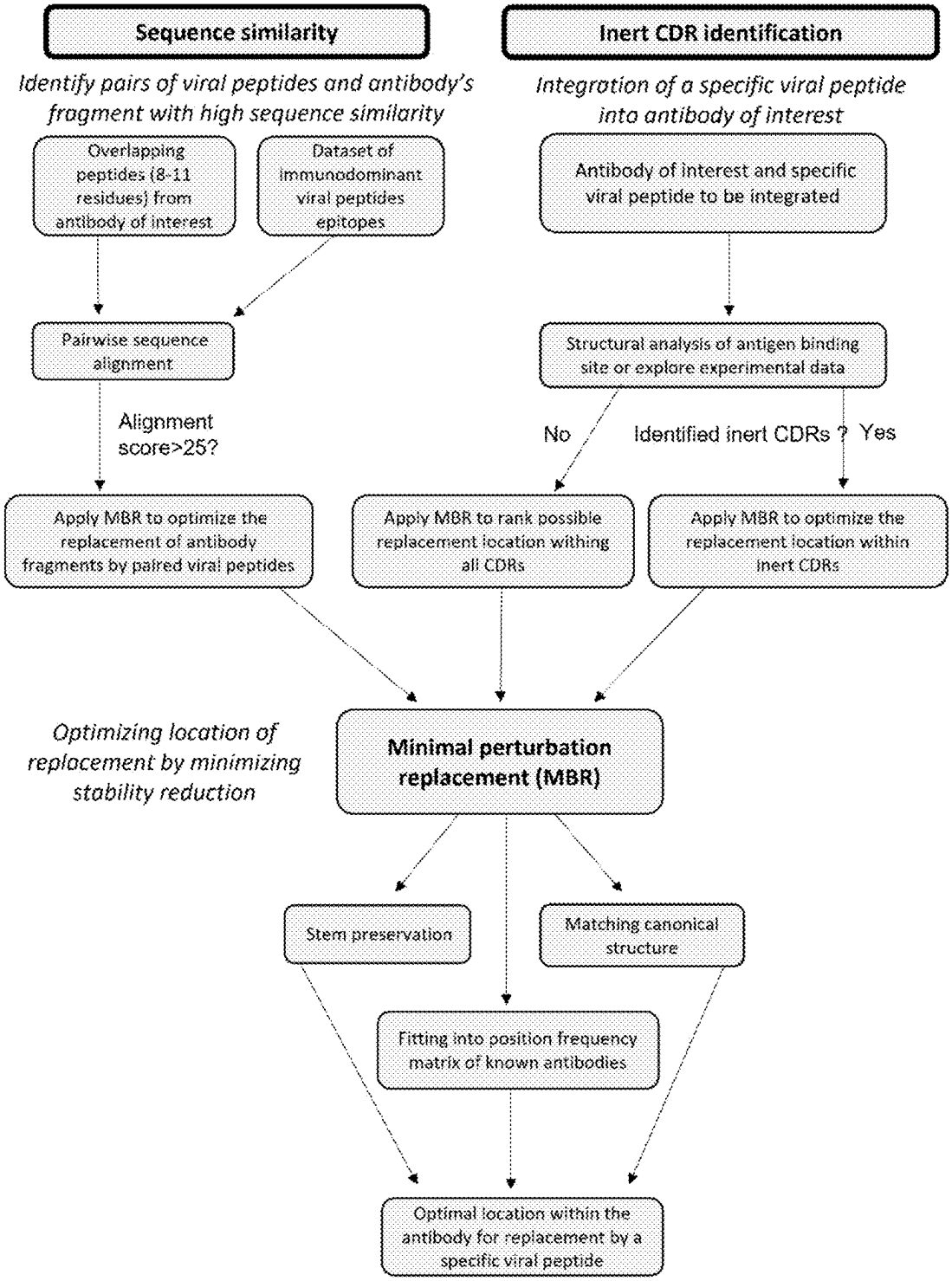

Sequence similarity
Inert CDR identification
Identify pairs of viral peptides and antibody's fragment with high sequence similarity
Integration of a specific viral peptide into antibody of interest
Overlapping peptides (8-11 residues) from antibody of interest
Dataset of immunodominant viral peptides epitopes
Antibody of interest and specific viral peptide to be integrated
Pairwise sequence alignment
Structural analysis of antigen binding site or explore experimental data
Alignment score>25?
No
Identified inert CDRs ?
Yes
Apply MBR to optimize the replacement of antibody fragments by paired viral peptides
Apply MBR to rank possible replacement location withing all CDRs
Apply MBR to optimize the replacement location within inert CDRs
Optimizing location of replacement by minimizing stability reduction
Minimal perturbation replacement (MBR)
Stem preservation
Matching canonical structure
Fitting into position frequency matrix of known antibodies
Optimal location within the antibody for replacement by a specific viral peptide

Figure 7A

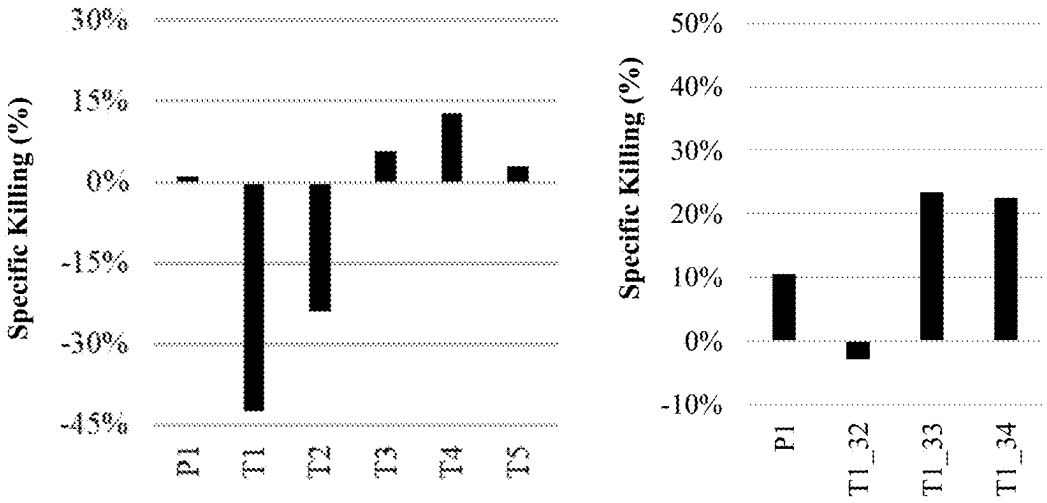


Figure 7B

Figure 7C

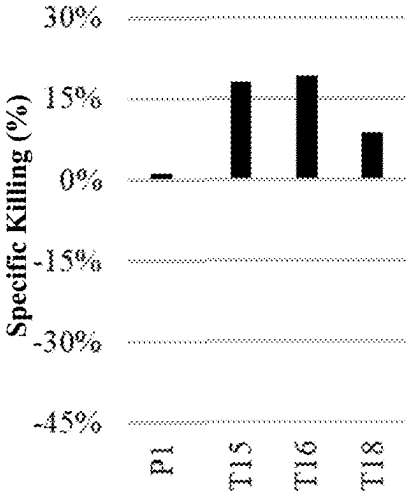


Figure 8

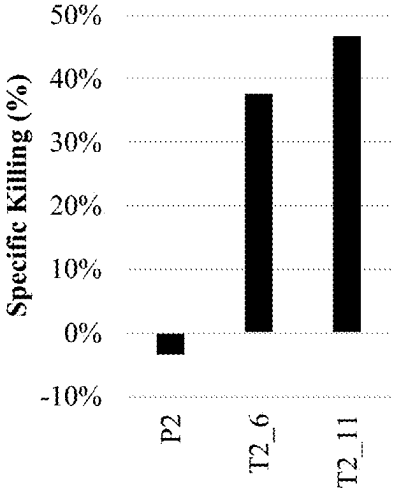


Figure 9A

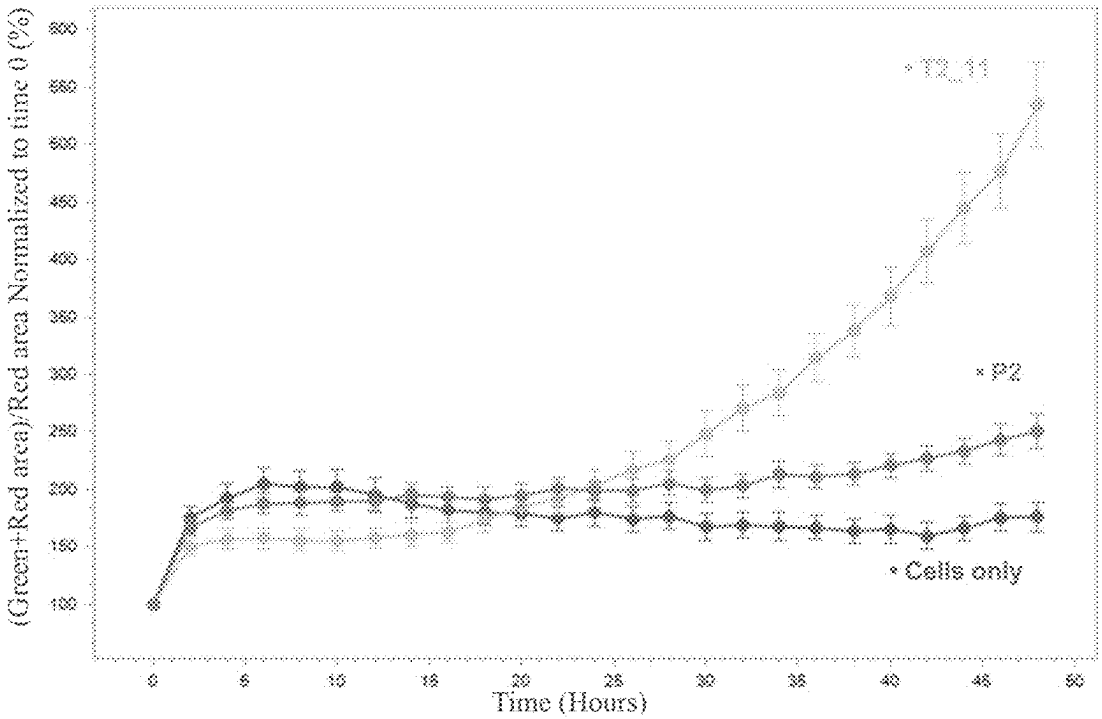
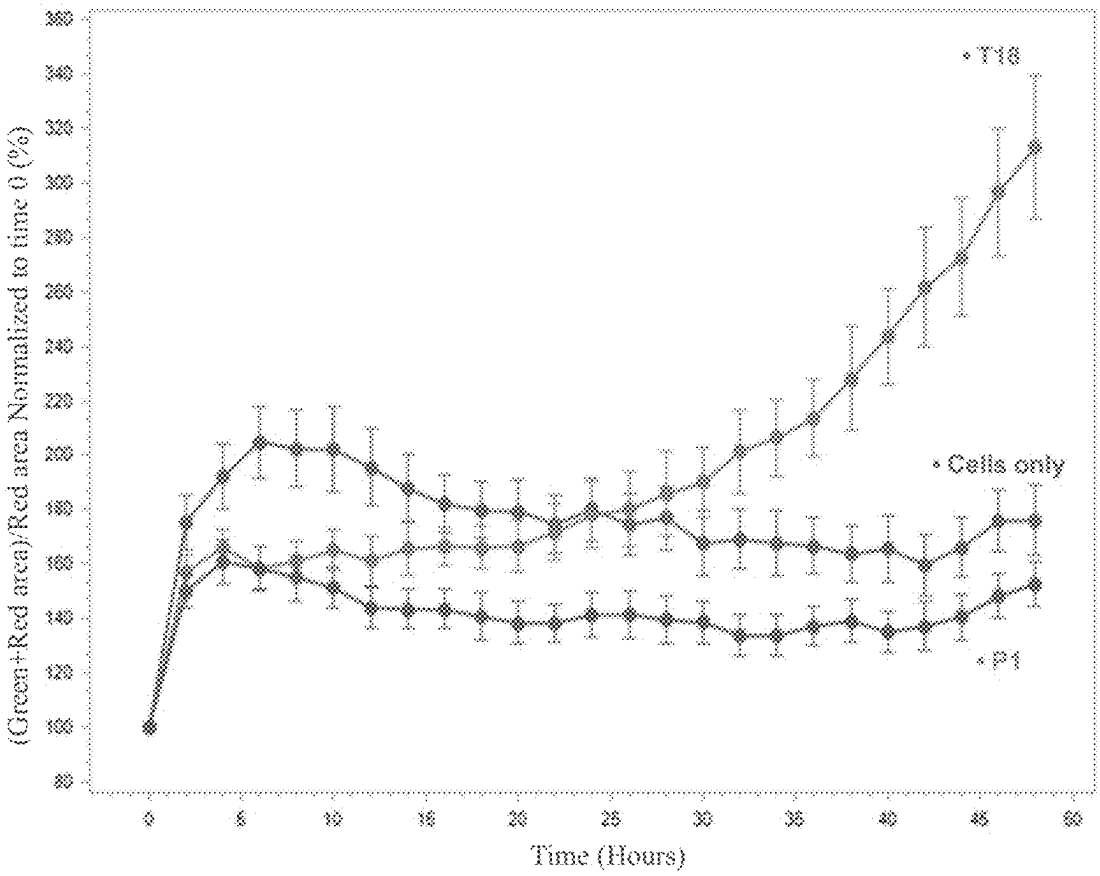


Figure 9B



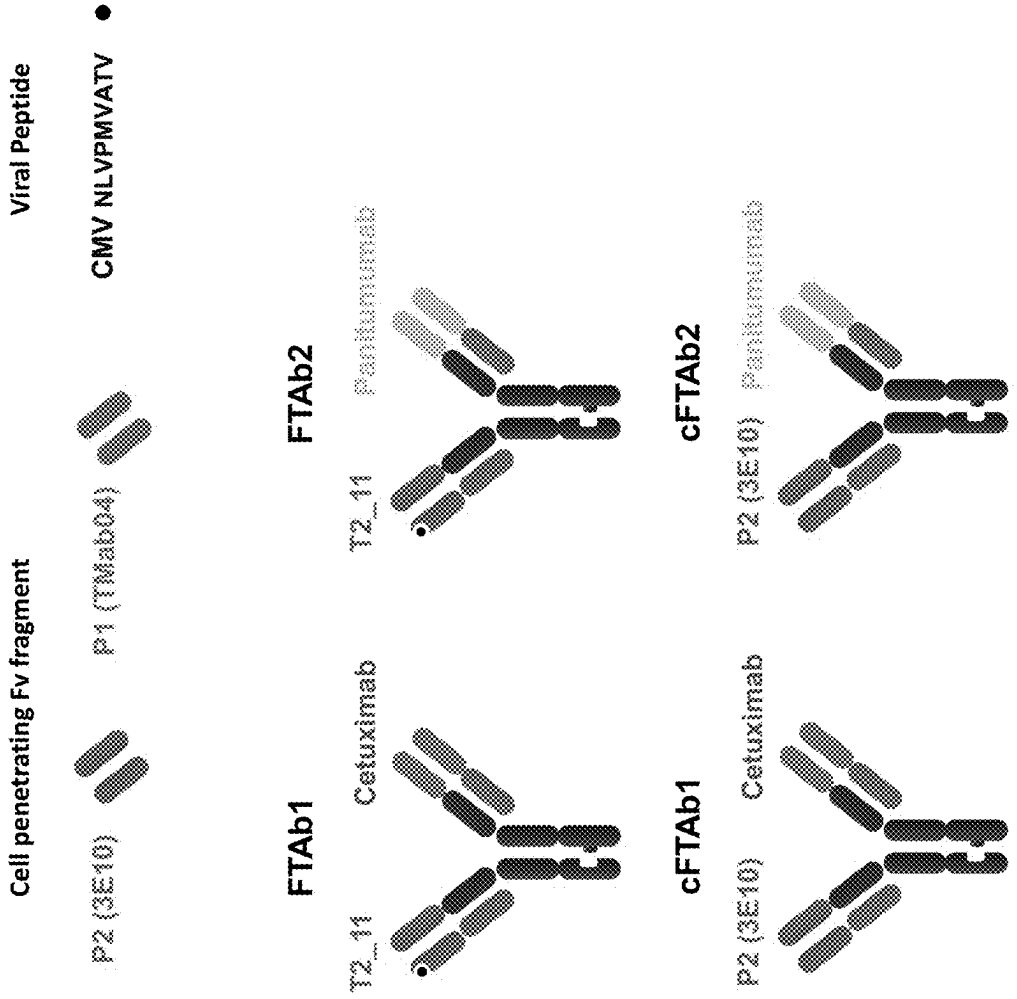

Cell penetrating Fv fragment
P2 (3E10)
P1 (TMab04)
Viral Peptide
CMV NLVPMVATV
FTAb1
T2_11
Cetuximab
FTAb2
T2_11
Panitumumab
cFTAb1
P2 (3E10)
Cetuximab
cFTAb2
P2 (3E10)
Panitumumab

Figure 10

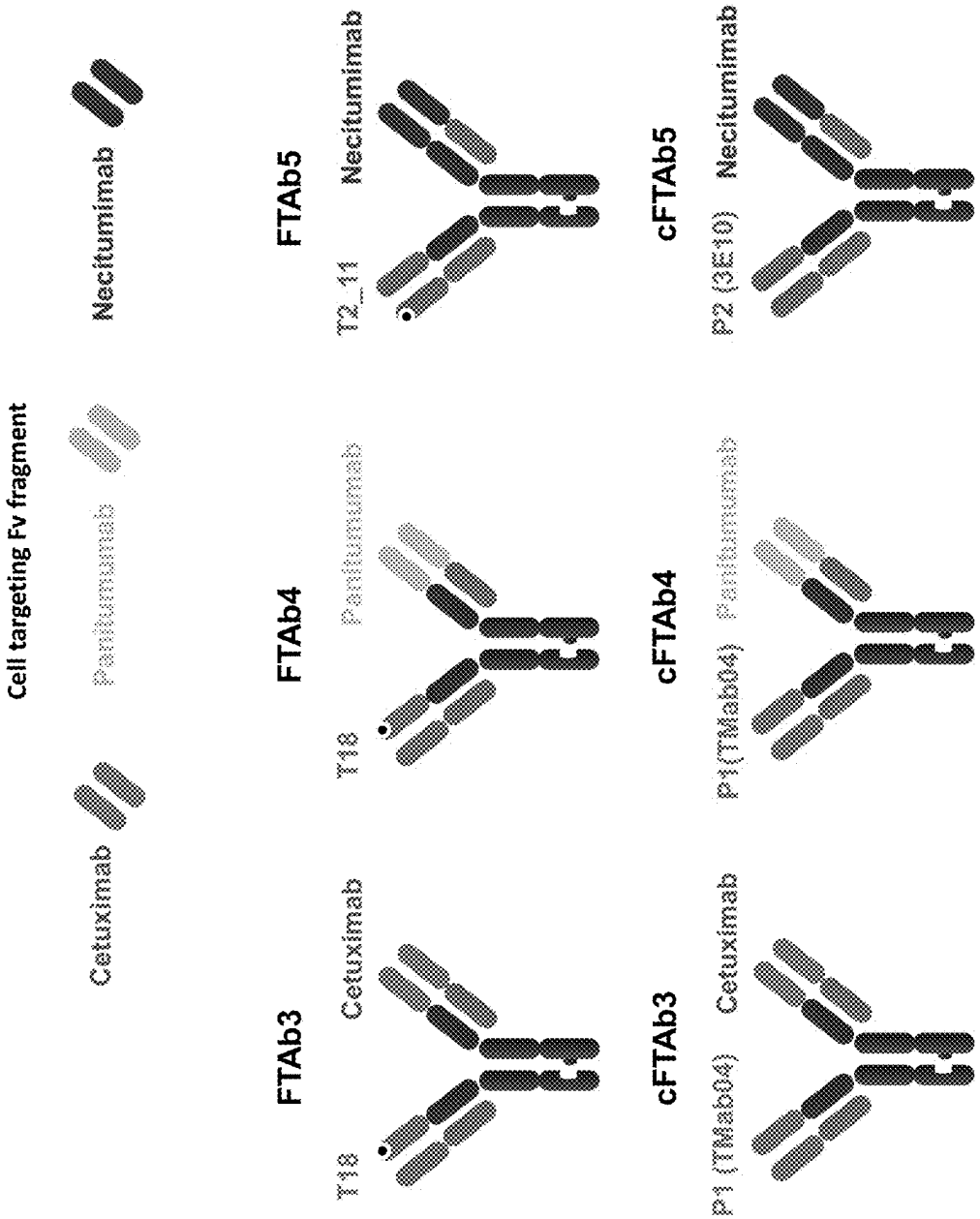


Figure 10 continued

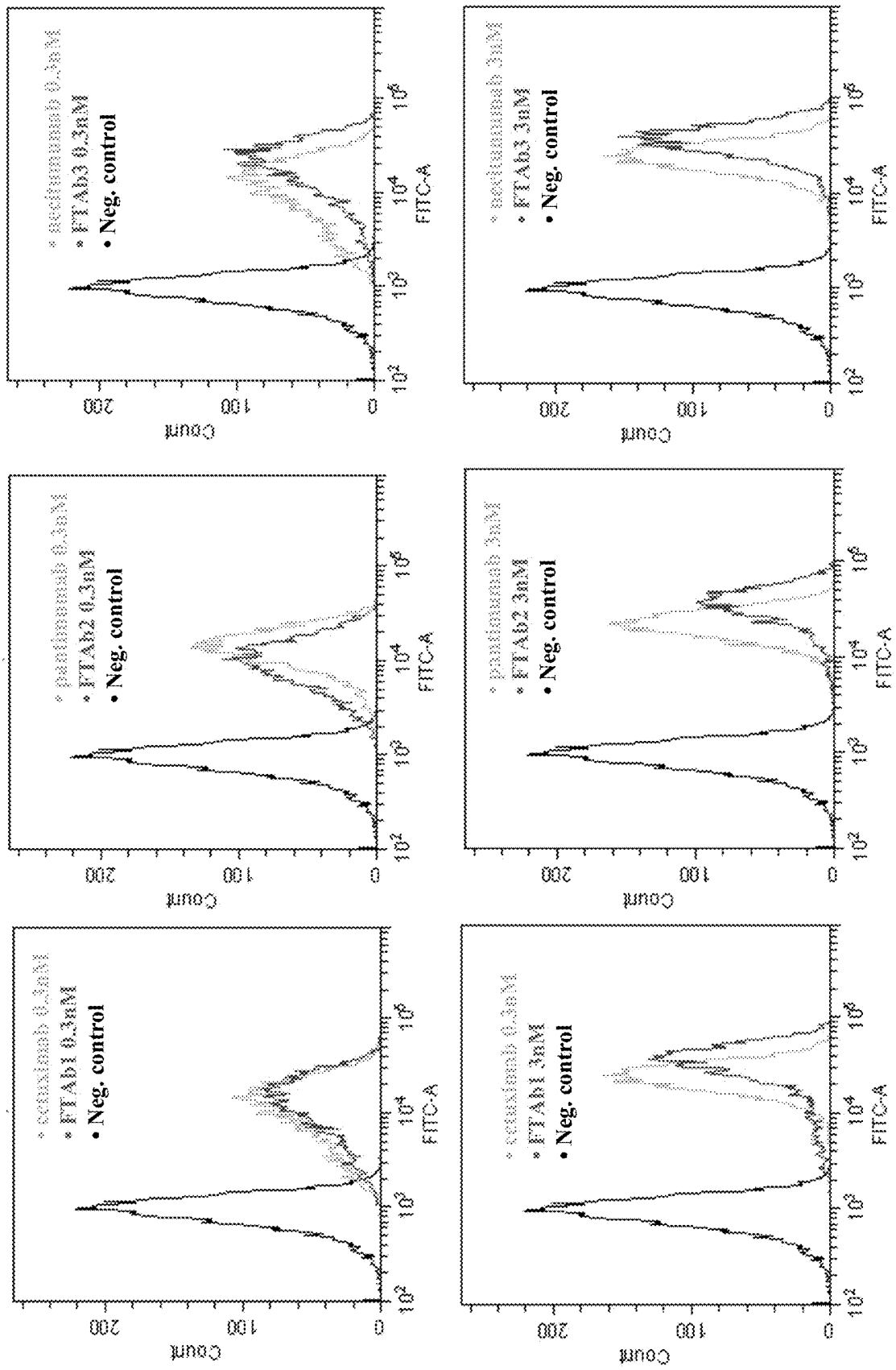

• FTAb1 0.3nM
• Neg. control
• FTAb2 0.3nM
• Neg. control
• FTAb3 0.3nM
• Neg. control
• FTAb1 3nM
• Neg. control
• FTAb2 3nM
• Neg. control
• FTAb3 3nM
• Neg. control
Count
FITC-A

Figure 11

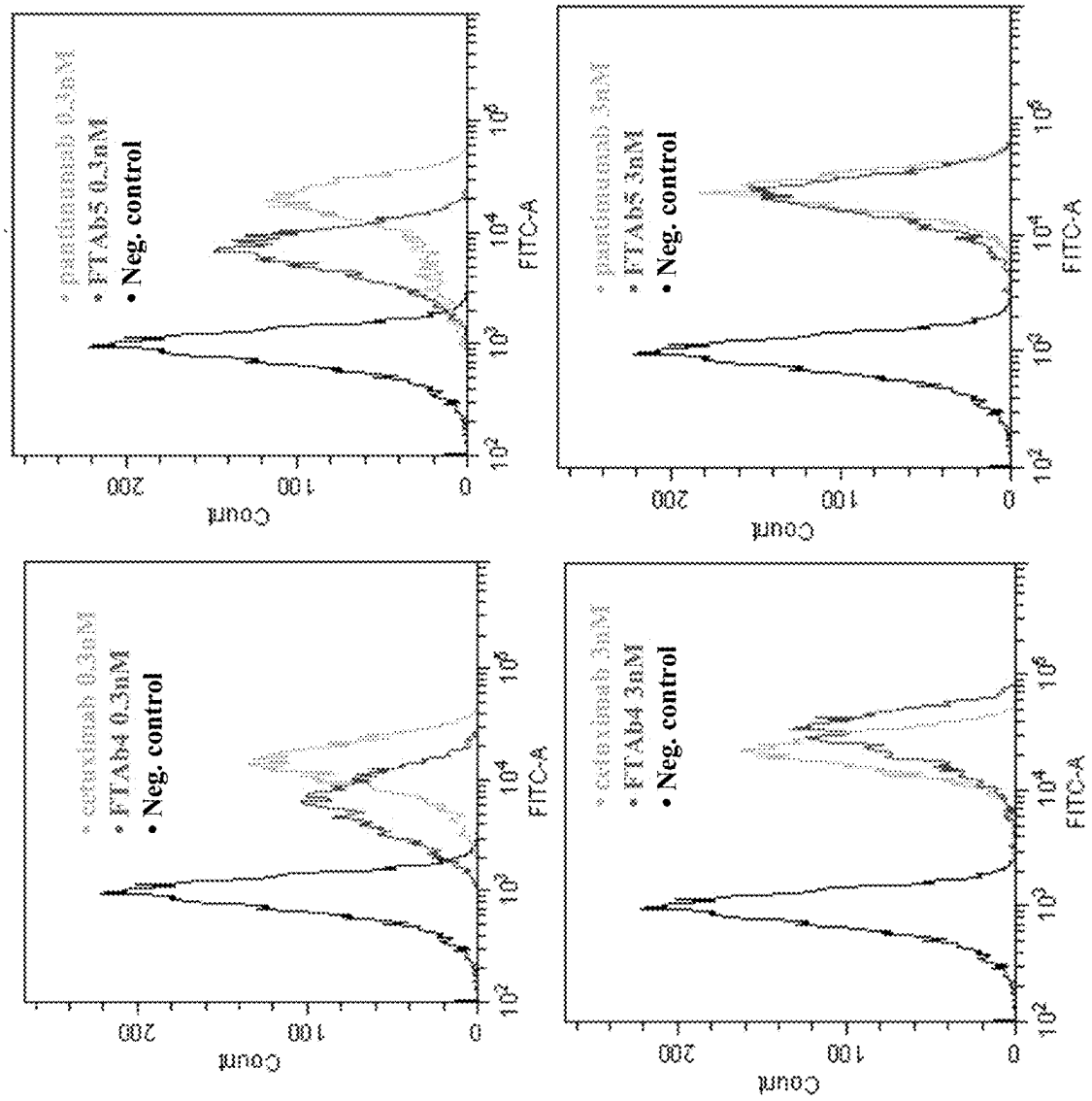


Figure 11 continued

Figure 12

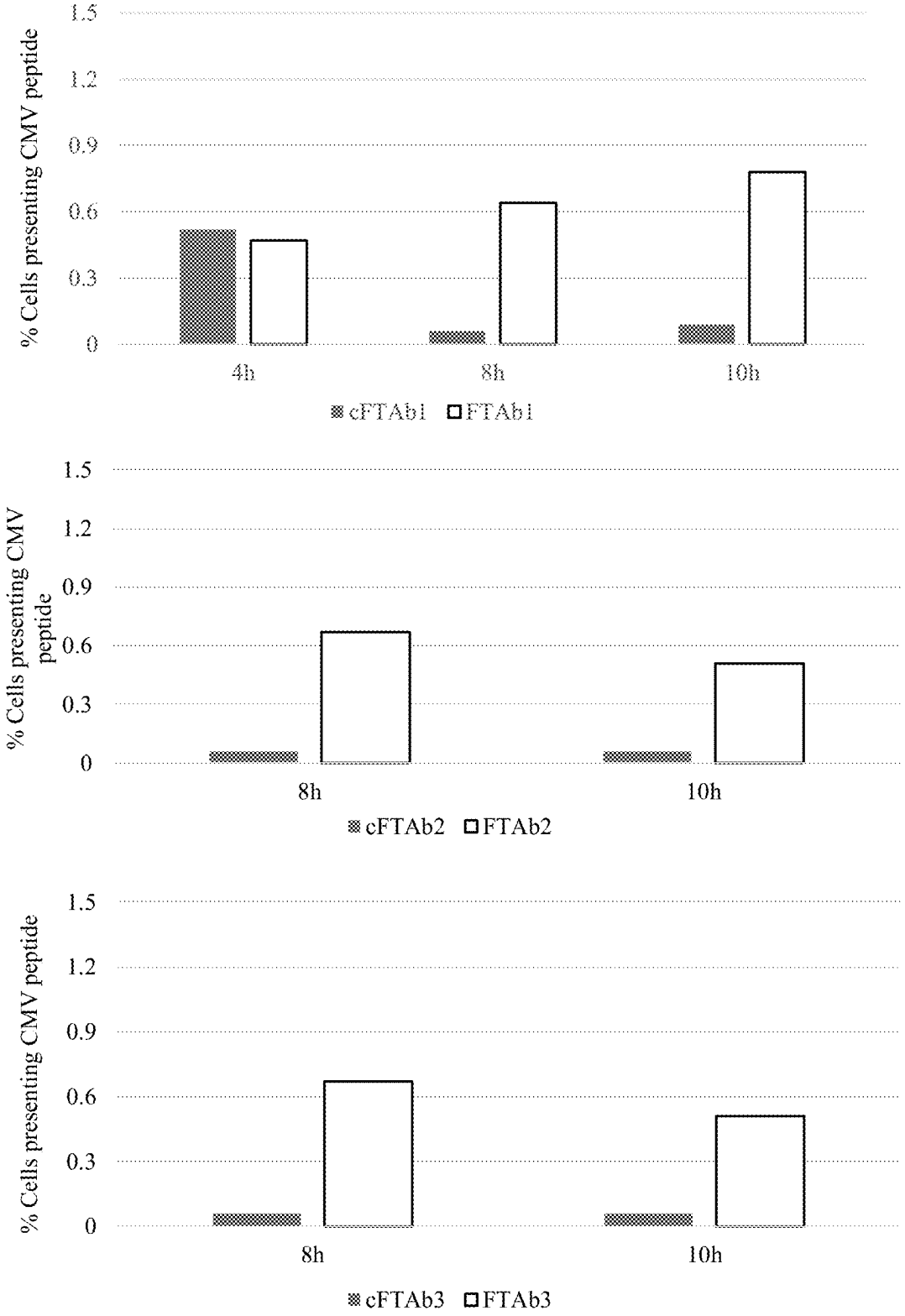
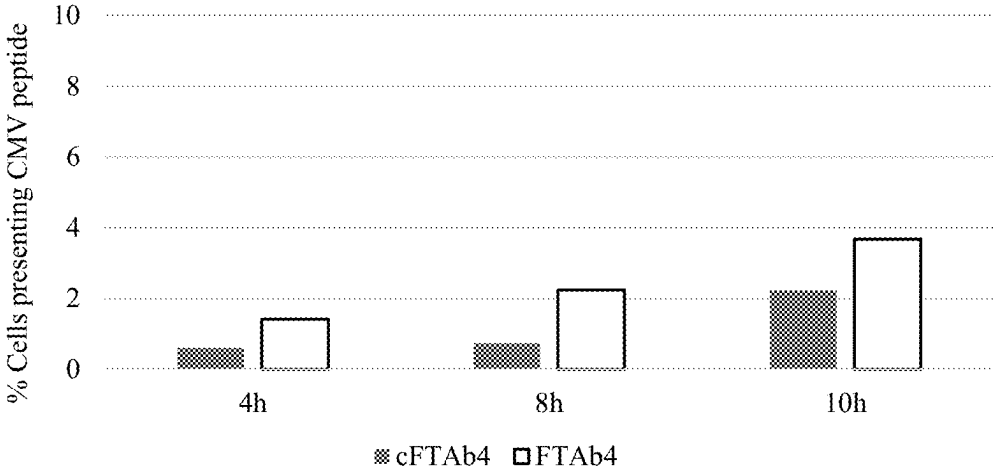

% Cells presenting CMV peptide
1.5
1.2
0.9
0.6
0.3
0
4h
8h
10h
cFTAb1
FTAb1
% Cells presenting CMV peptide
1.5
1.2
0.9
0.6
0.3
0
8h
10h
cFTAb2
FTAb2
% Cells presenting CMV peptide
1.5
1.2
0.9
0.6
0.3
0
8h
10h
cFTAb3
FTAb3

Figure 12 continued



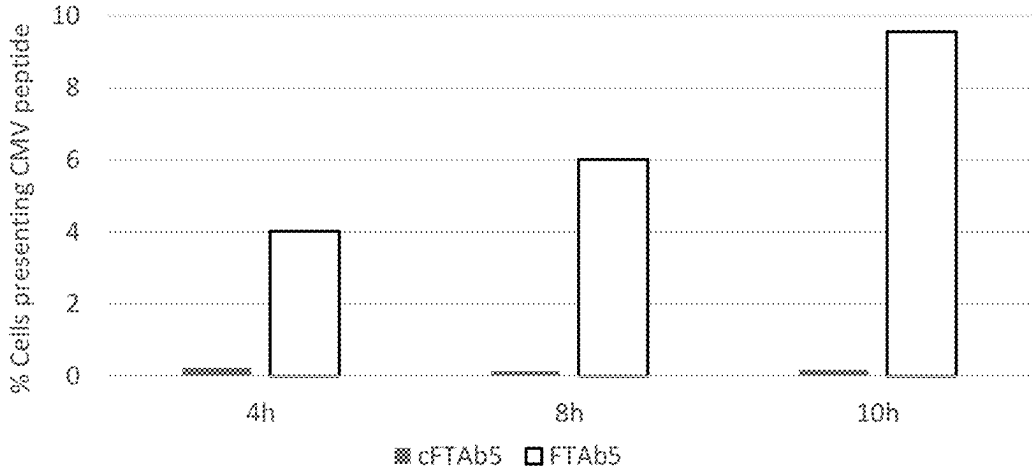
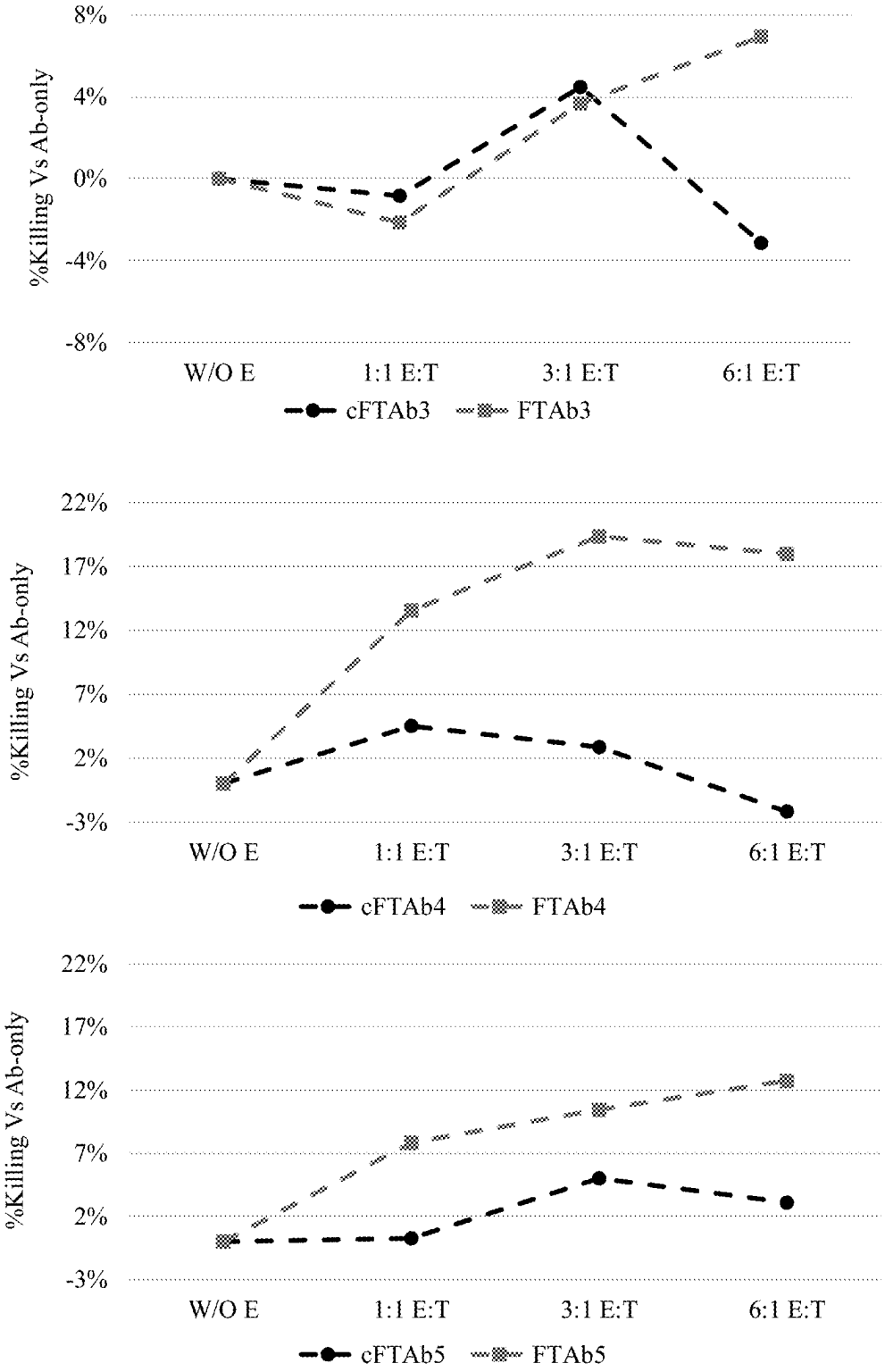


Figure 13


8%
4%
0%
-4%
-8%
%Killing Vs Ab-only
W/O E
1:1 E:T
3:1 E:T
6:1 E:T
cFTAb3
FTAb3
22%
17%
12%
7%
2%
-3%
%Killing Vs Ab-only
W/O E
1:1 E:T
3:1 E:T
6:1 E:T
cFTAb4
FTAb4
22%
17%
12%
7%
2%
-3%
%Killing Vs Ab-only
W/O E
1:1 E:T
3:1 E:T
6:1 E:T
cFTAb5
FTAb5

DUAL FUNCTION ANTIGEN BINDING MOLECULES

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of Israeli Patent Application No. 287372 filed on Oct. 18, 2021, the contents of which are incorporated herein by reference in its entirety.

FIELD OF INVENTION

[0002] The present invention is in the field of anti-cancer immunotherapy.

SUMMARY OF THE INVENTION

[0003] The present invention provides antibodies or antigen binding fragments thereof comprising at least one immunogenic peptide inserted into a variable region of the antibody or antigen binding fragment thereof. Dual-function antigen binding molecules comprising an antibody or antigen binding fragment of the invention and a second antibody or antigen binding fragment thereof capable of binding an antigen overexpressed on a target cell. Nucleic acid molecules encoding same, pharmaceutical compositions comprising same and methods of treating cancer by administrating same are also provided. Methods of producing antibodies or antigen binding fragments are also provided.

[0004] According to a first aspect, there is provided an antibody or antigen binding fragment thereof comprising at least one immunogenic peptide inserted into a variable region of the antibody or antigen binding fragment thereof, and where the insertion comprises removal of antibody or antigen binding fragment sequence.

[0005] According to another aspect, there is provided a dual-function antigen binding molecule comprising:

[0006] a. a first antibody or antigen binding fragment thereof comprising at least one immunogenic peptide inserted into a CDR of the antibody or antigen binding fragment thereof, and where the insertion comprises removal of CDR sequence; and

[0007] b. a second antibody capable of binding epidermal growth factor receptor (EGFR), wherein the antibody is selected from cetuximab, panitumumab and necitumumab or antibody comprising at least 85% sequence identity thereto.

[0008] According to some embodiments, the antibody or antigen binding fragment thereof binds to a target cell, and wherein the target cell is a cancer cell, a dendritic cell or both. According to some embodiments, the first antibody or antigen binding fragment thereof binds to a target cell, and wherein the target cell is a cancer cell, a dendritic cell or both.

[0009] According to some embodiments, the immunogenic peptide is a cancer specific peptide.

[0010] According to some embodiments, the cancer specific peptide is selected from a peptide sequence provided in Table 1.

[0011] According to some embodiments, the immunogenic peptide is a viral peptide.

[0012] According to some embodiments, the viral peptide is derived from Cytomegalovirus (CMV), Epstein-Barr virus (EBV), Severe acute respiratory syndrome coronavirus 2 (SARS-CoV2), Adenovirus, Human papilloma virus (HPV) or Influenza virus (FLU).

[0013] According to some embodiments, the viral peptide is selected from a peptide sequence provided in Table 2 or Table 3.

[0014] According to some embodiments, the antibody or antigen binding fragment thereof further comprises a cell penetration sequence that targets the antibody or antigen binding fragment thereof to a cytoplasm of a cell binding the antibody or antigen binding fragment thereof. According to some embodiments, the antibody or antigen binding fragment thereof further comprises a cell penetration sequence that targets the first antibody or antigen binding fragment thereof to a cytoplasm of a cell bound by the first antibody or antigen binding fragment thereof.

[0015] According to some embodiments, the cell penetration sequence is an endosomal escape domain (EED).

[0016] According to some embodiments, the antibody devoid of the immunogenic peptide is endocytosed into an endosomal pathway and is delivered to the cytoplasm. According to some embodiments, the first antibody or antigen binding fragment thereof is endocytosed into an endosomal pathway and is delivered to the cytoplasm.

[0017] According to some embodiments, at least one CDR or a portion thereof of the antibody or antigen binding fragment thereof is replaced with the immunogenic peptide. According to some embodiments, at least one CDR or a portion thereof of the first antibody or antigen binding fragment thereof is replaced with the immunogenic peptide.

[0018] According to some embodiments, the CDR is an inert CDR having little or no contribution to binding to a target antigen.

[0019] According to some embodiments, an inert CDR comprises two or fewer amino acids that contact the target antigen.

[0020] According to some embodiments, contact comprises a distance of not more than 5 angstroms between an amino acid of a CDR and an amino acid of the target antigen.

[0021] According to some embodiments, the insertion and removal produces no change or minimal change in the overall conformation of the antibody or antigen binding fragment thereof such that the antibody or antigen binding fragment thereof binds its target antigen at an equivalent affinity to the antibody or antigen binding fragment devoid of the immunogenic peptide. According to some embodiments, the insertion and removal produces no change or minimal change in the overall conformation of the first antibody or antigen binding fragment thereof such that the first antibody or antigen binding fragment thereof binds its target antigen at an equivalent affinity to the first antibody or antigen binding fragment devoid of the immunogenic peptide.

[0022] According to some embodiments, at least one inert CDR of an antigen binding region is replaced with a cell penetration sequence.

[0023] According to some embodiments, the target cell is a dendritic cell and a dendritic cell antigen is selected from CD40, CD205, CD206, CLEC9A, CLEC12A, CD209, and CD207.

[0024] According to some embodiments, the target cell is a malignant immune cell and an immune cell antigen is selected from CD20, CD19, CD21, and CD22.

[0025] According to some embodiments, the target cell is a cancer cell and a cancer cell antigen is selected from HER2, EGFR, EpCAM, PSMA, BCMA, CD123, CD33, CD38, CTLA, LAG-3, ICOS, 4-1BB and PD-L1.

[0026] According to some embodiments, the antibody or antigen binding fragment thereof is devoid of a chemical linker.

[0027] According to some embodiments, the antigen binding region, the immunogenic peptide and the cell penetrating sequence are each separated by a linker. According to some embodiments, within the first antibody or antigen binding fragment thereof the antigen binding region, the immunogenic peptide and the cell penetrating sequence are each separated by a linker.

[0028] According to some embodiments, the immunogenic peptide is recognized by CD4 T cells, CD8 T cells or both.

[0029] According to some embodiments, the antibody before the immunogenic peptide is inserted is selected from:

[0030] a. antibody TMab4 comprising a heavy chain variable region of SEQ ID NO: 1021 and a light chain variable region of SEQ ID NO: 1022;

[0031] b. antibody 3E10 comprising a heavy chain variable region of SEQ ID NO: 1023 and a light chain variable region of SEQ ID NO: 1024; and

[0032] c. antibody 71F12 comprising a heavy chain variable region of SEQ ID NO: 1026 and a light chain variable region of SEQ ID NO: 1027.

[0033] According to some embodiments, the first antibody before the immunogenic peptide is inserted is selected from:

[0034] a. antibody TMab4 comprising a heavy chain variable region of SEQ ID NO: 1021 and a light chain variable region of SEQ ID NO: 1022;

[0035] b. antibody 3E10 comprising a heavy chain variable region of SEQ ID NO: 1023 and a light chain variable region of SEQ ID NO: 1024; and

[0036] c. antibody 71F12 comprising a heavy chain variable region of SEQ ID NO: 1026 and a light chain variable region of SEQ ID NO: 1027.

[0037] According to some embodiments, at least one of:

[0038] a. the immunogenic peptide is inserted into CDRH1, CDRH2, CDRH3 or cDRL3 of the TMab4;

[0039] b. the immunogenic peptide is inserted into CDRL1 or CDRL2 of the 3E10; and

[0040] c. the immunogenic peptide is inserted into CDRL1 of the 71F12.

[0041] According to some embodiments, the antibody or antigen binding fragment thereof comprises at least one of:

[0042] a. a light chain variable region of SEQ ID NO: 1022 and a heavy chain variable region selected from SEQ ID NO: 1028-1040, 1043-1045, 1047-1055, and 1058-1059;

[0043] b. a heavy chain variable region of SEQ ID NO: 1021 and a light chain variable region selected from SEQ ID NO: 1041-1042, 1046, and 1056-1057;

[0044] c. a heavy chain variable region of SEQ ID NO: 1023 and a light chain variable region selected from SEQ ID NO: 1060-1065;

[0045] d. a heavy chain variable region of SEQ ID NO: 1026 and a light chain variable region of SEQ ID NO: 1066; and

[0046] e. a light chain variable region of SEQ ID NO: 1027 and a heavy chain variable region of SEQ ID NO: 1067.

[0047] According to some embodiments, the first antibody comprises at least one of:

[0048] a. a light chain variable region of SEQ ID NO: 1022 and a heavy chain variable region selected from SEQ ID NO: 1028-1040, 1043-1045, 1047-1055, and 1058-1059;

[0049] b. a heavy chain variable region of SEQ ID NO: 1021 and a light chain variable region selected from SEQ ID NO: 1041-1042, 1046, and 1056-1057;

[0050] c. a heavy chain variable region of SEQ ID NO: 1023 and a light chain variable region selected from SEQ ID NO: 1060-1065;

[0051] d. a heavy chain variable region of SEQ ID NO: 1026 and a light chain variable region of SEQ ID NO: 1066; and

[0052] e. a light chain variable region of SEQ ID NO: 1027 and a heavy chain variable region of SEQ ID NO: 1067.

[0053] According to another aspect, there is provided a dual-function antigen binding molecule comprising a first antibody or antigen binding fragment thereof comprising an antibody or antigen binding fragment of the invention and a second antibody or antigen binding fragment thereof capable of binding an antigen overexpressed on a target cancer cell.

[0054] According to some embodiments, the antigen overexpressed on a target cancer cell is EGFR and the second antibody is selected from cetuximab, panitumumab and necitumumab.

[0055] According to some embodiments, the first antibody and the second antibody comprise at least one modification that promotes heterodimerization and inhibit homodimerization.

[0056] According to some embodiments, one of the first and second antibody comprises a heavy chain constant region comprising SEQ ID NO: 1074 and the other antibody comprises a heavy chain constant region comprising SEQ ID NO: 1075.

[0057] According to some embodiments, the dual function antigen binding molecule comprises two heavy chains and two light chains, wherein:

[0058] a. the two heavy chains are SEQ ID NO: 1088 and 1080 and the two light chains are SEQ ID NO: 1087 and 1079;

[0059] b. the two heavy chains are SEQ ID NO: 1088 and 1082 and the two light chains are SEQ ID NO: 1087 and 1081;

[0060] c. the two heavy chains are SEQ ID NO: 1090 and 1080 and the two light chains are SEQ ID NO: 1089 and 1079;

[0061] d. the two heavy chains are SEQ ID NO: 1090 and 1082 and the two light chains are SEQ ID NO: 1089 and 1081; or

[0062] e. the two heavy chains are SEQ ID NO: 1088 and 1086 and the two light chains are SEQ ID NO: 1087 and 1085.

[0063] According to another aspect, there is provided a pharmaceutical composition comprising an antibody or antigen binding fragment or the invention or a dual-function antigen binding molecule of the invention and a pharmaceutically acceptable carrier excipient or adjuvant.

[0064] According to another aspect, there is provided a nucleic acid molecule comprising at least one open reading frame, wherein the open reading frame encodes an antibody

or antigen binding fragment thereof of the invention or a dual-function antigen binding molecule the invention.

[0065] According to another aspect, there is provided an expression vector comprising at least one regulatory element operatively linked to a nucleic acid molecule of the invention.

[0066] According to another aspect, there is provided a method of treating cancer in a subject in need thereof, the method comprising administering to the subject a pharmaceutical composition of the invention, thereby treating cancer in a subject.

[0067] According to some embodiments, the cancer overexpresses the cancer specific antigen.

[0068] According to some embodiments, the cancer is an EGFR positive cancer.

[0069] According to some embodiments, the dual-function antigen binding molecule is a cancer vaccine and comprises an antigen binding region capable of binding a dendritic cell antigen.

[0070] According to another aspect, there is provided a method of engineering an antibody or antigen binding fragment thereof, the method comprising:

[0071] a. selecting an antibody or antigen binding fragment thereof of interest;

[0072] b. receiving structural analysis of the selected antibody or antigen binding domain bound to its target;

[0073] c. determining at least one CDR of the selected antibody or antigen binding domain that is not required for binding to the target based on the structural analysis;

[0074] d. replacing the determined at least one CDR or a portion thereof with an immunogenic peptide;

thereby engineering an antibody or antigen binding fragment thereof.

[0075] According to another aspect, there is provided a method of engineering an antibody or antigen binding fragment thereof, the method comprising:

[0076] a. selecting an antibody or antigen binding fragment thereof of interest;

[0077] b. receiving a database of immunogenic peptides;

[0078] c. performing pairwise alignment of peptides of a variable region of the selected antibody or antigen binding fragment thereof of interest with immunogenic peptides of the database;

[0079] d. determining a peptide from the selected antibody or antigen binding fragment thereof and an immunogenic peptide with an alignment score above a predetermined threshold; and

[0080] e. replacing the determined peptide from the selected antibody or antigen binding fragment thereof with the determined immunogenic peptide;

thereby engineering an antibody or antigen binding fragment thereof.

[0081] According to some embodiments, the method further comprises optimizing the replacing to produce as little perturbation in the structure of the selected antibody or antigen binding fragment thereof of interest as possible.

[0082] According to some embodiments, the engineered antibody or antigen binding fragment thereof is an immunogenic peptide delivery antibody.

[0083] According to some embodiments, step (a) comprises selecting an antibody or antigen binding fragment thereof that binds to a surface of a target cell.

[0084] According to some embodiments, step (a) comprises selecting an antibody or antigen binding fragment thereof that upon binding to a surface is internalized and delivered to a cytosol of the target cell.

[0085] According to some embodiments, the method further comprises confirming at least one of: delivery of the immunogenic peptide to a cytosol of the target cell, delivery of the immunogenic peptide in complex with an HLA molecule to a surface of the target cell and specific killing of the target cell by an effector cell specific to the immunogenic peptide.

[0086] According to some embodiments, the method further comprises selecting a targeting antibody that binds to a protein on a surface of a target cell and producing a dual-function antigen binding molecule by combining the engineered antibody and the targeting antibody.

[0087] According to some embodiments, the combining comprises engineering a heavy chain constant region of the targeting antibody and a heavy chain constant region of the engineered antibody to promote heterodimerization and inhibit homodimerization.

[0088] Further embodiments and the full scope of applicability of the present invention will become apparent from the detailed description given hereinafter. However, it should be understood that the detailed description and specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0089] FIG. **1**: A schematic showing an antibody engaging its antigen and the presence of inert CDRs not involved in binding.

[0090] FIG. **2**: Images of an anti-PD-L1 antibody with an inert CDR and the Trojan antibody of the invention after the inert CDR is replace with an immunogenic peptide.

[0091] FIG. **3**: A stepwise diagram of dendritic cell vaccination method of the invention.

[0092] FIG. **4**: A stepwise diagram of a B cell targeting CD4+ T cell-mediated method of the invention.

[0093] FIG. **5**: A stepwise diagram of a CD8+ T cell-mediated cancer killing method of the invention.

[0094] FIG. **6**: An overview of embodiments of the Trojan antibody production method.

[0095] FIGS. **7**A-**7**C: Bar charts of specific killing of cancer cells contacted with (**7**A) TAbs containing immunogenic peptides inserted into CDRH1 of TMab4 (P1) antibody, (**7**B) TAbs containing immunogenic peptides inserted into CDRH3 of TMab4 (P1) antibody, and (**7**C) TAbs containing immunogenic peptides inserted into CDRL3 pr CDRH2 of TMab4 (P1) antibody, and then cocultured with peptide specific effector cells.

[0096] FIG. **8**: Bar charts of specific killing of cancer cells contacted with TAbs containing immunogenic peptides inserted into CDRL1 of 3E10 (P2) antibody and then cocultured with peptide specific effector cells.

[0097] FIGS. **9**A-**9**B: Line graphs of apoptotic cancer cells cultured with effector cells alone (Cells only), (**9**A) parental antibody 3E10 (P2) and TAb T2_11, and (**9**B) parental antibody TMab4 (P1) and TAb T18.

[0098] FIG. **10**: Schematics of bi-functional Trojan antibodies and corresponding controls. Bi-TAbs are labeled as FTAbs and control bi-TAbs are labeled as cFTAbs.

[0099] FIG. **11**: Histograms showing binding of bi-TAbs to EGFR on the surface of cancer cells. Therapeutic antibodies are used as the positive control and fluorescently labeled secondary antibodies are used as a negative control. Upper panels show 0.3 nM concentration and lower panels show 3 nM concentration. Bi-TAbs are labeled as FTAbs.

[0100] FIG. **12**: Bar graphs of the percentage of cancer cells displaying the HLA-peptide complex at different time points. Each bi-TAb (white bars) is compared to its negative control (grey bars) with the same killing module but without the immunogenic peptide. Bi-TAbs are labeled as FTAbs and control bi-TAbs are labeled as cFTAbs.

[0101] FIG. **13**: Line graphs of percentage of cancer cells killed by effector cells at various effector to target cell ratios. Each bi-TAb (light grey) is compared to its negative control (black lines). An antibody only point without effector cells is included. Bi-TAbs are labeled as FTAbs and control bi-TAbs are labeled as cFTAbs.

DETAILED DESCRIPTION OF THE INVENTION

[0102] The present invention, in some embodiments, provides antibodies or antigen binding fragments thereof comprising at least one immunogenic peptide inserted into a variable region of the antibody or antigen binding fragment thereof, wherein the insertion comprises removal of antibody or antigen binding fragment sequence. Dual-function antigen binding molecules comprising an antibody or antigen binding fragment of the invention and a second antibody or antigen binding fragment thereof capable of binding an antigen overexpressed on a target cell. Nucleic acid molecules encoding same, pharmaceutical compositions comprising same and methods of treating cancer by administrating same are also provided. Methods of producing antibodies or antigen binding fragments are also provided.

[0103] The invention is based on the surprising finding that antibodies/antigen binding molecules can be used as a delivery system for immunogenic peptides. That is, a highly immunogenic peptide can be delivered specifically to cancer cells and thereby increase immune surveillance against them. The antibody would in this case have an antigen binding domain to a cancer epitope which would cause the therapeutic molecule to bind the cancer cell. Upon endocytosis of the antibody/antigen binding molecule the immunogenic peptide would be delivered to the cytoplasm. This can be enhanced by the inclusion of a cell penetrating sequence, or specifically an endosomal escape sequence. Endosomal escape however is not essential as some mechanisms, such as receptor-mediated transcytosis of antibodies, deliver the antibody directly to the cytoplasm. The therapeutic molecule would be cleaved, releasing the immunogenic peptide which would then be displayed on the cell surface in complex with an HLA molecule, thus enhancing the immunogenicity of the cancer cell and increasing immune surveillance against the cancer and cancer killing.

[0104] Alternatively, the antigen binding region can bind a dendritic cell antigen, which would deliver the therapeutic molecule comprising a cancer cell antigen to a dendritic cell. The molecule would be endocytosed upon binding and the immunogenic cancer peptide will be cleaved from the rest of the molecule of the invention and displayed on the surface of the dendritic cell by HLA molecules. This will in turn train cytotoxic immune cells (T cell and NK cells) to target this immunogenic peptide and thereby the cancer.

[0105] By a first aspect, there is provided an antigen binding molecule.

[0106] By another aspect, there is provided a composition comprising the antigen binding molecule of the invention.

[0107] By another aspect, there is provided a nucleic acid molecule encoding the antigen binding molecule of the invention.

[0108] By another aspect, there is provided an expression vector comprising the nucleic acid molecule of the invention.

[0109] By another aspect, there is provided a method of expressing a peptide on a surface of a target cell, the method comprising contacting the target cell with an antigen binding molecule of the invention or a pharmaceutical composition of the invention, thereby expressing a peptide on a surface of a target cell.

[0110] By another aspect, there is provided a method of treating cancer in a subject in thereof, the method comprising administering to the subject an antigen binding molecule of the invention or a pharmaceutical composition of the invention, thereby treating cancer in a subject in need thereof.

[0111] By another aspect, there is provided a composition of the invention for use in expressing a peptide on a surface of a target cell. By another aspect, there is provided a composition of the invention for use in treating cancer. By another aspect, there is provided a composition of the invention for use in the production of a medicament for the treating of cancer.

[0112] In some embodiments, the antigen binding molecule is a dual-function molecule. In some embodiments, the first function is binding an antigen. In some embodiments, the second function is entering a cell. In some embodiments, the second function is delivering a peptide. In some embodiments, the peptide is an immunogenic peptide. In some embodiments, the second function is delivering an immunogenic peptide into a cytoplasm of a cell.

[0113] In some embodiments, the molecule comprises an antigen binding region. In some embodiments, the region is a domain. In some embodiments, the region binds the antigen. In some embodiments, the antigen is on a target cell. In some embodiments, the antigen binding region is capable of binding to a target cell. In some embodiments, the antigen is a cancer antigen. In some embodiments, a cancer antigen is a cancer specific antigen. In some embodiments, a cancer antigen is an antigen on a cancer cell. In some embodiments, the antigen is an immune cell antigen. In some embodiments, the immune cell is selected from a dendritic cell, a B cell, a T cell, a neutrophil, a macrophage and a natural killer (NK) cell. In some embodiments, the immune cell is a dendritic cell. In some embodiments, the antigen is a dendritic cell antigen. In some embodiments, the immune cell is a B cell. In some embodiments, the antigen is a B cell antigen. In some embodiments, an antigen is expressed on a cell. In some embodiments, an antigen is expressed on a cell surface. In some embodiments, an antigen is displayed on the cell surface as an MHC molecule. In some embodiments, an MHC molecule is an MHC class I or class II molecule. In some embodiments, an MHC molecule is a protein complex of the antigen and an HLA protein. In some embodiments, an antigen is a cell surface protein. In some

embodiments, a cell surface protein is a cell surface receptor. In some embodiments, the antigen binding region is capable of binding the antigen.

[0114] In some embodiments, a dendritic cell antigen is selected from CD40, CD205, CD206, CLEC9A, CLEC12A, CD209, and CD207. Markers of dendritic cells are well known in the art and any such surface marker may be used as the antigen. In some embodiments, the dendritic cell antigen is CD40. Antigen binding domains that target dendritic cell antigens are well known in the art and any such antigen binding domain may be employed. For a non-limiting example Fab516 binds specifically to CD40.

[0115] In some embodiments, an immune cell antigen is selected from CD20, CD19, CD21, and CD22. In some embodiments, the immune cell antigen is CD20. In some embodiments, the immune cell antigen is a B cell antigen. Markers of immune cells in general, and B cells in particular, are well known in the art and any such surface marker may be used as the antigen. Antigen binding domains that target immune cell antigens are well known in the art and any such antigen binding domain may be employed. For a non-limiting example Arzerra binds specifically to CD20

[0116] In some embodiments, a cancer cell antigen is selected from HER2, EGFR, EpCAM, PSMA, BCMA, CD123, CD33, CD38, CTLA, LAG-3, ICOS, 4-1BB and PD-L1. Markers of cancer cells are well known in the art and any such surface marker may be used as the antigen. In some embodiments, the cancer cell antigen is PD-L1. Antigen binding domains that target cancer cell antigens are well known in the art and any such antigen binding domain may be employed. For a non-limiting example Durvalumab binds specifically to PD-L1.

[0117] In some embodiments, the antigen binding domain is an antigen binding domain of an antibody. In some embodiments, the antigen binding domain is an antibody. In some embodiments, the antigen binding domain is an antibody or antigen binding fragment thereof. In some embodiments, the antibody is a single-chain antibody. In some embodiments, the antibody is a single domain antibody. In some embodiments, the antibody is a full antibody.

[0118] As used herein, the term "antibody" refers to a polypeptide or group of polypeptides that include at least one binding domain that is formed from the folding of polypeptide chains having three-dimensional binding spaces with internal surface shapes and charge distributions complementary to the features of an antigenic determinant of an antigen. An antibody typically has a tetrameric form, comprising two identical pairs of polypeptide chains, each pair having one "light" and one "heavy" chain. The variable regions of each light/heavy chain pair form an antibody binding site. An antibody may be oligoclonal, polyclonal, monoclonal, chimeric, camelised, CDR-grafted, multi-specific, bi-specific, catalytic, humanized, fully human, anti-idiotypic and antibodies that can be labeled in soluble or bound form as well as fragments, including epitope-binding fragments, variants or derivatives thereof, either alone or in combination with other amino acid sequences. An antibody may be from any species. The term antibody also includes binding fragments, including, but not limited to Fv, Fab, Fab', F(ab')2 single stranded antibody (svFC), dimeric variable region (Diabody) and disulphide-linked variable region (dsFv). In particular, antibodies include immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, i.e., molecules that contain an antigen binding site. Antibody fragments may or may not be fused to another immunoglobulin domain including but not limited to, an Fc region or fragment thereof. The skilled artisan will further appreciate that other fusion products may be generated including but not limited to, scFv-Fc fusions, variable region (e.g., VL and VH)~ Fc fusions and scFv-scFv-Fc fusions.

[0119] Immunoglobulin molecules can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass.

[0120] An "antigen" is a molecule or a portion of a molecule capable of eliciting antibody formation and being bound by an antibody. Antibody formation can occur in mice, rats, rabbits, pigs and other animals commonly used for generation of antibodies, but of course can also occur in humans as a response to a foreign antigen. An antigen may have one or more than one epitope. The specific reaction referred to above is meant to indicate that the antigen will react, in a highly selective manner, with its corresponding antibody and not with the multitude of other antibodies which may be evoked by other antigens.

[0121] The term "antigenic determinant" or "epitope" according to the invention refers to the region of an antigen molecule that specifically reacts with particular antibody. Peptide sequences derived from an epitope can be used, alone or in conjunction with a carrier moiety, applying methods known in the art, to immunize animals and to produce additional polyclonal or monoclonal antibodies. Immunoglobulin variable domains can also be analyzed using the IMGT information system (imgt. Cines.fr/) (IMGT®/V-Quest) to identify variable region segments, including CDRs. See, e.g., Brochet, X. et al, Nucl. Acids Res. J6:W503-508 (2008).

[0122] Kabat et al. also defined a numbering system for variable domain sequences that is applicable to any antibody. One of ordinary skill in the art can unambiguously assign this system of "Kabat numbering" to any variable domain sequence, without reliance on any experimental data beyond the sequence itself. As used herein, "Kabat numbering" refers to the numbering system set forth by Kabat et al, U.S. Dept. of Health and Human Services, "Sequence of Proteins of Immunological Interest" (1983).

[0123] The term "antibody" (also referred to as an "immunoglobulin") is used in the broadest sense and specifically encompasses monoclonal antibodies and antibody fragments so long as they exhibit the desired biological activity. In certain embodiments, the use of a chimeric antibody or a humanized antibody is also encompassed by the invention.

[0124] The basic unit of the naturally occurring antibody structure is a heterotetrameric glycoprotein complex of about 150,000 Daltons, composed of two identical light (L) chains and two identical heavy (H) chains, linked together by both noncovalent associations and by disulfide bonds. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Five human antibody classes (IgG, IgA, IgM, IgD and IgE) exist, and within these classes, various subclasses, are recognized based on structural differences, such as the number of immunoglobulin units in a single antibody molecule, the disulfide bridge structure of the individual units, and differences in chain length and sequence. The class and subclass of an antibody is its isotype.

[0125] The amino terminal regions of the heavy and light chains are more diverse in sequence than the carboxy

terminal regions, and hence are termed the variable domains. This part of the antibody structure confers the antigen-binding specificity of the antibody. A heavy variable (VH) domain and a light variable (VL) domain together form a single antigen-binding site, thus, the basic immunoglobulin unit has two antigen-binding sites. Particular amino acid residues are believed to form an interface between the light and heavy chain variable domains (Chothia et al., J. Mol. Biol. 186, 651-63 (1985); Novotny and Haber, (1985) Proc. Natl. Acad. Sci. USA 82 4592-4596).

[0126] The carboxy terminal portion of the heavy and light chains form the constant domains i.e., CH1, CH2, CH3, CL. While there is much less diversity in these domains, there are differences from one animal species to another, and further, within the same individual there are several different isotypes of antibody, each having a different function.

[0127] The term "framework region" or "FR" refers to the amino acid residues in the variable domain of an antibody, which are other than the hypervariable region amino acid residues as herein defined. The term "hypervariable region" as used herein refers to the amino acid residues in the variable domain of an antibody, which are responsible for antigen binding. The hypervariable region comprises amino acid residues from a "complementarity determining region" or "CDR". The CDRs are primarily responsible for binding to an epitope of an antigen. The extent of FRs and CDRs has been precisely defined (see, Kabat et al.). In some embodiments, CDRs are determined using the KABAT system. In some embodiments, CDRs are determined using the Clothia system. In some embodiments, the Clothia system is the enhanced Clothia system (Martin system).

[0128] In some embodiments, the antibody or antigen binding fragment thereof is the antibody or antigen binding fragment thereof devoid or without the immunogenic peptide. In some embodiments, devoid of without the immunogenic peptide is before insertion of the immunogenic peptide. In some embodiments, the antibody or antigen binding fragment thereof binds to a target cell. In some embodiments, the antibody or antigen binding fragment thereof adheres to a surface of a target cell. In some embodiments, the antibody or antigen binding fragment thereof is a cell penetrating antibody. In some embodiments, the antibody or antigen binding fragment thereof is phagocytosed into the cell. In some embodiments, the antibody or antigen binding fragment thereof is endocytosed into the cell. In some embodiments, into the cell is into the endosomal pathway of the cell. In some embodiments, the antibody or antigen binding fragment thereof is brought into the endosomal pathway. In some embodiments, the antibody or antigen binding fragment thereof escapes from the endosomal pathway. In some embodiments, the antibody or antigen binding fragment thereof is delivered into the cytoplasm of a cell that binds it. In some embodiments, the antibody or antigen binding fragment thereof is a DNA binding antibody. In some embodiments, the antibody or antigen binding fragment thereof is a lupus antibody.

[0129] In some embodiments, the antibody or antigen binding fragment thereof is the Tmab4 antibody. In some embodiments, the Tmab4 comprises a heavy chain variable region of SEQ ID NO: 1021 or an analog or homolog comprising at least 85% sequence identity and being capable of binding cells and reaching the cytosol. In some embodiments, the Tmab4 comprises a light chain variable region of SEQ ID NO: 1022 or an analog or homolog comprising at least 85% sequence identity and being capable of binding cells and reaching the cytosol. In some embodiments, the antibody or antigen binding fragment thereof is the 3E10 antibody. In some embodiments, the 3E10 comprises a heavy chain variable region of SEQ ID NO: 1023 or an analog or homolog comprising at least 85% sequence identity and being capable of binding cells and reaching the cytosol. In some embodiments, the 3E10 comprises a light chain variable region of SEQ ID NO: 1024 or an analog or homolog comprising at least 85% sequence identity and being capable of binding cells and reaching the cytosol. In some embodiments, the antibody or antigen binding fragment thereof is the 71F12 antibody. In some embodiments, the 71F12 comprises a heavy chain variable region of SEQ ID NO: 1026 or an analog or homolog comprising at least 85% sequence identity and being capable of binding cells and reaching the cytosol. In some embodiments, the 71F12 comprises a light chain variable region of SEQ ID NO: 1027 or an analog or homolog comprising at least 85% sequence identity and being capable of binding cells and reaching the cytosol.

[0130] In some embodiments, the antigen binding molecule comprises at least one immunogenic peptide. In some embodiments, the antigen binding molecule comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 immunogenic peptides. Each possibility represents a separate embodiment of the invention. In some embodiments, the immunogenic peptide is an exogenous immunogenic peptide. In some embodiments, the immunogenic peptide is inserted into the antigen binding molecule. In some embodiments, the immunogenic peptide is inserted into a variable region of the antibody or antigen binding fragment thereof. In some embodiments, the immunogenic peptide is not a natural part of the antigen binding molecule. In some embodiments, the peptide is a sequence of amino acids. In some embodiments, the sequence of immunogenic amino acids is inserted into the sequence of the antigen binding molecule. In some embodiments, the immunogenic peptide replaces amino acids of the antigen binding molecule. In some embodiments, insertion of the immunogenic peptide comprises removal of amino acid sequence. In some embodiments, the amino acid sequence is sequence of the antibody or antigen binding fragment thereof. In some embodiments, the immunogenic peptide is not artificially linked to antigen binding molecule. In some embodiments, the antigen binding molecule is a recombinant molecule. In some embodiments, the recombinant molecule comprises an amino acid sequence of the immunogenic peptide. In some embodiments, the immunogenic peptide is not linked by a chemical linkage to the antigen binding molecule. In some embodiments, a chemical linkage is any linkage other than a peptide linkage. In some embodiments, a chemical linkage is any linkage other than an amino acid linkage. In some embodiments, the immunogenic peptide is linked to the antigen binding molecule by a peptide bond, an amino acid linkage or both.

[0131] As used herein, the terms "peptide", "polypeptide" and "protein" are used interchangeably to refer to a polymer of amino acid residues. In another embodiment, the terms "peptide", "polypeptide" and "protein" as used herein encompass native peptides, peptidomimetics (typically including non-peptide bonds or other synthetic modifications) and the peptide analogues peptoids and semipeptoids or any combination thereof. In another embodiment, the peptides polypeptides and proteins described have modifi-

cations rendering them more stable while in the body or more capable of penetrating into cells. In one embodiment, the terms "peptide", "polypeptide" and "protein" apply to naturally occurring amino acid polymers. In another embodiment, the terms "peptide", "polypeptide" and "protein" apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid.

[0132] As used herein, the term "recombinant protein" refers to a protein which is coded for by a recombinant DNA and is thus not naturally occurring. The term "recombinant DNA" refers to DNA molecules formed by laboratory methods of genetic recombination. Generally, this recombinant DNA is in the form of a vector, plasmid or virus used to express the recombinant protein in a cell.

[0133] In some embodiments, the immunogenic peptide comprises at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the immunogenic peptide comprises at most 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the immunogenic peptide is between 3 and 20, 3 and 15, 3 and 12, 3 and 11, 3 and 10, 3 and 7, 5 and 20, 5 and 15, 5 and 12, 5 and 11, 5 and 10, 7 and 20, 7 and 15, 7 and 12, 7 and 11, or 7 and 10 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the immunogenic peptide is between 8 and 11 amino acids. In some embodiments, the immunogenic peptide consists of 8 amino acids. In some embodiments, the immunogenic peptide consists of 9 amino acids. In some embodiments, the immunogenic peptide consists of 10 amino acids. In some embodiments, the immunogenic peptide consists of 11 amino acids.

[0134] As used herein, the term "immunogenic peptide" refers to an amino acids sequence that produces an immune response when exposed to the human immune system. In some embodiments, an immunogenic peptide is a non-human peptide. In some embodiments, the immunogenic peptide produces an immune response from an immune cell. In some embodiments, the immunogenic peptide is recognized an immune response from an immune cell. In some embodiments, recognized is bound by. In some embodiments, an immunogenic peptide produces an immune response from a dendritic cell. In some embodiments, an immunogenic peptide is displayed on the cell surface. In some embodiments, an immunogenic peptide is displayed as an MHC molecule. In some embodiments, an immunogenic peptide is displayed in complex with HLA. In some embodiments, the immunogenic peptide produces an immune response from a T cell. In some embodiments, the immune cell is a dendritic cell. In some embodiments, the immune cell is a T cell. In some embodiments, a T cell is selected from a CD4 T cell and a CD8 T cell. In some embodiments, the T cell is a CD4 T cell. In some embodiments, the T cell is a CD8 T cell. In some embodiments, the immunogenic peptide comprises a CD4 epitope, a CD8 epitope or both. In some embodiments, the immunogenic peptide produces an immune response from an NK cell. In some embodiments, an immune response is an elevated immune response. In some embodiments, immunogenic comprises increase immunogenicity. In some embodiments, increased is as compared to a control peptide. In some embodiments, the control peptide is a human peptide. In some embodiments, a control peptide is a non-cancerous peptide. In some embodiments, a control peptide is a non-immunogenic peptide.

[0135] In some embodiments, the immunogenic peptide is a cancer peptide. In some embodiments, the cancer peptide is a cancer specific peptide. In some embodiments, the cancer peptide is a cancer elevated peptide. In some embodiments, the cancer peptide is a peptide with increased surface expression in cancer cells. In some embodiments, a cancer peptide is a peptide provided in Table 1. In some embodiments, a cancer peptide is selected from a sequence provided in Table 1. In some embodiments, a cancer peptide is selected from the sequences provided in SEQ ID NO: 702-1020. Cancer peptides are well known in the art and can found, for example at the Cancer Antigenic Peptide Database: caped.icp.ucl.ac.be/Peptide/search.

TABLE 1

Cancer peptides

Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
p53	SQKTYQGSY	702	99-107
NY-ESO-1/LAGE-2	KEFTVSGNILTI	703	124-135
MAGE-A6	MVKISGGPR	704	290-298
Melan-A/MART-1	AEEAAGIGIL(T)	705	24-33(34)
MAGE-A1	DPARYEFLW	706	258-266
MAGE-A10	DPARYEFLW	707	290-298
MAGE-A1	REPVTKAEML	708	120-129
MAGE-A2	REPVTKAEML	709	127-136
MAGE-A3	REPVTKAEML	710	127-136
MAGE-A4	SESLKMIF	711	156-163
MAGE-A6	REPVTKAEML	712	127-136

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
PBF	CTACRWKKACQR	713	499-510
HSDL1	CYMEAVAL	714	20-27
LAGE-1	LAAQERRVPR	715	ORF2
LAGE-1	LAAQERRVPR	716	(18-27)
NY-ESO-1/LAGE-2	ASGPGGGAPR	717	53-62
NY-ESO-1/LAGE-2	LAAQERRVPR	718	ORF2
NY-ESO-1/LAGE-2	LAAQERRVPR	719	(18-27)
TRP-1/gp75	MSLQRQFLR	720	alt. ORF
TRP-2	LLGPGRPYR	721	197-205
TRP-2	LLGPGRPYR	722	197-205
TRP-2	LLGPGRPYR	723	197-205
SNRPD1	SHETVIIEL	724	43739
tyrosinase	LHHAFVDSIF	725	388-397
NFYC	QQITKTEV	726	275-282
MAGE-A3	WQYFFPVIF	727	143-151
NY-ESO-1/LAGE-2	FATPMEAEL	728	96-104
GAGE-3,4,5,6,7	YYWPRPRRY	729	43374
NA88-A	QGQHFLQKV	730	
MAGE-A3	MEVDPIGHLY	731	167-176
MAGE-A3	AELVHFLLL	732	114-122
VEGF	SRFGGAVVR	733	-i
BAGE-1	AARAVFLAL	734	44471
MAGE-A1	SAYGEPRKL	735	230-238
MAGE-A6	ISGGPRISY	736	293-301
K-ras	GADGVGKSA	737	43374
K-ras	GADGVGKSAL	738	43739
gp100/Pmel17	SNDGPTLI	739	71-78
TRP-2	ANDPIFVVL	740	387-395
tyrosinase	QCSGNFMGF	741	90-98
gp100/Pmel17	RTKQLYPEW	742	40-42 and 47-52
Elongation factor 2	ETVSEQSNV	743	581-589
MUM-3	EAFIQPITR	744	322-330
LAGE-1	ELVRRILSR	745	103-111
MAGE-A1	EVYDGREHSA	746	222-231
NY-ESO-1/LAGE-2	TVSGNILTIR	747	127-136

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
TRP2-INT2	EVISCKLIKR	748	intron 2
gp100/Pmel17	HTMEVTVYHR	749	182-191
MAGE-A1	ITKKVADLVGF	750	102-112
MAGE-C2	ASSTLYLVF	751	42-50
MAGE-A1	SAFPTTINF	752	62-70
NY-ESO-1/LAGE-2	MPFATPMEA	753	94-102
NY-ESO-1/LAGE-2	FATPMEAELAR	754	96-106
CDK12	CILGKLFTK	755	924-932
CDKN2A	AVCPWTWLR	756	125-133 (p14ARF-ORF3)
MATN	KTLTSVFQK	757	226-234
HERV-E	ATFLGSLTWK	758	
gp100/Pmel17	ALNFPGSQK	759	87-95
KK-LC-1	RQKRILVNL	760	76-84
BCR-ABL fusion protein (b3a2)	GFKQSSKAL	761	922-930
TAG-1	LSRLSNRLL	762	42-50
TAG-2	LSRLSNRLL	763	42-50
RBAF600	RPHVPESAF	764	329-337
SYT-SSX1 or -SSX2 fusion protein	QRPYGYDQIM	765	402-410 (SYT)
LAGE-1	APRGVRMAV	766	ORF2
LAGE-1	APRGVRMAV	767	(46-54)
MAGE-A1	RVRFFFPSL	768	289-298
NY-ESO-1/LAGE-2	APRGPHGGAASGL	769	60-72
gp100/Pmel17	SSPGCQPPA	770	529-537
Intestinal carboxyl esterase	SPRWWPTCL	771	alt. ORF
RAGE-1	SPSSNRIRNT	772	44136
RU2AS	LPRWPPPQL	773	antisense
MAGE-A1	SAYGEPRKL	774	230-238
NY-ESO-1/LAGE-2	LAMPFATPM	775	92-100
MUM-2	FRSGLDSYV	776	126-134
GAGE-1,2,8	YRPRPRRY	777	42614
NY-ESO-1/LAGE-2	ARGPESRLL	778	80-88
beta-catenin	SYLDSGIHF	779	29-37
KM-HN-1	NYNNFYRFL	780	196-204
KM-HN-1	EYSKECLKEF	781	499-508
KM-HN-1	EYLSLSDKI	782	770-778

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
LY6K	RYCNLEGPPI	783	119-128
MAGE-A2	EYLQLVFGI	784	156-164
MAGE-A3	TFPDLESEF	785	97-105
MAGE-A3	VAELVHFLL	786	113-121
MAGE-A4	NYKRCFPVI	787	143-151
MAGE-A4	NYKRCFPVI	788	143-151
NY-ESO-1/LAGE-2	YLAMPFATPME	789	91-101
SAGE	LYATVIHDI	790	715-723
CEA	TYACFVSNL	791	652-660
CEA	QYSWFVNGTF	792	268-277
gp100/Pmel17	VYFFLPDHL	793	intron 4
OA1	LYSACFWWL	794	126-134
tyrosinase	IYMDGTADFSF	795	368-373 and 336-340e
tyrosinase	AFLPWHRLF	796	206-214
CD45	KFLDALISL	797	556-564
EpCAM	RYQLDPKFI	798	173-181
EZH2	KYDCFLHPF	799	291-299
EZH2	KYVGIEREM	800	735-743
glypican-3	EYILSLEEL	801	298-306
HER-2/neu	TYLPTNASL	802	63-71
HSPH1	NYGIYKQDL	803	180-188
MUC5AC	TCQPTCRSL	804	716-724
PRAME	LYVDSLFFLc	805	301-309
PSMA	NYARTEDFF	806	178-186
RNF43	NSQPVWLCL	807	721-729
WT1	CMTWNQMNL	808	235-243
CASP-8	FPSDSWCYF	809	476-484
K-ras	VVVGAVGVG	810	42186
MAGE-A1	EADPTGHSY	811	161-169
MAGE-A3	EVDPIGHLY	812	168-176
MAGE-A6	EVDPIGHVY	813	168-176
NY-ESO-1/LAGE-2	MPFATPMEAEL	814	94-104
gp100/Pmel17	VPLDCVLYRY	815	471-480
gp100/Pmel17	LPHSSSHWL	816	630-638
Melan-A/MART-1	EAAGIGILTV	817	26-35
tyrosinase	LPSSADVEF	818	312-320

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
tyrosinase	TPRLPSSADVEF	819	309-320
M-CSF	LPAVVGLSPGEQEY	820	alt. ORF
KIAA0205	AEPINIQTW	821	262-270
MUM-1	EEKLIVVLF	822	30-38
MUM-2	SELFRSGLDSY	823	123-133
OS-9	KELEGILLL	824	438-446
MAGE-A1	KEADPTGHSY	825	160-169
MAGE-A3	MEVDPIGHLY	826	167-176
MAGE-C2	SESIKKKVL	827	307-315
tyrosinase	SEIWRDIDFD	828	192-200
EFTUD2	KILDAVVAQK	829	668-677
GPNMB	TLDWLLQTPK	830	179-188
Myosin class I	KINKNPKYK	831	911-919
SIRT2	KIFSEVTLK	832	192-200
MAGE-A1	SLFRAVITK	833	96-104
CEA	HLFGYSWYK	834	61-69
gp100/Pmel17	LIYRRRLMK	835	614-622
gp100/Pmel17	IALNFPGSQK	836	86-95
gp100/Pmel17	ALLAVGATK	837	17-25
gp100/Pmel17	RSYVPLAHR	838	195-202 and 191 or 192e
gp100/Pmel17	ALNFPGSQK	839	87-95
mammaglobin-A	PLLENVISK	840	23-31
FGF5	NTYASPRFKf	841	172-176 and 217-220
HER-2/neu	VLRENTSPK	842	754-762
MMP-7	SLFPNSPKWTSK	843	96-107
RGS5	GLASFKSFLK	844	74-83
RhoC	RAGLQVRKNK	845	176-185
FLT3-ITD	YVDFREYEYY	846	591-600
MART2	FLEGNEVGKTY	847	446-455
N-ras	ILDTAGREEY	848	55-64
PPP1R3B	YTDFHCQYV	849	172-180
MAGE-A1	EADPTGHSY	850	161-169
MAGE-A3	EVDPIGHLY	851	168-176
MAGE-A4	EVDPASNTY	852	169-177
Sp17	ILDSSEEDK	853	103-111

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
tyrosinase	KCDICTDEY	854	243-251
tyrosinase	SSDYVIPIGTY	855	146-156
AIM-2	RSDSGQQARY	856	intron
WT1	TSEKRPFMCAY	857	317-327
MAGE-A1	RVRFFFPSL	858	289-298
MAGE-A12 m	VRIGHLYIL	859	170-178
MAGE-A12 m	VRIGHLYIL	860	170-178
MAGE-A12 m	EGDCAPEEK	861	212-220
MAGE-A2	EGDCAPEEK	862	212-220
MAGE-A3	EGDCAPEEK	863	212-220
MAGE-A6	EGDCAPEEK	864	212-220
Melan-A/MART-1	RNGYRALMDKS	865	51-61
alpha-actinin-4	FIASNGVKLV	866	118-127
BCR-ABL fusion protein (b3a2)	SSKALQRPV	867	926-934
CASP-5	FLIIWQNTM	868	67-75
CDK4	ACDPHSGHFV	869	23-32
CLPP	ILDKVLVHL	870	240-248
CSNK1A1	GLFGDIYLA	871	26-34
ETV6-AML1 fusion protein	RIAECILGM	872	334-342
FNDC3B	VVMSWAPPV	873	292-300
GAS7	SLADEAEVYL	874	141-150
HAUS3	ILNAMIAKI	875	154-162
hsp70-2	SLFEGIDIYT	876	286-295
ME1	FLDEFMEGV	877	224-232
OGT	SLYKFSPFPL	878	28-37
p53	VVPCEPPEV	879	217-225
PRDX5	LLLDDLLVSI	880	163-172
TGF-betaRII	RLSSCVPVA	881	131-139
TP53	VVPCEPPEV	882	217-225
CT37/FMRINB	YLCSGSSYFV	883	89-98
Cyclin-A1	SLIAAAAFCLA	884	341-351
Cyclin-A1	FLDRFLSCM	885	227-235
GnTV	VLPDVFIRC(V)	886	intron
HERV-K-MEL	MLAVISCAV	887	44440
LAGE-1	MLMAQEALAFL	888	ORF2
LAGE-1	MLMAQEALAFL	889	(1-11)

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
LAGE-1	SLLMWITQC	890	157-165
LRPAP1	FLGPWAAS	891	21-30
MAGE-A1	KVLEYVIKV	892	278-286
MAGE-A1	KVLEYVIKV	893	278-286
MAGE-A10	GLYDGMEHL	894	254-262
MAGE-A12m	FLWGPRALV	895	271-279
MAGE-A2	YLQLVFGIEV	896	157-166
MAGE-A3	KVAELVHFL	897	112-120
MAGE-A3	FLWGPRALV	898	271-279
MAGE-A4	GVYDGREHTV	899	230-239
MAGE-A9	ALSVMGVYV	900	223-231
MAGE-C1	ILFGISLREV	901	959-968
MAGE-C1	KVVEFLAML	902	1083-1091
MAGE-C2	ALKDVEERV	903	336-344
MAGE-C2	LLFGLALIEV	904	191-200
NY-ESO-1/LAGE-2	SLLMWITQC	905	157-165
NY-ESO-1/LAGE-2	SLLMWITQC	906	157-165
NY-ESO-1/LAGE-2	SLLMWITQC	907	157-165
NY-ESO-1/LAGE-2	MLMAQEALAFL	908	ORF2
NY-ESO-1/LAGE-2	MLMAQEALAFL	909	(1-11)
SSX-2	KASEKIFYV	910	41-49
TAG-1	SLGWLFLLL	911	78-86
XAGE-1b/GAGED2a	ROKKIRIQL	912	21-29
CEA	YLSGANLNL	913	605-613
CEA	GVLVGVALI	914	694-702
CEA	IMIGVLVGV	915	691-699
gp100/Pmel17	KTWGQYWQV	916	154-162
gp100/Pmel17	(A)MLGTHTMEV	917	177(8)-186
gp100/Pmel17	KTWGQYWQV	918	154-163
gp100/Pmel17	ITDQVPFSV	919	209-217
gp100/Pmel17	YLEPGPVTA	920	280-288
gp100/Pmel17	VLYRYGSFSV	921	476-485
gp100/Pmel17	LLDGTATLRL	922	457-466
gp100/Pmel17	RLMKQDFSV	923	619-627
gp100/Pmel17	SLADTNSLAV	924	570-579
gp100/Pmel17	RLPRIFCSC	925	639-647

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
Melan-A/MART-1	ILTVILGVL	926	32-40
Melan-A/MART-1	EAAGIGILTV	927	26(27)-35
NY-BR-1	SLSKILDTV	928	904-912
PAP	TLMSAMTNL	929	112-120
PAP	ALDVYNGLL	930	299-307
PAP	FLFLLFFWL	931	18-26
PSA	FLTPKKLQCV	932	165-174
PSA	VISNDVCAQV	933	178-187
RAB38/NY-MEL-1	VLHWDPETV	934	50-58
TRP-2	SVYDFFVWL	935	180-188
TRP-2	TLDSQVMSL	936	360-368
tyrosinase	MLLAVLYCL	937	44440
tyrosinase	CLLWSFQTSA	938	42948
tyrosinase	YMDGTMSQV	939	369-377
tyrosinase	YMDGTMSQV	940	369-377
adipophilin	SVASTITGV	94	129-137
ALDH1A1	LLYKLADLI	942	88-96
alpha-foetoprotein (AFP)	GVALQTMKQ	943	542-550
alpha-foetoprotein (AFP)	FMNKFIYEI	944	158-166
BCLX (L)	YLNDHLEPWI	945	173-182
BING-4	CQWGRLWQL	946	ORF2
CALCA	VLLQAGSLHA	947	16-25
CALCA	FLALSILVL	948	42979
CALCA	LLAALVQDYL	949	50-59
CALCA	CMLGTYTQDF	950	91-100
CD274	LLNAFTVTV	95	15-23
CPSF	LMLQNALTTM	952	1360-1369
CPSF	KVHPVIWSL	953	250-258
cyclin D1	LLGATCMFV	954	101-109
DKK1	ALGGHPLLGV	955	20-29
DKK1	ALGGHPLLGV	956	20-30
ENAH (hMena)	TMNGSKSPV	957	502-510
EZH2	FMVEDETVL	958	120-128
EZH2	FINDEIFVEL	959	165-174
G250/MN/CAIX	HLSTAFARV	960	254-262
glypican-3	FVGEFFTDV	961	144-152

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
glypican-3	TIHDSIQYV	962	325-334
HEPACAM	RLAPFVYLL	963	16-24
Hepsin	SLLSGDWVL	964	191-199
Hepsin	GLQLGVQAV	965	229-237
Hepsin	PLTEYIQPV	966	268-276
HER-2/neu	KIFGSLAFL	967	369-377
HER-2/neu	IISAVVGIL	968	654-662
HER-2/neu	ALCRWGLLL	969	44329
HER-2/neu	ILHNGAYSL	970	435-443
HER-2/neu	VVLGVVFGI	971	665-673
HER-2/neu	YMIMVKCWMI	972	952-961
HER-2/neu	YLVPQQGFFC	973	1023-1032
HER-2/neu	RLLQETELV	974	689-697
HER-2/neu	HLYQGCQVV	975	48-56
HER-2/neu	PLQPEQLQV	976	391-399
HER-2/neu	ALIHHNTHL	977	466-474
HER-2/neu	TLEEITGYL	978	402-410
HER-2/neu	PLTSIISAV	979	650-658
HLA-DOB	FLLGLIFLL	980	232-240
HSPH1	RLMNDMTAV	981	169-177
IDO1	ALLEIASCL	982	199-207
IGF2B3	NLSSAEVVV	983	515-523
IL13Ralpha2	WLPFGFILI	984	345-353
Kallikrein 4	FLGYLILGV	985	43770
KIF20A	AQPDTAPLPV	986	284-293
KIF20A	LLSDDDVVV	987	44166
KIF20A	CIAEQYHTV	988	809-817
Lengsin	FLPEFGISSA	989	270-279
mdm-2	VLFYLGQY	990	53-60
Meloe	TLNDECWPA	991	36-44
Midkine	ALLALTSAV	992	13-21
Midkine	AQCQETIRV	993	114-122
MMP-2	GLPPDVQRVh	994	560-568
MUC1	STAPPVHNV	995	950-958
MUC1	LLLLTVLTV	996	44166
nectin-4	VLVPPLPSL	997	145-153

TABLE 1-continued

Cancer peptides			
Gene/Protein	Peptide Sequence	SEQ ID NO:	Position
p53	RMPEAAPPV	998	65-73
p53	LLGRNSFEV	999	264-272
PAX5	TLPGYPPHV	1000	311-319
PLAC1	VLCSIDWFM	1001	28-36
PRAME	VLDGLDVLL	1002	100-108
PRAME	ALYVDSLFFL	1003	300-309
PRAME	SLYSFPEPEA	1004	142-151
PRAME	SLLQHLIGL	1005	425-433
RAGE-1	LKLSGVVRL	1006	352-360
RAGE-1	PLPPARNGGLg	1007	32-40
RGS5	LAALPHSCL	1008	41395
RNF43	ALWPWLLMA(T)	1009	11-19(20)
Secernin 1	KMDAEHPEL	1010	196-204
SOX10	AWISKPPGV	1011	332-340
SOX10	SAWISKPPGV	1012	331-340
STEAP1	MIAVFLPIV	1013	292-300
STEAP1	HQQYFYKIPILVINK	1014	102-116
survivin	ELTLGEFLKL	1015	95-104
survivin	ELTLGEFLKL	1016	95-104
Telomerase	ILAKFLHWLE	1017	540-548
Telomerase	RLVDDFLLV	1018	865-873
TPBG	RLARLALVL	1019	17-25
IGF2B3	RLLVPTQFV	1020	199-207

[0136] In some embodiments, the immunogenic peptide is a non-human peptide. In some embodiments, the immunogenic peptide is a viral peptide. In some embodiments, the immunogenic peptide is a bacterial peptide. Viral peptides are well known in the art and any such peptide may be employed. Such peptides can found, for example, at the Immune Epitope Database (IEDB) and VDJDB database: iedb.org and vdjdb.cdr3.net. In some embodiments, the viral peptide is derived from a virus selected from Cytomegalovirus (CMV), Epstein-Barr virus (EBV) or Influenza virus (FLU). In some embodiments, the viral peptide is derived from a virus selected from CMV, EBV, FLU, Severe acute respiratory syndrome coronavirus 2 (SARS-CoV2), Adenovirus and Human Papilloma virus (HPV). In some embodiments, the virus is CMV. In some embodiments, the virus is EBV. In some embodiments, the virus is FLU. In some embodiments, the virus is SARS-CoV2. In some embodiments, the virus is Adenovirus. In some embodiments, the virus is HPV. In some embodiments, the viral peptide is a peptide provided in Table 2. In some embodiments, the viral peptide is selected from a sequence provided in Table 2. In some embodiments, the viral peptide is a peptide provided in Table 3. In some embodiments, the viral peptide is selected from a sequence provided in Table 3. In some embodiments, the viral peptide is selected from SEQ ID NO: 1-701. In some embodiments, the viral peptide is selected from SEQ ID NO: 1-695. In some embodiments, the viral peptide is selected from SEQ ID NO: 1-11. In some embodiments, the viral peptide is selected from SEQ ID NO: 1-9. In some embodiments, the viral peptide is selected from SEQ ID NO: 1-5. In some embodiments, the viral peptide is SEQ ID NO: 1. In some embodiments, the viral peptide is SEQ ID NO: 2. In some embodiments, the viral peptide is SEQ ID NO: 3. In some embodiments, the viral peptide is SEQ ID NO: 4. In some embodiments, the viral peptide is SEQ ID NO: 5. In some embodiments, the viral peptide is SEQ ID NO: 6. In some embodiments, the viral peptide is SEQ ID NO: 7. In some embodiments, the viral peptide is SEQ ID NO: 8. In some embodiments, the viral peptide is SEQ ID NO: 9. In some embodiments, the viral peptide is SEQ ID NO: 10. In some embodiments, the viral peptide is SEQ ID NO: 11. In some embodiments, the viral peptide is selected from SEQ ID NO: 1, 2, 3, 4, 5, 151, 197, 471, 677, 696, 697, 698, 699, 700, and 701.

TABLE 2

Viral peptides		
Peptide	SEQ ID NO:	source
NLVPMVATV	1	CMV
GLCTLVAML	197	EBV
CLGGLLTMV	2	EBV
CTELKLSDY	677	FLU
CLGGLLTMV, GLCTLVAML, NLVPMVATV, GILGFVFTL	2, 197, 1, 3	EBV, CMV, FLU
DYNFVKQLF, GLCTLVAML, TYPVLEEMF, RYSIFFDYM, AVFDRKSDAK, TYSAGIVQI, IVTDFSVIK, SSCSSCPLSK, AYAQKIFKIL, VYALPLKML, QYDPVAALF, NLVPMVATV, GPISGHVLK,	696, 197, 697, 698, 4, 699, 151, 629, 471, 700, 5, 1, 701	EBV, CMV, FLU

TABLE 3

Full list of viral peptides	
Peptide	SEQ ID NO:
NLVPMVATV	1
CLGGLLTMV	2
GILGFVFTL	3
AVFDRKSDAK	4
QYDPVAALF	5
TPSVSSSISSL	6
LPFNDGVYF	7
FLGERVTLT	8
LLALHRSYL	9
STDVASLNY	10
TLGIVCPI	11
RYSIFFDY	12
CPLSKILL	13
SLGYITTV	14
RAKFKQLL	15
TNKIKEQL	16
QTRQKFHL	17
EMRLRMIL	18
MAREKNDL	19
CCKCDSTL	20
HDIILECV	21
LPQGFSAL	22
NLTTRTQL	23

TABLE 3-continued

Full list of viral peptides	
Peptide	SEQ ID NO:
AEHVNNSY	24
AEVQIDRL	25
EPLVDLPI	26
FPREGVFV	27
NITRFQTL	28
QPYRVVVL	29
RLQSLQTY	30
SPRRARSV	31
VYYPDKVF	32
YAWNRKRI	33
FLPFFSNV	34
APHGVVFL	35
GVYHKNNK	36
TYFNLGNKF	37
TDLGQNLLY	38
TLLYVLFEV	39
VLAWTRAFV	40
YVAGFLALY	41
ALMGAVTSL	42
MMLRDRWSL	43
AVLCLYLLY	44
FLWEDQTLL	45
FIPQYLSAV	46

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
FLIAYQPLL	47
SVYPYDEFV	48
VYMSPFYGY	49
FLGDDPSPA	50
RLTGYPAGI	51
APASVYQPA	52
CPRRPAVAF	53
VVRGPTVSL	54
LIDGIFLRY	55
SQLAHLVYV	56
FLGAGALAV	57
FLGGHVAVA	58
TLRGLFFSV	59
KYFYCNSLF	60
EYQRLYATF	61
APRIGGRRA	62
APRTWCRLL	63
ALMLRLLRI	64
RILGVLVHL	65
YMESVFQMY	66
ILIEGIFFA	67
YMANQILRY	68
VPRPDDPVL	69
VYTPSPYVF	70
AYLPRPVEF	71
AILTQYWKY	72
ATDSLNNEY	73
AYVSVLYRW	74
LASDPHYEY	75
LLAYVSVLY	76
RLNELLAYV	77
SIVHHHAQY	78
ALATVTLKY	79
ALLDRDCRV	80
FLADAVVRL	81
FTAPEVGTY	82

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
RLLGFADTV	83
RSSLGSLLY	84
ALHTALATV	85
TLLELVVSV	86
VPGWSRRTL	87
ALLAKMLFY	88
RMLGDVMAV	89
TMLEDHEFV	90
ALLGLTLGV	91
FVLATGDFV	92
GIFEDRAPV	93
LLTTPKFTV	94
NLLTTPKFT	95
TMYYKDVTV	96
YLANGGFLI	97
ALSALLTKL	98
FLTCTDRSV	99
DRLDNRLQL	100
KSRRPLTTF	101
RRAQMAPKR	102
GPHETITAL	103
PAWSRRTLL	104
ASDSLNNEY	105
FLVDAIVRV	106
GLADTVVAC	107
RPRGEVRFL	108
SAPLPSNRV	109
SLPRSRTPI	110
ALWALPHAA	111
ILIEGIFFV	112
VTEHDTLLY	113
ELNRKMIYM	114
IPSINVHHY	115
TRATKMQVI	116
QIKVRVKMV	117
DELRRKMMY	118

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
EEAIVAYTL	119
ELKRKMMYM	120
QIKVRVDMV	121
VLEETSVML	122
ARAKKDELK	123
ARAKKDELR	124
DELKRKMIY	125
FMDILTTCV	126
KEWAYCVEM	127
LITGRLAAL	128
LLLNCLWSV	129
TMLDIQPED	130
LPRWYFYYL	131
KLWHYCSTL	132
LLIEGIFFI	133
AFLGERVTL	134
KLGPGEEQV	135
RFIAQLLLL	136
TLTSYWRRV	137
VEDLFGANL	138
WQWEHIPPA	139
LPCVLWPVL	140
RAKFKQLLQ	141
SENDRLRLL	142
TLDTKPLSV	143
FMVFLQTHI	144
HPVGEADYF	145
VLKDAIKDL	146
AYSSWMYSY	147
QAKWRLQTL	148
RLRAEAQVK	149
SVRDRLARL	150
IVTDFSVIK	151
VSFIEFVGW	152
EGGVGWRHW	153
QPRAPIRPI	154

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
RRIYDLIEL	155
RPPIFIRLL	156
YPLHEQHGM	157
LMIIPLINV	158
SLVIVTTFV	159
TLFIGSHVV	160
YLQQNWWTL	161
ALLVLYSFA	162
GLGTLGAAL	163
LLSAWILTA	164
LLWTLVVLL	165
MGSLEMVPM	166
YLLEMLWRL	167
VLQWASLAV	168
FLYALALLL	169
IEDPPFNSL	170
RRRWRRLTV	171
TYGPVFMCL	172
FLRGRAYGL	173
LVLILYLCV	174
LLNGWRWRL	175
IGLITVLFL	176
DAAPAIQHI	177
KQYLGVYIW	178
TYATFLVTW	179
KENIAAYKF	180
KTNNWHAGW	181
APKTATSSW	182
QTTGRITNR	183
VEDINRVFL	184
CYDHAQTHL	185
TLDYKPLSV	186
YRSGIIAVV	187
RPPIFIRRL	188
FLDKGTYTL	189
ARYAYYLQF	190

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
RRRKGWIPL	191
LQHYREVAA	192
AENAGNDAC	193
RVRAYTYSK	194
YVLDHLIVV	195
DEVEFLGHY	196
GLCTLVAML	197
KDTWLDARM	198
VLFGLLCLL	199
ELRRKMMYM	200
ELKRKMIYM	201
EFKSKFSTL	202
EGRDRILTV	203
FEKERFLFL	204
EGRERILTV	205
NVKHKKNPL	206
VVKGKVLSI	207
EARRRLAEM	208
RSKPRHMCV	209
DFKSKYLTL	210
SPRSRLQQL	211
VLATAVREL	212
FQANTPPAV	213
IPYTAAVQV	214
KLAKLIIDL	215
RLPREKLKK	216
SPKAGLLSL	217
SLQQEITLL	218
ISDYFHNTY	219
KVLIRCYLC	220
SIDQLCKTF	221
HNNGICWGN	222
CYEQLGDSS	223
ITIRCIICQ	224
KTLEERVKK	225
MRGDKATIK	226

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
PYGVCIMCL	227
QLGDSSDEE	228
RLQCVQCKK	229
VYKFLFTDL	230
YYYAGSSRL	231
LQFIFQLCK	232
MTLCAEVKK	233
QYRVFRIKL	234
RIKLPDPNK	235
ILIRCIICQ	236
KCLNEILIR	237
KVCLRLLSK	238
ATEVRTLQQ	239
CTIVCPSCA	240
LCINSTATE	241
AVPDDLYIK	242
KYTFWEVNL	243
RVRLPDPNK	244
TSESQLFNK	245
YTFWEVNLK	246
YLTAPTGCI	247
DSAPILTAF	248
KSAIVTLTY	249
LAVSKNKAL	250
LQDVSLEVY	251
NPCHTTKLL	252
NTTPIVHLK	253
QVILCPTSV	254
RLECAIYYK	255
SPEIIRQHL	256
TLYTAVSST	257
VVEGQVDYY	258
YRFKKHCTL	259
ALQAIELQL	260
TLQDVSLEV	261
YIIFVYIPL	262

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
FAFRDLCIV	263
IILECVYCK	264
TTLEQQYNK	265
VCDKCLKFY	266
CPEEKQRHL	267
YGTTLEQQY	268
EYRHYCYSL	269
VYDFAFQDL	270
GTLGIVCPI	271
IVCPICSQK	272
QAEPDRAHY	273
RAHYNIVTF	274
TLHEYMLDL	275
LQPETTDLY	276
TPTLHEYML	277
LLMGTLGIV	278
TLGIVCPIC	279
IHSMNSTIL	280
ISEYRHYCY	281
KFYSKISEY	282
KLPQLCTEL	283
VYDFAFRDL	284
TIHDIILEC	285
YMLDLQPET	286
IHSMNSSIL	287
NVFPIFLQM	288
KLPDLCTEL	289
NLLIRCLRC	290
FQQLFLNTL	291
LFLNTLSFV	292
LLLGTLNIV	293
TIDQLCKTF	294
EADVQQWLT	295
FYTPLADQF	296
GLCPHCINV	297
GLENNVLYH	298

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
LHTDFEQVM	299
LLHTDFEQV	300
SESSFFNLI	301
SSHSGSFQI	302
TEADVQQWL	303
VQQWLTWCN	304
TAKSRVHPL	305
LLLIWFRPV	306
AVDTVLAKK	307
EPLVWIDCY	308
AITEVECFL	309
LLMWEAVTV	310
RARRELPRF	311
YLEKESIYY	312
NPKASLLSL	313
QVMLRWGVL	314
GILGFVFTL	315
SRYWAIRTR	316
NMLSTVLGV	317
LPFERATVM	318
LPFERATIM	319
LPFDKSTVM	320
LPFEKSTIM	321
LPFDKPTIM	322
LPFEKSTVM	323
CVNGSCFTV	324
LPFDRTTIM	325
KTGGPIYRR	326
LPFDRPTIM	327
GLDNHTILL	328
ILMWEAVTL	329
SITEVECFL	330
NLNESLIDL	331
RLDKVEAEV	332
VYDPLQPEL	333
TLKSFTVEK	334

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
HADQLTPTW	335
NATNVVIKV	336
VGYLQPRTF	337
YFQPRTFLL	338
FQFCNDPFL	339
ASVYAWNRK	340
GYLQPRTFL	341
YLQLRTFLL	342
YLQPRIFLL	343
AEVQIDRLI	344
ALNTLVKQL	345
CVADYSVLY	346
GSFCTQLNR	347
GVVFLHVTY	348
LLFNKVTLA	349
LLQYGSFCT	350
RLQSLQTYV	351
RVDFCGKGY	352
SVLNDILSR	353
VLNDILSRL	354
FVFKNIDGY	355
GTHWFVTQR	356
GTITSGWTF	357
KEIDRLNEV	358
LEPLVDLPI	359
LPPAYTNSF	360
NGVEGENCY	361
NQKLIANQF	362
RISNCVADY	363
RLFRKSNLK	364
TLDSKTQSL	365
TPINLVRDL	366
YFPLQSYGF	367
FQPTNGVGY	368
RFDNPVLPF	369
TSNQVAVLY	370

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
GLTVLPPLL	371
SIIAYTMSL	372
YLQPRTFLL	373
EPVLKGVKL	374
LTDEMIAQY	375
QYIKWPWYI	376
VLKGVKLHY	377
VTYVPAQEK	378
KCYGVSPTK	379
SPRRARSVA	380
YEQYIKWPW	381
AEIRASANL	382
GVYFASTEK	383
GVYYHKNNK	384
MIAQYTSAL	385
NSASFSTFK	386
NYNYLYRLF	387
ADAGFIKQY	388
ALDPLSETK	389
AYSNNSIAI	390
DAVRDPQTL	391
EILPVSMTK	392
ETKCTLKSF	393
EVFAQVKQI	394
EYVSQPFLM	395
FAMQMAYRF	396
FASVYAWNR	397
FERDISTEI	398
FPQSAPHGV	399
FTISVTTEI	400
FVIRGDEVR	401
FVSNGTHWF	402
GAAAYYVGY	403
GEVFNATRF	404
HLMSFPQSA	405
HVSGTNGTK	406

TABLE 3-continued

Full list of viral peptides	
Peptide	SEQ ID NO:
HWFVTQRNF	407
IAIPTNFTI	408
IANQFNSAI	409
INITRFQTL	410
IPFAMQMAY	411
IPTNFTISV	412
IYQTSNFRV	413
KIADYNYKL	414
KIYSKHTPI	415
KSNLKPFER	416
KVFRSSVLH	417
LGAENSVAY	418
LPFNDGVYF	419
LPLVSSQCV	420
LPPLLTDEM	421
NASVVNIQK	422
NATRFASVY	423
NSFTRGVYY	424
NSIAIPTNF	425
QELGKYEQY	426
QIAPGQTGK	427
QLTPTWRVY	428
QPTESIVRF	429
QTNSPRRAR	430
RSVASQSII	431
RVYSTGSNV	432
SANNCTFEY	433
SFKEELDKY	434
SVYAWNRKR	435
TLADAGFIK	436
VASQSIIAY	437
VFAQVKQIY	438
VFKNIDGYF	439
VGGNYNYLY	440
WFVTQRNFY	441
WTAGAAAYY	442

TABLE 3-continued

Full list of viral peptides	
Peptide	SEQ ID NO:
WTFGAGAAL	443
YGFQPTNGV	444
YNYLYRLFR	445
YQDVNCTEV	446
YYHKNNKSW	447
TQDLFLPFF	448
FVFLVLLPL	449
LVKNKCVNF	450
STQDLFLPF	451
NIADYNYKL	452
NYNYRYRLF	453
TIADYNYKL	454
LLYANSAHAL	455
SSGVVFGTWY	456
EYVHARWAAF	457
HTDLHPNNTY	458
AYLGAFLSVL	459
FVYTPSPYVF	460
AYSLLFPAPF	461
RPTERPRAPA	462
FTDALGIDEY	463
SALPTNADLY	464
LYPDAPPLRL	465
GFLIAYQPLL	466
FLVDAIVRVA	467
PHSVVNPFVK	468
MILIEGIFFV	469
TPRVTGGGAM	470
AYAQKIFKIL	471
YILEETSVML	472
RRKMMYMCYR	473
TYSQKIFKIL	474
RPPIFIRRLH	475
VEITPYKPTW	476
EENLLDFVRF	477
LLDFVRFMGV	478

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
PYLFWLAAIA	479
VMSNTLLSAW	480
QNGALAINTF	481
DTPLIPLTIF	482
ATVKTGNIKL	483
AERQGSPTPA	484
KPQGQRLIEV	485
QTDTYTLLGY	486
ILIEGIFFVS	487
HVFPHRFISF	488
RIRLVVPSAL	489
SLILIGITTL	490
KVEGEQHVIK	491
IAPYAGLIMI	492
KPAVGVYHIV	493
FSECNALGSY	494
STELNYNHLY	495
FLTEAIVHSV	496
YVLDLQPEAT	497
FACYDLCIVY	498
FAFSDLYVVY	499
FAFKDLCIVY	500
VAFTEIKIVY	501
YILDLQPETT	502
FVFADLRIVY	503
FAFSDLCIVY	504
ILTAFNSSHK	505
LTAPTGCIKK	506
TLKCLRYRFK	507
YYVHEGIRTY	508
YICEEASVTV	509
LLIRCINCOK	510
AVCDKCLKFY	511
CVYCKQQLLR	512
NPYAVCDKCL	513
RPRKLPQLCT	514

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
YAVCDKCLKF	515
QYNKPLCDLL	516
GIVCPICSQK	517
HGDTPTLHEY	518
HYNIVTFCCK	519
YMLDLQPETT	520
TIHDIILECV	521
HNIRGRWTGR	522
FAFRDLCIVY	523
QERPRKLPQL	524
RWTGRCMSCC	525
SSRTRRETQL	526
HPAATHTKAV	527
TLLQQYCLYL	528
GLCPHCINVG	529
HAKALKERMV	530
IDTCISATFR	531
LLHTDFEQVM	532
QSALKLAIYK	533
SALKLAIYKA	534
KLYQNPTTYI	535
RLYQNPTTYI	536
KFLPDLYDYK	537
VLRGFLILGK	538
GILGFVFTLT	539
RMVLASTTAK	540
SFSFGGFTFK	541
KNIDGYFKIY	542
CMTSCCSCLK	543
DSFKEELDKY	544
QPYRVVVLSF	545
SEPVLKGVKL	546
CALDPLSETK	547
EILDITPCSF	548
FTISVTTEIL	549
IGAEHVNNSY	550

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
ILPDPSKPSK	551
IYSKHTPINL	552
KLPDDFTGCV	553
KTSVDCTMYI	554
LSSTASALGK	555
STQDLFLPFF	556
SVLNDILSRL	557
TEKSNIIRGW	558
WIFGTTLDSK	559
YHLMSFPQSA	560
TQLNRALTGI	561
NESLIDLQEL	562
DGVYFASTEK	563
DSKVGGNYNY	564
EVFAQVKQIY	565
FDEDDSEPVL	566
FERDISTEIY	567
FEYVSQPFLM	568
FLPFFSNVTW	569
GVFVSNGTHW	570
GVYYPDKVFR	571
GYLQPRTFLL	572
HVTYVPAQEK	573
IHADQLTPTW	574
KFLPFQQFGR	575
KVGGNYNYLY	576
LPIGINITRF	577
NTSNQVAVLY	578
NVYADSFVIR	579
QIPFAMQMAY	580
QYIKWPWYIW	581
RASANLAATK	582
RFASVYAWNR	583
RVYSTGSNVF	584
SETKCTLKSF	585
STGSNVFQTR	586

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
SVASQSIIAY	587
SWMESEFRVY	588
TECSNLLLQY	589
TPCSFGGVSV	590
VFVSNGTHWF	591
VYSSANNCTF	592
YTNSFTRGVY	593
IYKTPPIKDF	594
LLTDEMIAQY	595
SYFIASFRLF	596
EITDTIDKFGK	597
LPEGMDPFAEK	598
ARLCDLPATPK	599
LQRGPQYSEHP	600
PSQEPMSIYVY	601
QEFFWDANDIY	602
QYDPVAALFFF	603
RLTVSGLAWTR	604
RNLVPMVATVQ	605
TPRVTGGGAMA	606
VFPTKDVALRH	607
VLCPKNMIIKP	608
YSEHPTFTSQY	609
YYTSAFVFPTK	610
QYTPDSTPCHR	611
RPHERNGFTVL	612
AKARAKKDELR	613
CYVLEETSVML	614
EFCRVLCCYVL	615
EQVTEDCNENP	616
ESLKTFEQVTE	617
FPKTTNGCSQA	618
GKSTHPMVTRS	619
KDELRRKMMYM	620
KNSAFPKTTNG	621
KQIKVRVDMVR	622

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
MAYAQKIFKIL	623
NIEFFTKNSAF	624
SVMKRRIEEIC	625
YPRNPTEQGNI	626
HPVGEADYFEY	627
QPRAPIRPIPT	628
SSCSSCPLSKI	629
EPLPQGOLTAY	630
AVYENPLSVEK	631
TEADVQQWLTW	632
FFAVGGDPLEM	633
IAVGLLLYCKA	634
TIAMELIRMIK	635
EILDITPCSFG	636
AQALNTLVKQL	637
FCNDPFLGVYY	638
FPQSAPHGVVF	639
KSWMESEFRVY	640
LQIPFAMQMAY	641
NYNYLYRLFRK	642
YEQYIKWPWYI	643
IPIGAGICASY	644
KPFERDISTEI	645
QEVFAQVKQIY	646
RFPNITNLCPF	647
YECDIPIGAGI	648
YENQKLIANQF	649
YYVGYLQPRTF	650
SFELLHAPATV	651
TYVPAQEKNFT	652
HPVGDADYFEY	653
HPVGQADYFEY	654
RVAGDSGFAAY	655
EFFWDANDIY	656
RPHERNGFTV	657
LPRRSGAAGA	658

TABLE 3-continued

Full list of viral peptides

Peptide	SEQ ID NO:
ALQIPFAMQM	659
QELIRQGTDY	660
RARSVASQSI	661
RLITGRLQSL	662
TLATHGLAAV	663
TTDPSFLGRY	664
VENPHLMGWD	665
YPDKVFRSSV	666
AYAQKIFKI	667
CRVLCCYVL	668
CVETMCNEY	669
DEEDAIAAY	670
FRCPRRFCF	671
KLGGALQAK	672
MLNIPSINV	673
VMAPRTLIL	674
YILEETSVM	675
MLDLQPETT	676
CTELKLSDY	677
FEDLRVLSF	678
ALSKGVHFV	679
ALWEIQQVV	680
DTDFVNEFY	681
FIAGLIAIV	682
FTSDYYQLY	683
KQIYKTPPI	684
KTFPPTEPK	685
LLLDRLNQL	686
LLYDANYFL	687
MLAKALRKV	688
MQLFFSYFA	689
PTDNYITTY	690
SPRWYFYYL	691
VYFLQSINF	692
VYIGDPAQL	693
FPTKDVAL	694

TABLE 3-continued

Full list of viral peptides	
Peptide	SEQ ID NO:
NEGVKAAW	695
DYNFVKQLF	696
TYPVLEEMF	697
RYSIFFDYM	698
TYSAGIVQI	699
VYALPLKML	700
GPISGHVLK	701

[0137] In some embodiments, the immunogenic peptide is inserted into a complementarity determining region (CDR) of the antibody or antigen binding fragment thereof. In some embodiments, insertion of the immunogenic peptide comprises removal of CDR sequence. In some embodiments, at least one CDR of the antibody or antigen binding fragment thereof is replaced with the immunogenic peptide. In some embodiments, the CDR is the whole CDR. In some embodiments, the CDR is at least a portion of the CDR. In some embodiments, CDR sequence comprises sequence of at least a portion of the CDR. In some embodiments, a portion is at least 4 amino acids. In some embodiments, a portion is at least 5 amino acids. In some embodiments, a portion is at least 6 amino acids. In some embodiments, a portion is at least 7 amino acids. In some embodiments, a portion is at least 8 amino acids. In some embodiments, a portion is at least 9 amino acids. In some embodiments, insertion of the immunogenic peptide comprises removal of the CDR. In some embodiments, insertion of the immunogenic peptide comprises removal of at least a portion of the CDR.

[0138] In some embodiments, replacement of the CDR or a portion of the CDR also comprises replacement of at least one amino acid flanking the CDR. In some embodiments, flanking is N-terminal to the CDR. In some embodiments, flanking is C-terminal to the CDR. In some embodiments, at least one amino acid is at least the 1, 2, 3, 4 or 5 amino acids directly flanking the CDR. Each possibility represents a separate embodiment of the invention. In some embodiments, at least one amino acid is 4-5 amino acids. In some embodiments, at least one amino acid is 4 amino acids. In some embodiments, at least one amino acid is 5 amino acids. In some embodiments, the flanking region is not more than 5, 6, 7, 8, 9 or 10 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the flanking region is not more than 5 amino acids. In some embodiments, the flanking region is not more than 10 amino acids. In some embodiments, a flanking region comprises a stem of the CDR loop. It will be understood by a skilled artisan that in order to preserve antibody structure and to produce as little perturbation as possible it may be necessary to also replace a portion of the CDR flanking regions along with the CDR itself (or a portion thereof).

[0139] In some embodiments, the CDRH1 of TMab4 comprises or consists of amino acid 26-33 of SEQ ID NO: 1021. In some embodiments, the CDRH2 of TMab4 comprises or consists of amino acid 51-58 of SEQ ID NO: 1021. In some embodiments, the CDRH3 of TMab4 comprises or consists of amino acid 97-109 of SEQ ID NO: 1021. In some embodiments, the CDRL1 of TMab4 comprises or consists of amino acid of 27-38SEQ ID NO: 1022. In some embodiments, the CDRL2 of TMab4 comprises or consists of amino acid 56-58 of SEQ ID NO: 1022. In some embodiments, the CDRL3 of TMab4 comprises or consists of amino acid 95-103 of SEQ ID NO: 1022. In some embodiments, the CDRH1 of 3E10 comprises or consists of amino acid 26-33 of SEQ ID NO: 1023. In some embodiments, the CDRH2 of 3E10 comprises or consists of amino acid 51-58 of SEQ ID NO: 1023. In some embodiments, the CDRH3 of 3E10 comprises or consists of amino acid 97-105 of SEQ ID NO: 1023. In some embodiments, the CDRL1 of 3E10 comprises or consists of amino acid 27-36 of SEQ ID NO: 1024. In some embodiments, the CDRL2 of 3E10 comprises or consists of amino acid 54-56 of SEQ ID NO: 1024. In some embodiments, the CDRL3 of 3E10 comprises or consists of amino acid 93-101 of SEQ ID NO: 1024. In some embodiments, the CDRH1 of 71F12 comprises or consists of amino acid 26-33 of SEQ ID NO: 1026. In some embodiments, the CDRH2 of 71F12 comprises or consists of amino acid 51-57 of SEQ ID NO: 1026. In some embodiments, the CDRH3 of 71F12 comprises or consists of amino acid 96-105 of SEQ ID NO: 1026. In some embodiments, the CDRL1 of 71F12 comprises or consists of amino acid 26-34 of SEQ ID NO: 1027. In some embodiments, the CDRL2 of 71F12 comprises or consists of amino acid 52-54 of SEQ ID NO: 1027. In some embodiments, the CDRL3 of 71F12 comprises or consists of amino acid 91-100 of SEQ ID NO: 1027.

[0140] In some embodiments, the antigen binding molecule comprises a cell penetration sequence. In some embodiments, the cell penetration sequence is a cell penetration domain. In some embodiments, the cell penetration sequence is a cell penetration peptide. In some embodiments, the cell penetration sequence targets the molecule to the inside of the cell. In some embodiments, the cell penetration sequence delivers the molecule to the inside of the cell. In some embodiments, the cell penetration sequence enables entrance of the molecule to the inside of the cell. In some embodiments, the inside of the cell is an endosome. In some embodiments, the inside of the cell is the cytoplasm. In some embodiments, delivery to the cytoplasm comprises exit from an endosome. In some embodiments, delivery to the cytoplasm comprises escape from an endosome. In some embodiments, an endosome is the endosomal pathway. In some embodiments, the cell penetration sequence is a peptide transduction domain (PTD). In some embodiments, the cell penetration sequence is a cell penetrating peptide (CPP). In some embodiments, the cell penetration sequence is an endosomal escape domain (EED). Peptide sequences that allow entrance into the cytoplasm and in particular escape from the endosomal pathway after endocytosis are well known in the art and any such peptide sequence may be employed.

[0141] It is known in the art that the CDRL1 and CDRL3 of Tmab4 are both play a role in antibody penetration (see Kim et al., "Endosomal acidic pH-induced conformational changes of a cytosol-penetrating antibody mediate endosomal escape", J Control Release, 2016, 10; 235:165-175 and Choi et al., "A general strategy for generating intact, full-length IgG antibodies that penetrate into the cytosol of living cells", Mabs, 2014; 6(6):1402-14, herein incorporated by reference in their entirety. In some embodiments, the cell

penetration sequence comprises the CDRL1 of Tmab4. In some embodiments, the cell penetration sequence consists of the CDRL1 of Tmab4. In some embodiments, the cell penetration sequence comprises the CDRL3 of Tmab4. In some embodiments, the cell penetration sequence consists of the CDRL3 of Tmab4. Methods of grafting the cell penetration sequence into other antibodies are known in the art, such as for example, the method provided in Choi et al.

[0142] In some embodiments, the antigen binding molecule is a bi-specific antibody. In some embodiments, the antigen binding molecule is a bi-specific antibody fragment of an antibody. In some embodiments, the antigen binding molecule comprises a plurality of antigen binding regions. In some embodiments, the antigen binding molecule comprises at least two antigen binding regions. In some embodiments, the antigen binding molecule comprises two antigen binding regions. In some embodiments, at least one of the antigen binding regions is the antigen binding region that is capable of binding to a target cell. In some embodiments, at least one of the antigen binding regions is mutated to comprises the immunogenic peptide. In some embodiments, at least one of the antigen binding regions is mutated to comprises the cell penetration sequence. In some embodiments, at least one of the antigen binding regions is mutated to comprises the immunogenic peptide, the cell penetration sequence or both. In some embodiments, the mutation is mutation of a complementarity determining region (CDR). In some embodiments, a CDR of an antigen binding region is mutated. In some embodiments, mutated is replaced. In some embodiments, replaced is replaced with the immunogenic peptide. In some embodiments, replaced is replaced with the cell penetration sequence.

[0143] In some embodiments, the CDR is an inert CDR. In some embodiments, an inert CDR does not contribute to binding to a target antigen. In some embodiments, binding is binding of the antigen binding region comprising the CDR to the target antigen. In some embodiments, an inert CDR comprises little or no contribution to binding. In some embodiments, an inert CDR comprises two or fewer amino acids that contact the target antigen. In some embodiments, an inert CDR comprises fewer than 2 amino acids that contact the target antigen. In some embodiments, an inert CDR comprises 2, 1 or 0 amino acids that contact the target antigen. In some embodiments, an inert CDR comprises 2 amino acid that contacts the target antigen. In some embodiments, an inert CDR comprises 1 amino acid that contacts the target antigen. In some embodiments, an inert CDR does not comprise an amino acid that contacts the target antigen. In some embodiments, an inert CDR does not contact the target antigen. In some embodiments, contact comprises a distance of not more than 3, 5, 7, 9 or 10 angstroms. Each possibility represents a separate embodiment of the invention. In some embodiments, contact comprises a distance of not more than 5 angstroms.

[0144] In some embodiments, the distance is between the amino acid of the CDR and an amino acid of the target antigen. In some embodiments, the distant is the distance present when the antigen binding domain is bound to the antigen. In some embodiments, the distance is the distance during crystallography studies of the binding.

[0145] In some embodiments, mutation or replacement of an inert CDR does not diminish binding. In some embodiments, not diminishing binding is not significantly diminishing binding. In some embodiments, mutation or replacement of an inert CDR does not abrogate binding. In some embodiments, a significant diminishment is a reduction in binding of more than 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 75, 80, 90, 95 or 99%. Each possibility represents a separate embodiment of the invention. In some embodiments, a significant diminishment is a reduction in binding of more than 10%. In some embodiments, a significant diminishment is a reduction in binding of more than 20%. In some embodiments, mutation or replacement of an inert CDR does not reduce binding by 100%.

[0146] In some embodiments, mutation or replacement of an inert CDR does not diminish cell penetrance. In some embodiments, not diminishing cell penetrance is not significantly diminishing cell penetrance. In some embodiments, mutation or replacement of an inert CDR does not abrogate cell penetrance. In some embodiments, a significant diminishment is a reduction in penetrance of more than 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 75, 80, 90, 95 or 99%. Each possibility represents a separate embodiment of the invention. In some embodiments, a significant diminishment is a reduction in penetrance of more than 10%. In some embodiments, a significant diminishment is a reduction in penetrance of more than 20%. In some embodiments, mutation or replacement of an inert CDR does not reduce penetrance by 100%. In some embodiments, mutation or replacement of an inert CDR does not reduce penetrance to the level of a control antibody. In some embodiments, a control antibody is an antibody that does not enter a cell. Antibodies that do not enter cells are well known in the art, and include for example adalimumab and muromonab. In some embodiments, not diminishing cell penetrance comprises retaining penetrance that is substantially equal to the binding of the antibody or antigen binding fragment thereof devoid of or without the immunogenic peptide.

[0147] In some embodiments, insertion of the immunogenic peptide and removal of CDR sequence produces no change in the conformation of the antibody or antigen binding fragment thereof. In some embodiments, insertion of the immunogenic peptide and removal of CDR sequence produces minimal change in the conformation of the antibody or antigen binding fragment thereof. In some embodiments, conformation is overall conformation. In some embodiments, conformation is 3D structure. In some embodiments, conformation is tertiary structure. In some embodiments, change is perturbation. In some embodiments, minimal change is without a loss of a bond. In some embodiments, minimal change is a change of less than 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50%. Each possibility represents a separate embodiment of the invention. In some embodiments, minimal change comprises binding of a target antigen at an equivalent affinity to the antibody or antigen binding fragment thereof devoid or without the immunogenic peptide. In some embodiments, equivalent is with no reduction in affinity. In some embodiments, equivalent is with a reduction in affinity of not more than 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50%. Each possibility represents a separate embodiment of the invention. In some embodiments, equivalent is with a reduction in affinity of not more than 10%. In some embodiments, equivalent is with a reduction in affinity of not more than 20%

[0148] In some embodiments, the mutated CDR is in the antigen binding region capable of binding the target cell. In some embodiments, the mutated CDR is not in the antigen binding region capable of binding the target cell. In some

embodiments, the mutated CDR is in an antigen binding region other than the antigen binding region capable of binding the target cell. In some embodiments, the immunogenic peptide replaces a CDR in the antigen binding region capable of binding the target cell. In some embodiments, the cell penetrating sequence replaces a CDR in an antigen binding region that is not the antigen binding region that binds the target cell. In some embodiments, the immunogenic peptide and the cell penetration sequence are in the same antigen binding region. In some embodiments, the immunogenic peptide and the cell penetration sequence are in different antigen binding regions.

[0149] In some embodiments, the target cell is a dendritic cell, the dendritic cell antigen is CD40, the antigen binding region capable of binding to CD40 is Fab516 and light chain CDR L2 is replaced with said cell penetrating sequence, said immunogenic peptide or both.

[0150] In some embodiments, the target cell is a B cell, the B cell antigen is CD20, the antigen binding region capable of binding to CD20 is Arzerra and at least one of heavy chain CDR H1, light chain CDR L1 and light chain CDR L2 is replaced with said cell penetrating sequence, said immunogenic peptide or both. In some embodiments, replaced is mutated to include the peptide or sequence. In some embodiments, heavy chain CDR H1 is replaced. In some embodiments, the light chain CDR L1 is replaced. In some embodiments, the light chain CDR L2 is replaced.

[0151] In some embodiments, the target cell is a cancer cell, the cancer cell antigen is PD-L1, the antigen binding region capable of binding to PD-L1 is Durvalumab and at least one of heavy chain CDR H1, and light chain CDR L2 is replaced with said cell penetrating sequence, said immunogenic peptide or both. In some embodiments, replaced is mutated to include the peptide or sequence. In some embodiments, heavy chain CDR H1 is replaced. In some embodiments, the light chain CDR L2 is replaced.

[0152] In some embodiments, the antibody is TMab4 and the immunogenic peptide is inserted into any one of CDRH1, CDRH2, CDRH3 and CDRL3. In some embodiments, the antibody is TMab4 and the immunogenic peptide is inserted into CDRH1. In some embodiments, the antibody is TMab4 and the immunogenic peptide is inserted into CDRH2. In some embodiments, the antibody is TMab4 and the immunogenic peptide is inserted into CDRH3. In some embodiments, the antibody is TMab4 and the immunogenic peptide is inserted into CDRL3. In some embodiments, SEQ ID NO: 1 is inserted into CDRH1 of TMab4. In some embodiments, SEQ ID NO: 2 is inserted into CDRH1 of TMab4. In some embodiments, SEQ ID NO: 3 is inserted into CDRH1 of TMab4. In some embodiments, SEQ ID NO: 4 is inserted into CDRH1 of TMab4. In some embodiments, SEQ ID NO: 5 is inserted into CDRH1 of TMab4. In some embodiments, SEQ ID NO: 1 is inserted into CDRH2 of TMab4. In some embodiments, SEQ ID NO: 2 is inserted into CDRH2 of TMab4. In some embodiments, SEQ ID NO: 3 is inserted into CDRH2 of TMab4. In some embodiments, SEQ ID NO: 4 is inserted into CDRH2 of TMab4. In some embodiments, SEQ ID NO: 5 is inserted into CDRH2 of TMab4. In some embodiments, SEQ ID NO: 1 is inserted into CDRH3 of TMab4. In some embodiments, SEQ ID NO: 2 is inserted into CDRH3 of TMab4. In some embodiments, SEQ ID NO: 3 is inserted into CDRH3 of TMab4. In some embodiments, SEQ ID NO: 4 is inserted into CDRH3 of TMab4. In some embodiments, SEQ ID NO: 5 is inserted into CDRH3 of TMab4. In some embodiments, SEQ ID NO: 1 is inserted into CDRL3 of TMab4. In some embodiments, SEQ ID NO: 2 is inserted into CDRL3 of TMab4. In some embodiments, SEQ ID NO: 3 is inserted into CDRL3 of TMab4. In some embodiments, SEQ ID NO: 4 is inserted into CDRL3 of TMab4. In some embodiments, SEQ ID NO: 5 is inserted into CDRL3 of TMab4. In some embodiments, SEQ ID NO: 6 is inserted into CDRH1 of TMab4. In some embodiments, SEQ ID NO: 7 is inserted into CDRH23 of TMab4. In some embodiments, SEQ ID NO: 8 is inserted in place of amino acids 14-22 of the light chain of TMab4. In some embodiments, into CDRH1 comprises replacing amino acids 25-33 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 26-33 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 26-32 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 27-33 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 28-33 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 22-30 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 22-29 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 26-31 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 23-32 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 23-31 of the heavy chain. In some embodiments, into CDRH1 comprises replacing amino acids 28-35 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 100-108 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 99-106 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 99-105 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 100-106 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 100-105 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 100-104 of the heavy chain. In some embodiments, into CDRH3 comprises replacing amino acids 99-107 of the heavy chain. In some embodiments, into CDRH2 comprises replacing amino acids 52-59 of the heavy chain. In some embodiments, into CDRH2 comprises replacing amino acids 52-60 of the heavy chain. In some embodiments, into CDRL3 comprises replacing amino acids 97-103 of the light chain. In some embodiments, into CDRL3 comprises replacing amino acids 98-103 of the light chain. In some embodiments, into CDRL3 comprises replacing amino acids 96-104 of the light chain. In some embodiments, into CDRL3 comprises replacing amino acids 98-104 of the light chain.

[0153] In some embodiments, the antibody is 3E10 and the immunogenic peptide is inserted into any one of CDRL1 and CDRL2. In some embodiments, the antibody is 3E10 and the immunogenic peptide is inserted into CDRL1. In some embodiments, the antibody is 3E10 and the immunogenic peptide is inserted into CDRL2. In some embodiments, SEQ ID NO: 1 is inserted into CDRL1 of 3E10. In some embodiments, SEQ ID NO: 2 is inserted into CDRL1 of 3E10. In some embodiments, SEQ ID NO: 3 is inserted into CDRL1 of 3E10. In some embodiments, SEQ ID NO: 4 is inserted into CDRL1 of 3E10. In some embodiments, SEQ ID NO: 5 is inserted into CDRL1 of 3E10. In some embodiments, SEQ ID NO: 1 is inserted into CDRL2 of

3E10. In some embodiments, SEQ ID NO: 2 is inserted into CDRL2 of 3E10. In some embodiments, SEQ ID NO: 3 is inserted into CDRL2 of 3E10. In some embodiments, SEQ ID NO: 4 is inserted into CDRL2 of 3E10. In some embodiments, SEQ ID NO: 5 is inserted into CDRL2 of 3E10. In some embodiments, SEQ ID NO: 6 is inserted into CDRL1 of 3E10. In some embodiments, SEQ ID NO: 9 is inserted into CDRL2 of 3E10. In some embodiments, into CDRL1 comprises replacing amino acids 27-35 of the light chain. In some embodiments, into CDRL1 comprises replacing amino acids 28-36 of the light chain. In some embodiments, into CDRL2 comprises replacing amino acids 50-58 of the light chain.

[0154] In some embodiments, the antibody is 71F12 and the immunogenic peptide is inserted into CDRL1. In some embodiments, SEQ ID NO: 1 is inserted into CDRL1 of 71F12. In some embodiments, SEQ ID NO: 2 is inserted into CDRL1 of 71F12. In some embodiments, SEQ ID NO: 3 is inserted into CDRL1 of 71F12. In some embodiments, SEQ ID NO: 4 is inserted into CDRL1 of 71F12. In some embodiments, SEQ ID NO: 5 is inserted into CDRL1 of 71F12. In some embodiments, into CDRL1 comprises replacing amino acids 28-36 of the light chain. In some embodiments, into CDRL1 comprises replacing amino acids 26-34 of the light chain. In some embodiments, into CDRL2 comprises replacing amino acids 50-58 of the light chain.

[0155] In some embodiments, the antibody is a commercially available antibody. In some embodiments, the antibody penetrates into a bound cell at a level comparable to any one of TMab4, 3E10 and 71F12. In some embodiments, the antibody penetrates into a bound cell at a level comparable to TMab4. In some embodiments, the antibody penetrates into a bound cell at a level comparable to 3E10. In some embodiments, the antibody penetrates into a bound cell at a level comparable to 71F12. In some embodiments, comparable is with a penetrance that is at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 92, 95, 97, 99 or 100% of the original antibody. Each possibility represents a separate embodiment of the invention. In some embodiments, comparable is with a penetrance that is at least 80% of the original antibody. In some embodiments, comparable is with a penetrance that is at least 90% of the original antibody.

[0156] In some embodiments, the antigen binding region and the immunogenic peptide are part of the same amino acid chain. In some embodiments, the antigen binding region and the cell penetration sequence are part of the same amino acid chain. In some embodiments, the immunogenic peptide and the cell penetration sequence are part of the same amino acid chain. In some embodiments, the antigen binding molecule of the invention is a single fusion protein. In some embodiments, the antigen binding molecule of the invention is a single amino acid chain.

[0157] In some embodiments, the antigen binding region and the immunogenic peptide are separated by a linker. In some embodiments, the antigen binding region and the cell penetrating sequence are separated by a linker. In some embodiments, the immunogenic peptide and the cell penetrating sequence are separated by a linker. In some embodiments, the linker is not a chemical linker. In some embodiments, the linker is not an artificial linker. In some embodiments, the linker is a peptide linker. In some embodiments, the linker is an amino acid linker. In some embodiments, the linker comprises or consists of at least 1, 2, 3, 4 or 5 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the linker comprises or consists of at most 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the linker comprises or consists of 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acids. Each possibility represents a separate embodiment of the invention.

[0158] In some embodiments, the antibody is selected from antibodies T1-T19, T1_30-T1_35, T1_39-T1_45 and T1_47. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising a sequence selected from SEQ ID NO: 1028-1040, 1043-1045, 1047-1055, and 1058-1059 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, an analog or homolog comprises the immunogenic peptide. In some embodiments, an analog or homolog is capable of binding cells. In some embodiments, an analog or homolog is delivered to the cytosol upon cell binding. In some embodiments, reaching the cytosol comprises displaying the immunogenic peptide on the surface of the bound cell. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1028 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1029 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1030 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1031 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1032 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1033 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1034 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1035 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1036 or analogs or homologs

comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1037 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1038 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1039 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1040 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1043 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1044 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1045 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1047 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1048 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1049 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1050 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1051 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1052 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1053 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1054 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1055 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1058 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a light chain variable region comprising SEQ ID NO: 1022 and a heavy chain variable region comprising SEQ ID NO: 1059 or analogs or homologs comprising at least 85% sequence identity.

[0159] In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1021 and a light chain variable region comprising a sequence selected from SEQ ID NO: 1041-1042, 1046, and 1056-1057 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1021 and a light chain variable region comprising SEQ ID NO: 1041 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1021 and a light chain variable region comprising SEQ ID NO: 1042 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1021 and a light chain variable region comprising SEQ ID NO: 1046 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1021 and a light chain variable region comprising SEQ ID NO: 1056 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1021 and a light chain variable region comprising SEQ ID NO: 1057 or analogs or homologs comprising at least 85% sequence identity.

[0160] In some embodiments, the antibody is selected from antibodies T2_6, T2_11-T2_13, T2_20 and T2_23. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light chain variable region comprising a sequence selected from SEQ ID NO: 1060-1065 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light

chain variable region comprising SEQ ID NO: 1060 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light chain variable region comprising SEQ ID NO: 1061 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light chain variable region comprising SEQ ID NO: 1062 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light chain variable region comprising SEQ ID NO: 1063 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light chain variable region comprising SEQ ID NO: 1064 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1023 and a light chain variable region comprising SEQ ID NO: 1065 or analogs or homologs comprising at least 85% sequence identity.

[0161] In some embodiments, the antibody is selected from antibodies T4_1 and T4_3. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1026 and a light chain variable region comprising SEQ ID NO: 1066 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the antibody or antigen binding fragment thereof comprises a heavy chain variable region comprising SEQ ID NO: 1027 and a light chain variable region comprising SEQ ID NO: 1067 or analogs or homologs comprising at least 85% sequence identity.

[0162] In some embodiments, at least 85% identity is at least 90, 92, 95, 97, 99 or 100% identity. Each possibility represents a separate embodiment of the invention. It will be understood by a skilled artisan that while certain regions in the antibodies are required for function, such as the antigen binding CDRs, the immunogenic peptide and the cell penetrating moiety, other regions may bear alterations without altering function. Other inert CDRs are such a region as are many inter-CDR sequences as well as sequences within the constant region of an antibody. Analogs and homologs that retain function but contain alterations with these other regions are also encompassed within the invention.

[0163] In some embodiments, the antigen biding region is a single-chain antibody. In some embodiments, the antigen binding molecule of the invention comprises a first single-chain antibody and a second single chain antibody. In some embodiments, the first single-chain antibody is capable of binding the antigen of the target cell. In some embodiments, the second single-chain antibody is not functional. In some embodiments, the second single-chain antibody comprises the cell penetrating sequence. In some embodiments, the first single-chain antibody comprises the immunogenic peptide. In some embodiments, the second single-chain antibody comprises the immunogenic peptide. In some embodiments, the first single-chain antibody comprises an inert CDR replaced with the immunogenic peptide. In some embodiments, the first single-chain antibody comprises an inert CDR replaced with the cell penetrating sequence. In some embodiments, the first single-chain antibody and the second single-chain antibody are separated by a linker. In some embodiments, the linker is a peptide linker or an amino acid linker. In some embodiments, the peptide linker is an amino acid linker. In some embodiments, a peptide linker is a peptide bond.

[0164] In some embodiments, the antigen biding molecule is an antibody. In some embodiments, the antigen biding molecule comprises a first heavy chain and a first light chain. In some embodiments, the first antigen binding region comprises a first heavy chain and a first light chain. In some embodiments, the first heavy chain and the first light chain are capable of binding the antigen on a target cell. In some embodiments, a CDR of the first heavy chain is inert. In some embodiments, a CDR of the first light chain is inert. In some embodiments, an inert CDR of the first heavy chain is replaced with the immunogenic peptide. In some embodiments, an inert CDR of the first light chain is replaced with the immunogenic peptide. In some embodiments, an inert CDR of the first heavy chain is replaced with the cell penetration sequence. In some embodiments, an inert CDR of the first light chain is replaced with the cell penetration sequence.

[0165] In some embodiments, the antigen biding molecule comprises a second heavy chain. In some embodiments, the antigen biding molecule comprises a second light chain. In some embodiments, the antigen biding molecule comprises a second heavy chain and a second light chain. In some embodiments, the second antigen binding region comprises a second heavy chain. In some embodiments, the second antigen binding region comprises a second light chain. In some embodiments, the second antigen binding region comprises a second heavy chain and a second light chain. In some embodiments, a CDR of the second heavy chain is inert. In some embodiments, a CDR of the second light chain is inert. In some embodiments, the second heavy chain comprises the immunogenic peptide. In some embodiments, the second light chain comprises the immunogenic peptide. In some embodiments, the second heavy chain comprises the cell penetrating sequence. In some embodiments, the second light chain comprises the cell penetrating sequence. In some embodiments, a CDR of the second light chain is replaced. In some embodiments, a CDR of the second heavy chain is replaced. In some embodiments, an inert CDR of the second heavy chain is replaced with the immunogenic peptide. In some embodiments, an inert CDR of the second light chain is replaced with the immunogenic peptide. In some embodiments, an inert CDR of the second heavy chain is replaced with the cell penetration sequence. In some embodiments, an inert CDR of the second light chain is replaced with the cell penetration sequence.

[0166] In some embodiments, the antigen binding molecule is a dual-function antigen binding molecule. In some embodiments, the composition comprises a dual-function antigen binding molecule. In some embodiments, the dual-function antigen binding molecule comprises an antibody or antigen binding fragment of the invention. In some embodiments, the dual-function antigen binding molecule is a bi-specific antibody. In some embodiments, the dual function antigen binding molecule comprises a first antibody or antigen binding molecule and a second antibody or antigen binding molecule. In some embodiments, the first antibody

is a first heavy chain and a first light chain and the second antibody and a second heavy chain and a second light chain. In some embodiments, the heavy chain and light chain are hybridized between the CH1 domain of the heavy chain and the CL domain of the light chain. In some embodiments, hybridized is bonded. In some embodiments, hybridized comprises disulfide bonds. In some embodiments, the second antibody or antigen binding fragment thereof is capable of binding an antigen overexpressed on a target cell. In some embodiments, the target cell is a cancer cell. In some embodiments, the antigen is a cancer antigen.

[0167] Examples of cancer antigens include but are not limited to epidermal growth factor (EGFR), Receptor tyrosine-protein kinase erbB2 (HER2), Nectin cell adhesion molecule 4 (NECTIN-4), Tumor-associated calcium signal transducer 2 (TROP-2/TACSTD2), Tissue Factor (TF/F3), B-cell maturation antigen (BCMA/TNFRSF17), Programmed death-ligand 1 (PDL-1), T cell immunoreceptor with Ig and ITIM domains (TIGIT), Epithelial cell adhesion molecule (EpCAM), TNF receptor superfamily member 8 (CD3/TNFRSF8), B-lymphocyte antigen CD19 (CD19), cluster of differentiation-22 (CD22), Siglec-3 (CD33), cluster of differentiation 38 (CD38), Cluster of differentiation 79 (CD79), Lymphocyte-activation gene 3 (LAG-3), C-C MotifChemokine Receptor 4 (CCR4), vascular endothelial growth factor receptor 2 (VEGFR2/KDR), Folate receptor 1 (FOLR1), CAMPATH-1 antigen (CD52), platelet-derived growth factor receptor A (PDGFRα), disialoganglio side GD2, mono sialodihexo sylganglio side (GM3), insulin-like growth factor 1 (IGF-1) receptor (IGF1R), SLAM family member 7 (SLAMF7), and cytotoxic T-lymphocyte-associated protein 4 (CTLA-4). Antibodies that bind to these cancer antigens are well known in the art and any such antibody can be used as the targeting module of the invention. In some embodiments, the cancer antigen targeted by the targeting molecule is selected from HER2, EGFR, EpCAM, BCMA, CD33, CD38, CTLA, LAG-3, and PD-L1. Examples of antibodies that can be used for the targeting moiety are provided in Table 4.

TABLE 4

targeting moiety antibodies

International Non-Proprietary Name	Target
Omburtamab	B7-H3 (CD276)
Belantamab mafodotin (belantamab mafodotin-blmf)	BCMA
Teclistamab	BCMA, CD3
Mogamulizumab (mogamulizumab-kpkc)	CCR4
Loncastuximab tesirine	CD19
Tafasitamab (tafasitamab-cxix)	CD19
Blinatumomab	CD19, CD3
Ibritumomab tiuxetan	CD20
Obinutuzumab	CD20
Ofatumumab	CD20
Ripertamab	CD20
Rituximab	CD20
Tositumomab-I131	CD20
Mosunetuzumab	CD20, CD3
Glofitamab	CD20, CD3e
Inotuzumab ozogamicin	CD22
Moxetumomab pasudotox (moxetumomab pasudotox-tdfk)	CD22
Brentuximab vedotin	CD30
Gemtuzumab ozogamicin	CD33
Daratumumab	CD38
Isatuximab (isatuximab-irfc)	CD38
Alemtuzumab	CD52

TABLE 4-continued

targeting moiety antibodies

International Non-Proprietary Name	Target
Polatuzumab vedotin (polatuzumab vedotin-piiq)	CD79
Ipilimumab	CTLA-4
Tremelimumab	CTLA-4
Cetuximab	EGFR
Necitumumab	EGFR
Nimotuzumab	EGFR
Panitumumab	EGFR
Amivantamab	EGFR, cMET
Edrecolomab	EpCAM
Oportuzumab monatox	EpCAM
Catumaxomab	EPCAM, CD3
Mirvetuximab soravtansine	FOLR1
Dinutuximab	GD2
Naxitamab-gqgk	GD2
Racotumomab	GM3
[fam-]trastuzumab deruxtecan, (fam-trastuzumab deruxtecan-nxki)	HER2
Ado-trastuzumab emtansine	HER2
Disitamab vedotin	HER2
Inetetamab	HER2
Margetuximab-cmkb	HER2
Pertuzumab	HER2
Trastuzumab	HER2
Teprotumumab (teprotumumab-trbw)	IGF-1R
Relatlimab	LAG-3
Enfortumab vedotin (enfortumab vedotin-ejfv)	Nectin-4
Olaratumab	PDGFRα
Adebrelimab	PD-L1
Atezolizumab	PD-L1
Avelumab	PD-L1
Durvalumab	PD-L1
Envafolimab	PD-L1
Socazolimab	PD-L1
Sugemalimab	PD-L1
Tagitanlimab	PD-L1
Elotuzumab	SLAMF7
Sacituzumab govitecan (sacituzumab govitecan-hziy)	TROP-2
Ramucirumab	VEGFR2

[0168] In some embodiments, the antigen is epidermal growth factor receptor (EGFR). In some embodiments, the second antibody is selected from: cetuximab, panitumumab and necitumumab. In some embodiments, the second antibody is cetuximab. In some embodiments, the second antibody is panitumumab. In some embodiments, the second antibody is necitumumab. In some embodiments, cetuximab comprises a heavy chain comprising SEQ ID NO: 1069 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, cetuximab comprises a light chain comprising SEQ ID NO: 1068 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, panitumumab comprises a heavy chain comprising SEQ ID NO: 1071 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, panitumumab comprises a light chain comprising SEQ ID NO: 1070 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, necitumumab comprises a heavy chain comprising SEQ ID NO: 1073 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, necitumumab comprises a light chain comprising SEQ ID NO: 1072 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the analog or homolog retains target binding function. In some embodiments, the analog or homolog retains the CDRs of the antibody. In some embodiments, the CDRs are all of the CDRs that are not inert.

[0169] In some embodiments, at least one inert CDR of the second antibody is replaced with an immunogenic peptide. In some embodiments, the second antibody is a targeting antibody. In some embodiments, CDRH1 of cetuximab is replaced. In some embodiments, CDRL1 of cetuximab is replaced. In some embodiments, CDRL2 of cetuximab is replaced. In some embodiments, CDRL1 of panitumumab is replaced. In some embodiments, CDRL2 of panitumumab is replaced. In some embodiments, CDRL1 of necitumumab is replaced. In some embodiments, CDRL2 of necitumumab is replaced. In some embodiments, the CDR is replaced with a peptide selected from those provided in Tables 1-3. In some embodiments, the CDR is replaced with a peptide selected from those provided in Table 1. In some embodiments, the CDR is replaced with a peptide selected from those provided in Table 2. In some embodiments, the CDR is replaced with a peptide selected from those provided in Table 3. In some embodiments, the CDR is replaced with a peptide selected from SEQ ID NO: 1-11. In some embodiments, the CDR is replaced with a peptide selected from SEQ ID NO: 1-5. In some embodiments, the CDR is replaced with SEQ ID NO: 1. In some embodiments, the second antibody comprises an immunogenic peptide in place of amino acid sequence from an inert CDR. In some embodiments, the inert CDRs are provided in Table 14.

[0170] In some embodiments, the first antibody comprises at least one modification that promotes heterodimerization. In some embodiments, the first antibody comprises at least one modification that inhibits homodimerization. In some embodiments, the second antibody comprises at least one modification that promotes heterodimerization. In some embodiments, the second antibody comprises at least one modification that inhibits homodimerization. In some embodiments, the modification are knob-in-holes modifications. In some embodiments, the modification is a mutation. In some embodiments, the modification is in the constant region. In some embodiments, the constant region is the Fc region.

[0171] In some embodiments, the Fc region comprises an Ig CH2 domain. In some embodiments, the Fc region comprises an Ig heavy chain CH2 domain. In some embodiments, the Fc region comprises an Ig CH3 domain. In some embodiments, the Fc region comprises an Ig heavy chain CH3 domain. In some embodiments, the Fc region comprises or consists of both an Ig CH2 domain and Ig CH3 domain. In some embodiments, the Fc region comprises or consists of both an Ig heavy chain CH2 and an Ig heavy chain CH3 domain. In some embodiments, the first chain comprises a first portion of an Fc region and the second chain comprises a second portion of the Fc region. In some embodiments, the first portion comprises a CH2 domain, a CH3 domain or both. In some embodiments, the second portion comprises a CH2 domain, a CH3 domain or both. In some embodiments, interface of the first portion of an Fc region and the second portion of an Fc region produces a functional Fc region. In some embodiments, interface comprises contact. In some embodiments, interface comprises adjacent positioning. In some embodiments, interface comprises formation of the protein complex of the invention. In some embodiments, interface comprises dimerization of the first and second dimerization domains. In some embodiments, the CH2 domain is an Ig CH2 domain. In some embodiments the CH2 domain is a heavy chain CH2 domain. In some embodiments, the CH3 domain is an Ig CH3 domain. In some embodiments, the CH3 domain is a heavy chain CH3 domain.

[0172] In some embodiments, a CH2 domain comprises the amino acid sequence SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK (SEQ ID NO: 1097) or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the CH2 domain consists of SEQ ID NO: 1097. In some embodiments, SEQ ID NO: 1097 is the IgG1 CH2 domain.

[0173] In some embodiments, a CH3 domain comprises the amino acid sequence GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 1098) or analogs or homologs comprising at least 85% sequence identity. In some embodiments, a CH3 domain comprises the amino acid sequence GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 1099) or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the CH3 domain consists of SEQ ID NO: 1098. In some embodiments, the CH3 domain consists of SEQ ID NO: 1099. In some embodiments, SEQ ID NO: 1098 is the IgG1 CH3 domain. In some embodiments, SEQ ID NO: 1099 is the IgG1 CH3 domain. In some embodiments, the SEQ ID NO: 1098 sequence is the sequence found predominantly is humans of European and American descent. In some embodiments, SEQ ID NO: 1099 is the sequence found predominantly in humans of Asian descent.

[0174] In some embodiments, a CH3 domain comprises a mutation. In some embodiments, the first CH3 domain comprises a first mutation. In some embodiments, the second CH3 domain comprises a second mutation. In some embodiments, a CH2 domain comprises a mutation. In some embodiments, the first CH2 domain comprises a first mutation. In some embodiments, the second CH2 domain comprises a second mutation. In some embodiments, the CH2 and CH3 domains both comprise mutations. In some embodiments, the first CH2 domain and first CH3 domains each comprise a first mutation. In some embodiments, the second CH2 domain and the second CH3 domain each comprise a second mutation. In some embodiments, the mutations inhibit homodimerization of the first polypeptide chain. In some embodiments, the first mutation inhibits homodimerization of the first polypeptide chain. In some embodiments, the mutations inhibit homodimerization of the second polypeptide chain. In some embodiments, the second mutation inhibits homodimerization of the second polypeptide chain. In some, embodiments, the mutations permit heterodimerization. In some embodiments, the mutations permit heterodimerization of the first and second chains. In some embodiments, permitting is promoting. In some embodiments, permitting is enhancing.

[0175] Mutations that promote heavy chain heterodimerization and/or inhibit homodimerization are well known in the art. Any such mutations or alterations may be used for constructing the polypeptides of the invention. In some embodiments, a region from an IgG is replaced with a region

from an IgA. In some embodiments, a region from a TCRa is inserted into the first CH3 domain and a region from TCRb is inserted in to the second CH3 domain. In some embodiments, the mutation is insertion of a region from a TCR. In some embodiments, the TCR is selected from TCRa and TCRb. In some embodiments, the mutation is insertion of a region from a different Ig. Examples of these mutations can be found in Table 5. In some embodiments, the mutation is selected from a mutation in Table 5. In some embodiments, the first mutation is selected from a group of mutation provided in a row and the second column of Table 5 and the second mutation is the group of mutations provided in that same row of Table 5 in the third column. The mutations in Table 5 are provided with the Kabat numbering for IgG1 unless otherwise stated; corresponding mutations can be made in other IGs and specifically in other IgGs. In some embodiments, the first mutation is T366Y, and the second mutation is Y407T. In some embodiments, the first mutation is S354C and T366W and the second mutation is Y349C, T366S, L368A, and Y407V. In some embodiments, the first mutation is S364H and F405A and the second mutation is Y349T and T392F. In some embodiments, the first mutation is T350V, L351Y, F405A, and Y407V and the second mutation is T350V, T366L, K392L, and T394W. In some embodiments, the first mutation is K392D, and K409D and the second mutation is E356K, and D399K. In some embodiments, the first mutation is D221E, P228E, and L368E and the second mutation is D221R, P228R, and K409R. In some embodiments, the first mutation is K360E, and K409W and the second mutation is Q347R, D399V, and F405T. In some embodiments, the first mutation is K360E, K409W, and Y349C and the second mutation is Q347R, D399V, F405T, and S354C. In some embodiments, the first mutation is F405L and the second mutation is K409R. In some embodiments, the first mutation is K360D, D399M, and Y407A and the second mutation is E345R, Q347R, T366V, and K409V. In some embodiments, the first mutation is Y349S, K370Y, T366M, and K409V and the second mutation is E356G, E357D, S364Q, and Y407A. In some embodiments, the first mutation is T366K, and the second mutation is selected from C351D, Y349E, Y349D, L368E, L368D, Y349E and R355E, Y349E and R355D, Y349D and R355E, and Y349D and R355D. In some embodiments, the first mutation is T366K and C351K and the second mutation is selected from C351D, Y349E, Y349D, L368E, L368D, Y349E and R355E, Y349E and R355D, Y349D and R355E, and Y349D and R355D. In some embodiments, the first mutation is L351D and L368E and the second mutation is L351K and T366K. In some embodiments, the first mutation is L368D and K370S and the second mutation is E357Q and S364K. In some embodiments, the first mutation is T366W, and the second mutation is T366S, L368A and Y407V. In some embodiments, the Ig is IgG2, and the first mutation is C223E, P228E, and L368E and the second mutation is C223R, E225R, P228R, and K409R. In some embodiments, the first mutation is S354C or T366W and the second mutation is Y349C, T366S, L368A, or Y407V. In some embodiments, the first mutation is S364H or F405A and the second mutation is Y349T or T392F. In some embodiments, the first mutation is T350V, L351Y, F405A, or Y407V and the second mutation is T350V, T366L, K392L, or T394W. In some embodiments, the first mutation is K392D, or K409D and the second mutation is E356K, or D399K. In some embodiments, the first mutation is D221E, P228E, or L368E and the second mutation is D221R, P228R, or K409R. In some embodiments, the first mutation is K360E, or K409W and the second mutation is Q347R, D399V, or F405T. In some embodiments, the first mutation is K360E, K409W, or Y349C and the second mutation is Q347R, D399V, F405T, or S354C. In some embodiments, the first mutation is K360D, D399M, or Y407A and the second mutation is E345R, Q347R, T366V, or K409V. In some embodiments, the first mutation is Y349S, K370Y, T366M, or K409V and the second mutation is E356G, E357D, S364Q, or Y407A. In some embodiments, the first mutation is L351D or L368E and the second mutation is L351K or T366K. In some embodiments, the first mutation is L368D or K370S and the second mutation is E357Q or S364K. In some embodiments, the first mutation is T366W, and the second mutation is T366S, L368A or Y407V. In some embodiments, the Ig is IgG2, and the first mutation is C223E, P228E, or L368E and the second mutation is C223R, E225R, P228R, or K409R. In some embodiments, the first heavy chain constant region comprises or consists of SEQ ID NO: 1074 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the second heavy chain constant region comprises or consists of SEQ ID NO: 1074. In some embodiments, the first heavy chain constant region comprises or consists of SEQ ID NO: 1075 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the second heavy chain constant region comprises or consists of SEQ ID NO: 1075. It will be understood that SEQ ID NO: 1074 and SEQ ID NO: 1075 heterodimerize with each other, but inhibit homodimerization. In some embodiments, the CL domain comprises or consists of SEQ ID NO: 1076 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the light chain constant region comprises or consists of SEQ ID NO: 1076. In some embodiments, the analog or homolog retains the mutations that promote heterodimerization and inhibit homodimerization.

TABLE 5

Mutations for enhancing heterodimerization and inhibiting homodimerization of CH3 domains.

	Strategy	CH3 domain Chain 1	CH3 domain Chain 2
1	Knobs-into-holes (Y-T)	T366Y	Y407T
2	Knobs-into-holes (CW-CSAV)	S354C, T366W	Y349C, T366S, L368A, Y407V
3	HA-TF	S364H, F405A	Y349T, T394F
4	ZW1 (VYAV-VLLW)	T350V, L351Y, F405A, Y407V	T350V, T366L, K392L, T394W
5	CH3 charge pairs (DD-KK)	K392D, K409D	E356K, D399K

TABLE 5-continued

Mutations for enhancing heterodimerization and inhibiting homodimerization of CH3 domains.

	Strategy	CH3 domain Chain 1	CH3 domain Chain 2
6	Hinge/CH3 charge (EEE-RRR)	D221E, P228E, L368E	D221R, P228R, K409R
7	EW-RVT	K360E, K409W,	Q347R, D399V, F405T
8	EW-RVTS-S	K360E, K409W, Y349C	Q347R, D399V, F405T, S354C
9	(L-R)	F405L	K409R
10	7.8.60 (DMA-RRVV)	K360D, D399M, Y407A	E345R, Q347R, T366V, K409V
11	20.8.34 (SYMV-GDQA)	Y349S, K370Y, T366M, K409V	E356G, E357D, S364Q, Y407A
12	Electrostatic steering effects	366K or 366K+ C351K	C351D or E or D at 349, 368, 349, or 349 +355
13	"DEKK"	L351D and L368E	L351K and T366K
14	XmAb	L368D/K370S	E357Q/S364K
15	KiH	T366W	T366S/L368A/Y407V
16	IgG2 hinge/CH3 charge (EEE-RRRR)	IgG2: C223E, P228E, L368E	IgG2: C223R, E225R, P228R, K409R
17	SEEDbody	IgG/A chimera	IgG/A chimera
18	BEAT	residues from TCRa interface	residues from TCRb interface

[0176] In some embodiments, the dual-function antigen binding molecule comprises two heavy chains and two light chains. In some embodiments, the two heavy chains are SEQ ID NO: 1088 and 1080 and the two light chains are SEQ ID NO: 1087 and 1079 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the two heavy chains are SEQ ID NO: 1088 and 1082 and the two light chains are SEQ ID NO: 1087 and 1081 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the two heavy chains are SEQ ID NO: 1090 and 1082 and the two light chains are SEQ ID NO: 1089 and 1079 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the two heavy chains are SEQ ID NO: 1090 and 1082 and the two light chains are SEQ ID NO: 1089 and 1081 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the two heavy chains are SEQ ID NO: 1088 and 1086 and the two light chains are SEQ ID NO: 1087 and 1085 or analogs or homologs comprising at least 85% sequence identity. It will be understood that analogs or homologs will target to the target protein by the targeting module, bind the cell and be delivered to the cytosol by the killing module and the will contain the immunogenic peptide which is displayed on the cell surface in complex with HLA.

[0177] In some embodiments, the composition is a pharmaceutical composition. In some embodiments, the composition comprises a pharmaceutically acceptable carrier, excipient or adjuvant. In some embodiments, the composition if formulated for administration to a subject. In some embodiments, the composition is formulated for systemic administration. In some embodiments, the composition if formulated for administration to a tumor. In some embodiments, the composition is formulated for intravenous administration. In some embodiments, the composition is formulated for administration to a subject. In some embodiments, the subject is a human.

[0178] As used herein, the term "carrier," "excipient," or "adjuvant" refers to any component of a pharmaceutical composition that is not the active agent. As used herein, the term "pharmaceutically acceptable carrier" refers to non-toxic, inert solid, semi-solid liquid filler, diluent, encapsulating material, formulation auxiliary of any type, or simply a sterile aqueous medium, such as saline. Some examples of the materials that can serve as pharmaceutically acceptable carriers are sugars, such as lactose, glucose and sucrose, starches such as corn starch and potato starch, cellulose and its derivatives such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt, gelatin, talc; excipients such as cocoa butter and suppository waxes; oils such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol, polyols such as glycerin, sorbitol, mannitol and polyethylene glycol; esters such as ethyl oleate and ethyl laurate, agar; buffering agents such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline, Ringer's solution; ethyl alcohol and phosphate buffer solutions, as well as other non-toxic compatible substances used in pharmaceutical formulations. Some non-limiting examples of substances which can serve as a carrier herein include sugar, starch, cellulose and its derivatives, powered tragacanth, malt, gelatin, talc, stearic acid, magnesium stearate, calcium sulfate, vegetable oils, polyols, alginic acid, pyrogen-free water, isotonic saline, phosphate buffer solutions, cocoa butter (suppository base), emulsifier as well as other non-toxic pharmaceutically compatible substances used in other pharmaceutical formulations. Wetting agents and lubricants such as sodium lauryl sulfate, as well as coloring agents, flavoring agents, excipients, stabilizers, antioxidants, and preservatives may also be present. Any non-toxic, inert, and effective carrier may be used to formulate the compositions contemplated herein. Suitable pharmaceutically acceptable carriers, excipients, and diluents in this regard are well known to those of skill in the art, such as those described in The Merck Index, Thirteenth Edition, Budavari et al., Eds., Merck & Co., Inc., Rahway, N.J. (2001); the CTFA (Cosmetic, Toiletry, and Fragrance Association) International

Cosmetic Ingredient Dictionary and Handbook, Tenth Edition (2004); and the "Inactive Ingredient Guide," U.S. Food and Drug Administration (FDA) Center for Drug Evaluation and Research (CDER) Office of Management, the contents of all of which are hereby incorporated by reference in their entirety. Examples of pharmaceutically acceptable excipients, carriers and diluents useful in the present compositions include distilled water, physiological saline, Ringer's solution, dextrose solution, Hank's solution, and DMSO. These additional inactive components, as well as effective formulations and administration procedures, are well known in the art and are described in standard textbooks, such as Goodman and Gillman's: The Pharmacological Bases of Therapeutics, 8th Ed., Gilman et al. Eds. Pergamon Press (1990); Remington's Pharmaceutical Sciences, 18th Ed., Mack Publishing Co., Easton, Pa. (1990); and Remington: The Science and Practice of Pharmacy, 21st Ed., Lippincott Williams & Wilkins, Philadelphia, Pa., (2005), each of which is incorporated by reference herein in its entirety. The presently described composition may also be contained in artificially created structures such as liposomes, ISCOMS, slow-releasing particles, and other vehicles which increase the half-life of the peptides or polypeptides in serum. Liposomes include emulsions, foams, micelies, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. Liposomes for use with the presently described peptides are formed from standard vesicle-forming lipids which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally determined by considerations such as liposome size and stability in the blood. A variety of methods are available for preparing liposomes as reviewed, for example, by Coligan, J. E. et al, Current Protocols in Protein Science, 1999, John Wiley & Sons, Inc., New York, and see also U.S. Pat. Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

[0179] The carrier may comprise, in total, from about 0.1% to about 99.99999% by weight of the pharmaceutical compositions presented herein.

[0180] As used herein, the terms "administering," "administration," and like terms refer to any method which, in sound medical practice, delivers a composition containing an active agent to a subject in such a manner as to provide a therapeutic effect. One aspect of the present subject matter provides for intravenous administration of a therapeutically effective amount of a composition of the present subject matter to a patient in need thereof. Other suitable routes of administration can include parenteral, subcutaneous, oral, intramuscular, intratumoral or intraperitoneal.

[0181] In some embodiments, the nucleic acid molecule comprises an open reading frame. In some embodiments, the open reading frame encodes the antigen binding molecule of the invention. In some embodiments, the nucleic acid molecule comprises a plurality of open reading frames which collectively encode the antigen binding molecule of the invention.

[0182] In some embodiments, the vector is an expression vector. In some embodiments, the vector comprises at least one regulatory element operatively linked to a nucleic acid molecule of the invention. In some embodiments, the vector comprises at least one regulatory element operatively linked to an open reading frame encoding the antigen binding molecule of the invention. In some embodiments, the vector comprises a plurality of regulatory elements each operatively linked to an open reading frame which collectively encode the antigen binding molecule of the invention. In some embodiments, a composition comprises a plurality of vectors each comprising at least one regulatory element operatively linked to an open reading frame wherein the plurality of open reading frames collectively encodes the antigen binding molecule of the invention.

[0183] The term "expression" as used herein refers to the biosynthesis of a gene product, including the transcription and/or translation of said gene product. Thus, expression of a nucleic acid molecule may refer to transcription of the nucleic acid fragment (e.g., transcription resulting in mRNA or other functional RNA) and/or translation of RNA into a precursor or mature protein (polypeptide).

[0184] Expressing of a gene within a cell is well known to one skilled in the art. It can be carried out by, among many methods, transfection, viral infection, or direct alteration of the cell's genome. In some embodiments, the gene is in an expression vector such as plasmid or viral vector.

[0185] A vector nucleic acid sequence generally contains at least an origin of replication for propagation in a cell and optionally additional elements, such as a heterologous polynucleotide sequence, expression control element (e.g., a promoter, enhancer), selectable marker (e.g., antibiotic resistance), poly-Adenine sequence.

[0186] The vector may be a DNA plasmid delivered via non-viral methods or via viral methods. The viral vector may be a retroviral vector, a herpesviral vector, an adenoviral vector, an adeno-associated viral vector or a poxviral vector. The promoters may be active in mammalian cells. The promoters may be a viral promoter.

[0187] In some embodiments, the gene is operably linked to a promoter. The term "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory element or elements in a manner that allows for expression of the nucleotide sequence (e.g. in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell).

[0188] In some embodiments, the vector is introduced into the cell by standard methods including electroporation (e.g., as described in From et al., Proc. Natl. Acad. Sci. USA 82, 5824 (1985)), Heat shock, infection by viral vectors, high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface (Klein et al., Nature 327. 70-73 (1987)), and/or the like.

[0189] The term "promoter" as used herein refers to a group of transcriptional control modules that are clustered around the initiation site for an RNA polymerase i.e., RNA polymerase II. Promoters are composed of discrete functional modules, each consisting of approximately 7-20 bp of DNA, and containing one or more recognition sites for transcriptional activator or repressor proteins.

[0190] In some embodiments, nucleic acid sequences are transcribed by RNA polymerase II (RNAP II and Pol II). RNAP II is an enzyme found in eukaryotic cells. It catalyzes the transcription of DNA to synthesize precursors of mRNA and most snRNA and microRNA.

[0191] In some embodiments, mammalian expression vectors include, but are not limited to, pcDNA3, pcDNA3.1 (±), pGL3, pZeoSV2(±), pSecTag2, pDisplay, pEF/myc/cyto, pCMV/myc/cyto, pCR3.1, pSinRep5, DH26S, DHBB, pNMT1, pNMT41, pNMT81, which are available from Invitrogen, pCI which is available from Promega, pMbac,

pPbac, pBK-RSV and pBK-CMV which are available from Strategene, pTRES which is available from Clontech, and their derivatives.

[0192] In some embodiments, expression vectors containing regulatory elements from eukaryotic viruses such as retroviruses are used by the present invention. SV40 vectors include pSVT7 and pMT2. In some embodiments, vectors derived from bovine papilloma virus include pBV-1MTHA, and vectors derived from Epstein Bar virus include pHEBO, and p2O5. Other exemplary vectors include pMSG, pAV009/A+, pMTO10/A+, pMAMneo-5, baculovirus pDSVE, and any other vector allowing expression of proteins under the direction of the SV-40 early promoter, SV-40 later promoter, metallothionein promoter, murine mammary tumor virus promoter, Rous sarcoma virus promoter, polyhedrin promoter, or other promoters shown effective for expression in eukaryotic cells.

[0193] In some embodiments, recombinant viral vectors, which offer advantages such as lateral infection and targeting specificity, are used for in vivo expression. In one embodiment, lateral infection is inherent in the life cycle of, for example, retrovirus and is the process by which a single infected cell produces many progeny virions that bud off and infect neighboring cells. In one embodiment, the result is that a large area becomes rapidly infected, most of which was not initially infected by the original viral particles. In one embodiment, viral vectors are produced that are unable to spread laterally. In one embodiment, this characteristic can be useful if the desired purpose is to introduce a specified gene into only a localized number of targeted cells.

[0194] Various methods can be used to introduce the expression vector of the present invention into cells. Such methods are generally described in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Springs Harbor Laboratory, New York (1989, 1992), in Ausubel et al., Current Protocols in Molecular Biology, John Wiley and Sons, Baltimore, Md. (1989), Chang et al., Somatic Gene Therapy, CRC Press, Ann Arbor, Mich. (1995), Vega et al., Gene Targeting, CRC Press, Ann Arbor Mich. (1995), Vectors: A Survey of Molecular Cloning Vectors and Their Uses, Butterworths, Boston Mass. (1988) and Gilboa et at. [Biotechniques 4 (6): 504-512, 1986] and include, for example, stable or transient transfection, lipofection, electroporation and infection with recombinant viral vectors. In addition, see U.S. Pat. Nos. 5,464,764 and 5,487,992 for positive-negative selection methods.

[0195] In one embodiment, plant expression vectors are used. In one embodiment, the expression of a polypeptide coding sequence is driven by a number of promoters. In some embodiments, viral promoters such as the 35S RNA and 19S RNA promoters of CaMV [Brisson et al., Nature 310:511-514 (1984)], or the coat protein promoter to TMV [Takamatsu et al., EMBO J. 6:307-311 (1987)] are used. In another embodiment, plant promoters are used such as, for example, the small subunit of RUBISCO [Coruzzi et al., EMBO J. 3:1671-1680 (1984); and Brogli et al., Science 224:838-843 (1984)] or heat shock promoters, e.g., soybean hsp17.5-E or hsp17.3-B [Gurley et al., Mol. Cell. Biol. 6:559-565 (1986)]. In one embodiment, constructs are introduced into plant cells using Ti plasmid, Ri plasmid, plant viral vectors, direct DNA transformation, microinjection, electroporation and other techniques well known to the skilled artisan. See, for example, Weissbach & Weissbach [Methods for Plant Molecular Biology, Academic Press, NY, Section VIII, pp 421-463 (1988)]. Other expression systems such as insects and mammalian host cell systems, which are well known in the art, can also be used by the present invention.

[0196] It will be appreciated that other than containing the necessary elements for the transcription and translation of the inserted coding sequence (encoding the polypeptide), the expression construct of the present invention can also include sequences engineered to optimize stability, production, purification, yield or activity of the expressed polypeptide.

[0197] In some embodiments, the method is a method of treating cancer. In some embodiments, the antigen binding molecule of the invention is for use in treating cancer. In some embodiments, the dual function antigen binding molecule of the invention is for use in treating cancer. In some embodiments, the composition of the invention is for use in treating cancer. In some embodiments, the cancer is a cancer that expresses the cancer specific antigen. In some embodiments, the cancer is a cancer that overexpresses the cancer specific antigen. In some embodiments, overexpresses is expresses at a level higher than in non-cancerous cells. In some embodiments, the non-cancerous cells are of the same cell type or tissue as the cancerous cells. In some embodiments, the cancer is a cancer that expresses the immunogenic cancer peptide. In some embodiments, the cancer is a hematopoietic cancer. In some embodiments, the cancer comprises a malignant immune cell. In some embodiments, the immune cell is a B cell. In some embodiments, the cancer is a solid cancer. In some embodiments, the cancer is a PD-L1 positive cancer. In some embodiments, the cancer is an EGFR positive cancer. In some embodiments, the cancer is an EGFR overexpressing cancer.

[0198] As used herein "cancer" refers to diseases associated with cell proliferation. Non-limiting types of cancer include carcinoma, sarcoma, lymphoma, leukemia, blastoma and germ cells tumors. In one embodiment, carcinoma refers to tumors derived from epithelial cells including but not limited to breast cancer, prostate cancer, lung cancer, pancreas cancer, and colon cancer. In one embodiment, sarcoma refers of tumors derived from mesenchymal cells including but not limited to sarcoma botryoides, chondrosarcoma, ewings sarcoma, malignant hemangioendothelioma, malignant schwannoma, osteosarcoma and soft tissue sarcomas. In one embodiment, lymphoma refers to tumors derived from hematopoietic cells that leave the bone marrow and tend to mature in the lymph nodes including but not limited to hodgkin lymphoma, non-hodgkin lymphoma, multiple myeloma and immunoproliferative diseases. In one embodiment, leukemia refers to tumors derived from hematopoietic cells that leave the bone marrow and tend to mature in the blood including but not limited to acute lymphoblastic leukemia, chronic lymphocytic leukemia, acute myelogenous leukemia, chronic myelogenous leukemia, hairy cell leukemia, T-cell prolymphocytic leukemia, large granular lymphocytic leukemia and adult T-cell leukemia. In one embodiment, blastoma refers to tumors derived from immature precursor cells or embryonic tissue including but not limited to hepatoblastoma, medulloblastoma, nephroblastoma, neuroblastoma, pancreatoblastoma, pleuropulmonary blastoma, retinoblastoma and glioblastoma-multiforme. In one embodiment, germ cell tumors refers to tumors derived from germ cells including but not limited to germinomatous or seminomatous germ cell tumors (GGCT, SGCT) and

nongerminomatous or nonseminomatous germ cell tumors (NGGCT, NSGCT). In one embodiment, germinomatous or seminomatous tumors include but not limited to germinoma, dysgerminoma and seminoma. In one embodiment, nongerminnomatous or nonseminomatous tumors refers to pure and mixed germ cells tumors including but not limited to embryonal carcinoma, endodermal sinus tumor, choriocarcinoma, tearoom, polyembryoma, gonadoblastoma and teratocarcinoma.

[0199] In some embodiments, the antigen binding molecule of the invention is a cancer vaccine. In some embodiments, cancer vaccine is an antigen binding molecule comprising an antigen binding region capable of binding a dendritic cell antigen. It will be understood by a skilled artisan that upon entrance into a dendritic cell, the immunogenic cancer peptide will be cleaved from the rest of the molecule of the invention and displayed on the surface of the dendritic cell by HLA molecules. This will in turn train cytotoxic immune cells (T cell and NK cells) to target this immunogenic peptide and thereby the cancer.

[0200] In some embodiments, treating further comprises administering effector cells specific to the immunogenic peptide to the subject. In some embodiments, an effector cell is an immune cell. In some embodiments, an effector cell is a cytotoxic cell. In some embodiments, an effector cell is a lymphocyte. In some embodiments, an effector cell is a CD8 T cell. In some embodiments, an effector cell is a natural killer (NK) cell. In some embodiments, the effector cell has been exposed to the peptide. In some embodiments, the effector cell has been exposed to an antigen presenting cell presenting the peptide in complex with an HLA.

[0201] In some embodiments, the treating further comprises providing a vaccine comprising the immunogenic peptide. In some embodiments, the subject has previously received a vaccine comprising the immunogenic peptide. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human. In some embodiments, the subject suffers from cancer. In some embodiments, the subject is suitable to be treated by a method of the invention. In some embodiments, the subject has previously been exposed to the immunogenic peptide. In some embodiments, the subject has previously been infected by the pathogen from which the immunogenic peptide originates. In some embodiments, a pathogen is a virus. In some embodiments, the subject is capable of mounting an immune response against the peptide. In some embodiments, the subject comprises T cells comprising a TCR that recognizes the peptide or a portion thereof. In some embodiments, the subject comprises memory B cells comprising a BCR that recognizes the peptide or a portion thereof.

[0202] In some embodiments, the method is a method of producing surface display of the peptide in a target cell. In some embodiments, the surface display is display of HLA complexed with the peptide. In some embodiments, expressing is surface display. In some embodiments, expressing is expressing in an HLA complex.

[0203] By another aspect, there is provided a method of engineering an antibody or antigen binding fragment thereof, the method comprising:

[0204] a. selecting an antibody or antigen binding fragment thereof of interest;

[0205] b. determining at least one CDR of the selected antibody or antigen binding fragment thereof is not required for binding to a target;

[0206] c. replacing the determined at least one CDR or a portion thereof with a peptide;

thereby engineering an antibody or antigen binding fragment thereof.

[0207] By another aspect, there is provided a method of engineering an antibody or antigen binding fragment thereof, the method comprising:

[0208] a. selecting an antibody or antigen binding fragment thereof of interest;

[0209] b. receiving a database of peptides;

[0210] c. performing alignment of peptides of a variable region of the selected antibody or antigen binding fragment thereof with peptides of the database;

[0211] d. determining a peptide from the selected antibody of antigen binding fragment thereof and a peptide from the database with an alignment score above a predetermined threshold; and

[0212] e. replacing the determined peptide from the selected antibody or antigen binding fragment thereof with the determined peptide from the database;

thereby engineering an antibody or antigen binding fragment thereof.

[0213] In some embodiments, the engineered antibody or antigen binding fragment thereof is an antibody or antigen binding fragment of the invention. In some embodiments, the engineered antibody or antigen binding fragment thereof is an antigen binding molecule of the invention. In some embodiments, the engineered antibody or antigen binding fragment thereof is a dual-function antigen binding molecule of the invention. In some embodiments, the engineered antibody or antigen binding fragment thereof is an immunogenic peptide delivery antibody. In some embodiments, the engineered antibody or antigen binding fragment thereof is for use in a method of the invention. In some embodiments, the antibody or antigen binding fragment thereof before engineering is a cell penetrating antibody. In some embodiments, the selecting is selecting an antibody that penetrates into cells to which it binds. In some embodiments, the antibody or antigen binding fragment thereof before engineering is a commercially available antibody.

[0214] In some embodiments, the antibody or antigen binding fragment thereof before engineering binds to the surface of a target cell. In some embodiments, the target cell is a cancer cell. In some embodiments, step (a) comprises selecting an antibody or antigen binding fragment thereof that binds to a surface of a target cell. In some embodiments, binding the surface is binding a surface antigen. In some embodiments, antibody or antigen binding fragment thereof before engineering is a DNA binding antibody. In some embodiments, antibody or antigen binding fragment thereof before engineering is endocytosed into the endocytic pathway of a cell. In some embodiments, antibody or antigen binding fragment thereof before engineering is transported into the cytoplasm of a cell to which it binds. In some embodiments, antibody or antigen binding fragment thereof before engineering is capable of endosomal escape. In some embodiments, antibody or antigen binding fragment thereof before engineering is delivered to the cytosol of a cell to which it binds. In some embodiments, the method further comprises inserting into the antibody or antigen binding fragment thereof a cell penetrating moiety. In some embodiments, the cell penetrating moiety is inserted before the immunogenic peptide. In some embodiments, the cell penetrating moiety is inserted after the immunogenic peptide. In

some embodiments, the cell penetrating moiety is inserted concomitantly to the insertion of the immunogenic peptide. In some embodiments, step (a) comprises selecting an antibody or antigen binding fragment thereof that upon binding to a surface of a target cell is internalized and delivered to a cytosol of the target cell.

[0215] In some embodiments, the antibody or antigen binding fragment thereof before engineering penetrates/internalizes into a bound cell at a level comparable to any one of TMab4, 3E10 and 71F12. In some embodiments, the antibody or antigen binding fragment thereof before engineering penetrates/internalizes into a bound cell at a level comparable to TMab4. In some embodiments, the antibody or antigen binding fragment thereof before engineering penetrates/internalizes into a bound cell at a level comparable to 3E10. In some embodiments, the antibody or antigen binding fragment thereof before engineering penetrates/internalizes into a bound cell at a level comparable to 71F12. In some embodiments, comparable is with a penetrance that is at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 92, 95, 97, 99 or 100% of the original antibody. Each possibility represents a separate embodiment of the invention. In some embodiments, comparable is with a penetrance that is at least 80% of the original antibody. In some embodiments, comparable is with a penetrance that is at least 90% of the original antibody.

[0216] In some embodiments, the determining is determining at least one inert CDR. In some embodiments, the determining is determining at least one CDR not involved in transport into the cell. In some embodiments, the determining is determining at least one CDR not involved in endosomal escape. In some embodiments, the determining is based on structural analysis of the antibody or antigen binding fragment thereof bound to its target. In some embodiments, the structural analysis is in silico analysis. In some embodiments, the structural analysis is crystallographic analysis. In some embodiments, the method further comprises receiving the structural analysis. In some embodiments, the method further comprises performing the structural analysis. In some embodiments, the analysis provides the distance of each amino acid of the antibody or antigen binding fragment thereof to an amino acid of the target. In some embodiments, the analysis provides the distance of each amino acid of a CDR of the antibody or antigen binding fragment thereof to an amino acid of the target. In some embodiments, the determining comprises determining the distance of each amino acid of a CDR to the target. In some embodiments, a CDR with two or fewer amino acids in contact with the antigen is determined as not required for binding. In some embodiments, the determining comprises determining the distance of each amino acid of a CDR to the target. In some embodiments, a CDR with one or fewer amino acids in contact with the antigen is determined as not required for binding. In some embodiments, a CDR not required for binding is an inert CDR. In some embodiments, a CDR not required for binding is a CDR in which mutations have been shown not to effect antibody function. In some embodiments, the function is binding.

[0217] In some embodiments, the peptide is an immunogenic peptide. In some embodiments, the peptide comprises at least 5, 6, 7, 8, 9, 10, or 11 amino acids. Each possibility represents a separate embodiment of the invention. In some embodiments, the peptide comprises at least 7 amino acids. In some embodiments, the peptide comprises at least 8 amino acids. In some embodiments, the peptide comprises between 8 and 11 amino acids. In some embodiments, the peptide is an immunogenic peptide provided hereinabove. In some embodiments, peptide is from the variable region of the antibody or antigen binding fragment thereof. In some embodiments, peptide is from a CDR of the antibody or antigen binding fragment thereof. Methods of determining the position of CDRs are well known in the art and the Clothia and Kabat systems may be used. Given the sequence of a variable domain of an antibody a skilled artisan will be readily able to identify the CDRs.

[0218] In some embodiments, the at least one CDR is removed. In some embodiments, a portion of the at least one CDR is removed. In some embodiments, the removed amino acids are replaced with the immunogenic peptide. In some embodiments, the replacing is optimized. In some embodiments, the method further comprises optimizing the replacement. In some embodiments, optimizing is structural optimization. In some embodiments, optimizing comprises performing an optimization algorithm. In some embodiments, optimizing comprises producing as little perturbation in the structure of the selected antibody or antigen binding fragment thereof as possible. In some embodiments, optimizing comprises in silico analysis or the insertion of the immunogenic peptide into the at least one determined CDR with removal of all possible portions of the CDR and selected the insertion and removal of a portion that produces the least perturbation. In some embodiments, optimization comprise insertion of at least one filler amino Acid. some embodiments, optimization comprise producing at least one compensatory mutation outside the determined CDR. In some embodiments, the optimization algorithm is a minimal perturbation replacement (MBR) algorithm. In some embodiments, optimization comprises optimization of CDR flanking sequence. In some embodiments, optimization of flanking sequence comprises antibody stem preservation. In some embodiments, the structure of the stems flanking the CDRs are maintained. In some embodiments, the stems are the ends of the beta sheets flanking the CDR. In some embodiments, the end comprises the 1, 2, 3, 4, or 5 amino acids directly adjacent to the CDR. Each possibility represents a separate embodiment of the invention.

[0219] In some embodiments, the method further comprises confirming binding of the engineered antibody or antigen binding fragment thereof to the same target that was bound by the selected antibody or antigen binding fragment thereof. In some embodiments, the method further comprises measuring binding of the engineered antibody or antigen binding fragment thereof to the same target that was bound by the selected antibody or antigen binding fragment thereof. In some embodiments, the method further comprises determining binding of the engineered antibody or antigen binding fragment thereof to the same target that was bound by the selected antibody or antigen binding fragment thereof. In some embodiments, binding is equivalent to the binding of the selected antibody or antigen binding fragment thereof. In some embodiments, the measuring further comprises determining that the binding is not significantly reduced as compared to the binding of the selected antibody or antigen binding fragment thereof. In some embodiments, significantly is statistically significantly. In some embodiments, significantly reduced comprises a greater than 10% reduction. In some embodiments, significantly reduced comprises a greater than 20% reduction. In some embodiments,

significantly reduced comprises a greater than 50% reduction. In some embodiments, significantly reduced is abolished.

[0220] In some embodiments, the method further comprises measuring levels of peptide in the cytosol of the target cell. In some embodiments, the method further comprises determining delivery of the peptide to the cytosol. In some embodiments, the method further comprises measuring delivery of the peptide to the cytosol.

[0221] In some embodiments, the method further comprises confirming delivery of the peptide to a cytosol of the target cell. In some embodiments, the method further comprises measuring levels of peptide in the cytosol of the target cell. In some embodiments, the method further comprises determining delivery of the peptide to the cytosol. In some embodiments, the method further comprises measuring delivery of the peptide to the cytosol.

[0222] In some embodiments, the method further comprises confirming delivery of the peptide to the surface of the target cell. In some embodiments, delivery is surface display of the peptide. In some embodiments, delivery is delivery of the peptide in complex with an HLA molecule to the surface of the target cell. In some embodiments, the method further comprises measuring levels of peptide on the surface of the target cell. In some embodiments, levels is levels of the peptide in complex with HLA. In some embodiments, the method further comprises determining delivery of the peptide to the surface of the target cell. In some embodiments, the method further comprises measuring delivery of the peptide to the surface of the target cell.

[0223] In some embodiments, the method further comprises confirming killing of the target cell by effector cells. In some embodiments, killing is specific killing. In some embodiments, effector cells are specific to the peptide. In some embodiments, effector cells are immune cells. In some embodiments, the method further comprises measuring killing of the target cell by effector cells. In some embodiments, the method further comprises determining killing of the target cell by effector cells. In some embodiments, the method is an in vitro method. In some embodiments, the confirming, measuring and determining is performed in vitro. In some embodiments, in vitro is ex vivo. Examples of methods of performing the confirming, measuring and determining are provided hereinbelow, but any assay known in the art for such measuring/confirming/determining may be used.

[0224] Databases of peptides and specifically immunogenic peptides are known in the art and any such database may be used. In some embodiments, the peptide is a cancer peptide. In some embodiments, database comprises or consists of Table 3. In some embodiments, the alignment is a pairwise alignment. In some embodiments, the alignment is alignment of one peptide from the selected antibody or antigen binding fragment thereof and one peptide of the database to produce an alignment pair. In some embodiments, an alignment pair with an alignment score above a predetermined threshold is used for replacement in step (e)

[0225] In some embodiments, the method further comprises inserting the engineered antibody into a dual-function antigen binding molecule. In some embodiments, the dual-function antigen binding molecule is a molecule of the invention. In some embodiments, the method further comprises selecting a targeting antibody that binds to a protein on a target cell. In some embodiments, on a target cell is on the surface of a target cell. In some embodiments, the target cell is a cancer cell. In some embodiments, the protein is a receptor. In some embodiments, the protein is a cancer antigen. In some embodiments, the protein is a protein only expressed on cancer cells and not counterpart healthy cell. In some embodiments, the protein is a protein overexpressed on cancer cells as compared to counterpart healthy cells. In some embodiments, counterpart cell are cells of the same tissue or cell type as the cancer cells. In some embodiments, counterpart cells are control cells. In some embodiments, the selected targeting antibody is combined with the engineered antibody. In some embodiments, the combining produces the dual-function antigen binding molecule. In some embodiments, a dual-function antigen binding molecule is a bi-specific antibody.

[0226] In some embodiments, the engineered antibody comprises one heavy chain and one light chain. In some embodiments, the targeting antibody or antigen binding fragment comprises one heavy chain and one light chain. In some embodiments, the engineered antibody is a single chain antibody. In some embodiments, the targeting antibody is a single chain antibody. In some embodiments, a single chain antibody comprises a heavy chain variable domain and a light chain variable domain linked in a single polypeptide by an amino acid linker. In some embodiments, the heavy chain constant region of the targeting antibody is engineered to promote heterodimerization and/or inhibit homodimerization. In some embodiments, the heavy chain constant region of the engineered antibody is engineered to promote heterodimerization and/or inhibit homodimerization. In some embodiments, engineered is modified. In some embodiments, modified is mutated. In some embodiments, the method comprises engineering the constant regions of the engineered antibody and/or the targeting antibody. In some embodiments, the engineering is producing a set of mutations provided in Table 5. In some embodiments, the heavy chain constant regions used comprise or consist of SEQ ID NO: 1074 and 1075 or analogs or homologs comprising at least 85% sequence identity. In some embodiments, the analogs or homologs retain the knob-in-holes mutations.

[0227] As used herein, the term "about" when combined with a value refers to plus and minus 10% of the reference value. For example, a length of about 1000 nanometers (nm) refers to a length of 1000 nm+−100 nm.

[0228] It is noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to "a polynucleotide" includes a plurality of such polynucleotides and reference to "the polypeptide" includes reference to one or more polypeptides and equivalents thereof known to those skilled in the art, and so forth. It is further noted that the claims may be drafted to exclude any optional element. As such, this statement is intended to serve as antecedent basis for use of such exclusive terminology as "solely," "only" and the like in connection with the recitation of claim elements, or use of a "negative" limitation.

[0229] In those instances where a convention analogous to "at least one of A, B, and C, etc." is used, in general such a construction is intended in the sense one having skill in the art would understand the convention (e.g., "a system having at least one of A, B, and C" would include but not be limited to systems that have A alone, B alone, C alone, A and B

together, A and C together, B and C together, and/or A, B, and C together, etc.). It will be further understood by those within the art that virtually any disjunctive word and/or phrase presenting two or more alternative terms, whether in the description, claims, or drawings, should be understood to contemplate the possibilities of including one of the terms, either of the terms, or both terms. For example, the phrase "A or B" will be understood to include the possibilities of "A" or "B" or "A and B."

[0230] It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments pertaining to the invention are specifically embraced by the present invention and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations of the various embodiments and elements thereof are also specifically embraced by the present invention and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

[0231] Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

[0232] Various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below find experimental support in the following examples.

EXAMPLES

[0233] Generally, the nomenclature used herein and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, "Molecular Cloning: A laboratory Manual" Sambrook et al., (1989); "Current Protocols in Molecular Biology" Volumes I-III Ausubel, R. M., ed. (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (eds) "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998); methodologies as set forth in U.S. Pat. Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; "Cell Biology: A Laboratory Handbook", Volumes I-III Cellis, J. E., ed. (1994); "Culture of Animal Cells—A Manual of Basic Technique" by Freshney, Wiley-Liss, N. Y. (1994), Third Edition; "Current Protocols in Immunology" Volumes I-III Coligan J. E., ed. (1994); Stites et al. (eds), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (eds), "Strategies for Protein Purification and Characterization—A Laboratory Course Manual" CSHL Press (1996); all of which are incorporated by reference. Other general references are provided throughout this document.

Materials and Methods

[0234] Cell penetration assay: The penetration ability of all Abs is screened by intracellular antibody detection followed by flow cytometry analysis. A fluorescent labeled anti-Fc-FITC is used to detect intracellular antibody. Briefly, breast cancer cells are seeded in 24 well plates and incubated for 6 hours with 0.5-1 uM of either control antibody or Trojan Ab. Next, cells are washed with PBS and low pH buffer (Glycine pH=2.5) to remove antibodies that are bound on the cell surface. The cells are then fixed, permeabilized and intracellularly fluorescently labeled by anti-Fc-FITC antibody (0.1% Saponin 1% BSA in PBS two hours at room temperature). Labeled cells are analyzed by flow cytometry for FITC and unlabeled cells are used as a negative control. To determine the level of proteasomal degradation of intracellular Trojan Abs a proteasomal inhibitor MG132 is added to cells prior to Trojan antibody addition.

[0235] Luciferase killing assay: Luciferase expressing target cancer cells (T) are seeded on 96-well plates and treated with the Trojan-Abs at various concentrations (0.5-4 μM). After 3-24 hours antigen-specific effector cells (E), specific to the relevant peptide within the Trojan-Ab, are added at various E:T ratios. Cells are then cocultured for 18-24 hours, followed by Luciferase substrate (Bio-Glo; Promega) addition. To quantify the number of viable cells, luminescence intensity (lum) is recorded. Killing is assessed by calculating % Killing=1−lum (Treated Target+Effectors)/Lum (Control non-Treated), this can also be calculated vs. other controls.

[0236] Image based killing assay (IncuCyte Imaging system): Target cells (T) are first labeled with a cytosolic red dye (IncuCyte® Cytolight Rapid Red) enabling tracking of target cell proliferation on the IncuCyte imager. Labeled target cell are then seeded on clear 96-well plates and treated with the Trojan-Abs at various concentrations (0.5-4 PM). After 3-24 hours antigen-specific effector cells (E), specific to the relevant peptide within the Trojan-Ab, are added at various E:T ratios. Next, plates are placed in the IncuCyte (37° C.; 5% CO2) and imaged at 2-hour intervals for 48 hours. Alternatively, a Caspase3/7 green dye was added to the media to enable apoptosis assessment of the target cells. Data is analyzed by the IncuCyte software analysis tool comparing two main parameters: Proliferation: The confluence of the red dye normalized to time 0 h; and Apoptosis: (Red+Green area)/Red-area normalized to time 0 h.

[0237] EGFR binding assay: To assess the ability of full Trojan antibodies (FTAbs) to bind EGFR on the cancer cell surface, a flow cytometry binding assay was established. Pre-plated cells are trypsinized, washed and then incubated on ice for 1 hour with 0.3 or 3 nM FTAb or EGFR bivalent therapeutic antibodies serving as a positive control. Then cells are washed with 2% FBS in PBS buffer three times and labeled with a fluorescent secondary antibody (anti-human Fc-FITC) for 30 minutes on ice. Cells are then washed with the same buffer three times and analyzed by flow cytometry. FTAbs binding is proportional to the FITC fluorescence level.

[0238] Presentation of HLA-peptide complex on the cancer cell surface: To quantify the level of presentation of HLA-peptide complex on the cancer cells upon incubation with FTAbs, TCR-like antibodies that are able bind specific

HLA-peptide complex were used. Briefly, cells are seeded in 24 well plates and incubated for different time durations (4 h, 8 h and 10 h) with 1 M of FTAb or cFTAb (control FTAb) at 37C, 5% CO2. Next, cells are incubated on ice for 30 minutes with C1-17 antibody (see Lee et al. "Affinity Maturation of a T-Cell Receptor-Like Antibody Specific for a Cytomegalovirus pp65-Derived Peptide Presented by HLA-A*02:01" Int. J. Mol. Sci. 2021, 22, 2349, herein incorporated by reference in its entirety.) that is conjugated to fluorescein (FITC) and analyzed by flow cytometry.

Example 1: Trojan Antibody Design

[0239] It is known that immunogenic peptides that are presented by cancer cells can lead to immune cell activation and cancer cell killing. Lymphocytes within the subject recognize the immunogenic peptide and the subject's immune system is brought to bear against the cancer cell. This mechanism can be harnessed by actively delivering the immunogenic peptide into cancer cells, who intern display the immunogenic peptide on their cell surface. Two classes of immunogenic peptides can be employed: 1) non-self-peptides/peptides not found in humans such as viral or bacterial peptides and 2) modified self-peptides which are human peptides that are mutated or otherwise altered to provide cancer specificity so that the immune system is not activated against healthy cells.

[0240] It has previously been hypothesized that the immunogenic peptide can be delivered via an antibody. Sefrin et al., 2019 "Sensitization of tumors for attack by virus-specific CD8+ T-cells through antibody-mediated delivery of immunogenic T cell epitopes", Front. Immunol., August 21; 10:1962 made use of a full-sized antibody conjugated to a peptide via a disulfide bond. However, this construct may have very low stability, resulting in high rates of deconjugation in serum. This in turn may lead to poor delivery to the target cells, reduced potency and high off target effects (side effects). Gaston et al., 2019, "Intracellular delivery of therapeutic antibodies into specific cells using antibody-peptide fusions", Sci. Rep., December 10; 9(1):18688 employed a fusion protein construct in which the peptide was integrated into an end of the amino acid chain of the heavy or light chain or was placed next to the hinge domain within the chain. This method led to decreased production yield, increased aggregation and reduced in vitro stability.

[0241] To alleviate the problems inherent to these methods, rather than insert the immunogenic peptide at the end of the chain or between structures the immunogenic peptide is inserted into the antibody variable region. In particular, the immunogenic peptide is use to replace all or part of "inert", non-essential CDRs within the heavy or light chain of the antibody (FIG. **1**). In silico modeling is used to identify inert CDR loops in known therapeutic antibodies. The inert CDR is then replaced by the immunogenic peptide (FIG. **2**). In this conformation the engineered antibody maintains high stability and antigen binding affinity. If the immunogenic peptide is shorter than the CDR filler amino acids can be added so as not to change the antibody conformation. Similarly, if the CDR is longer than the immunogenic peptide only a portion of the CDR is removed. Flanking regions next to the inert CDRs can also be replaced but their overall structure should be conserved as these regions are often important for overall antibody conformation. These engineered antibodies are referred to as Trojan antibodies.

Example 2: Trojan Antibody Uses

[0242] One use of the Trojan antibodies of the invention is dendritic cell vaccination. An antibody against a dendritic cell surface marker (e.g., CD40) is used for engineering. In this case anti-human CD40 antibody Fab516 is employed, and a modified self-antigen expressed by the target cancer is inserted into an inert CDR. After antibody binding to CD40, the antibody is digested and short peptides, including the immunogenic peptide, are displayed on the cell surface by MHCI molecules. CD8+ T cells are activated by these dendritic cells and become tumor specific leading to increased tumor cell killing (FIG. **3**).

[0243] The Trojan antibodies of the invention are also used for treating B cell malignancies, such as leukemia. In this instance an antibody against a B cell surface marker (e.g., CD20) is used. For example, the Arzerra antibody has an inert CDR replaced with a viral epitope (e.g., a CD4 viral epitope/epitope recognized by CD4 T cells). After endocytosis, the antibody is processed and presented on the B cell's surface by MHCII molecules. Cytotoxic T cells recognize the viral epitope and kill the malignant cells (FIG. **4**).

[0244] The Trojan antibodies of the invention are also used for treating solid tumors or general cancers. Antibodies that bind cancer specific epitopes such as HER2, EGFR, EpCAM and PSMA are used and in particular bi-specific antibodies are employed. In the case of a bi-specific molecule only one of the antigen binding domains is required to bring the agent to the cancer cell; the other can be substituted with one or more peptides recognized by CD8+ T cells and/or with a cell penetrating component. It will of course be understood that a cell penetrating component can also be inserted into a non-bispecific antibody if there are two inert CDRs (one for the penetrating component and one for the immunogenic peptide). Alternatively, an antibody can be used which is known to be internalized, so long as insertion of the immunogenic peptide does not interfere with internalization. After binding the target protein, the antibody is digested and released to the cytosol (endosomal escape). From there it is displayed on the cancer cell's surface via MHCII molecules (FIG. **5**).

Example 3: Trojan Antibody Pipeline with Inert CDR Identification (FIG. **6**, Right Pathway)

[0245] Trojan antibodies are designed by first selecting an antibody of interest. Structural analysis of the binding of the antibody to its target is undertaken and inert CDRs are identified. An inert CDR is one that does not directly contact the protein target (a distance of at great than 5 angstroms from the protein target). A suitable immunogenic peptide that can replace the CDR is identified and inserted into the engineered antibody. The immunogenic peptide can be preselected, or an immunogenic peptide can be selected based on its similarity to the CRD being removed. Computational modeling is used to select the suitable peptide and confirm correct antibody conformation. This computational modeling is referred to as the minimal perturbation replacement (MBR) and it can be applied to optimize the replacement location within the CDR. For example, if the CDR is longer than the immunogenic peptide, filling amino acids may need to be added for minimal perturbation of antigen binding. Similarly, if the CDR is shorter than the immunogenic peptide, amino acids from the inter-CDR regions may also be removed. Flanking amino acids are often also involved in

binding and antibody confirmation and structural similarity/minimal perturbation in the flanking regions is also desirous. The MBR optimizes the positioning of the immunogenic peptide.

[0246] If an antibody is selected without an obvious inert CDR, the MBR is applied to rank possible replacement locations within the antibody and specifically the CDRs. If a location can be found that does not perturb binding (or perturbs it by less than a predetermined threshold) than the immunogenic peptide is inserted in this location.

[0247] The MBR analysis takes into account the canonical structure of the antibody and selects positions/replacement location that most closely maintains this structure. Antibody stem preservation is highly conserved. The stem refers to the section of the beta-sheet directly adjacent to the CDR loop. This area is also referred to as the CDR flanking region. These 1-5 amino acids are important for loop position and tend to be highly rigid, whereas the loop itself, especially an inert CDR loop, may be less ordered. Stem preservation is thus important during MBR analysis. The MBR also takes into account the position frequency matrix of other known antibodies. The computational model has imputed hundreds of known antibodies and the frequency of each amino acid at each position is considered. Peptide replacement that most closely conforms to the positional frequency of the known antibodies is preferred. Finally, the MBR outputs the optimal location within the antibody for peptide replacement, or if there is more than one acceptable location it outputs a hierarchy positions.

Example 4: Trojan Antibody Pipeline by Sequence Similarity (FIG. **6**, Left Pathway)

[0248] Trojan antibodies can alternatively be generated based on sequence similarity. A target antibody is selected, as is a list of immunogenic peptides (see for example Tables 1-3). Pairwise sequence alignment is done between the various viral peptides and the antibody. Overlapping peptides within the antibody of 8-11 amino acids are compared with the immunogenic peptides and an alignment score is given for each pair (1 peptide from the antibody and one immunogenic peptide). The score was calculated based on blosum62 and a palanty of −3 per gap opening and per gap extension. A threshold was set for acceptable alignment (for example >25 was used in the below example) Immunogenic peptides and the peptides in the antibody to be replaced that meet the threshold for alignment score are selected and the MBR is applied to optimize replacement position.

Example 5: Trojan Antibody Functional Confirmation (Inert CDRs)

[0249] Replacement based on sequence similarity is not limited to CDRs but can be done anywhere in the antibody. Because of the similarity in sequence, minimal perturbation is expected. Nevertheless, this method and the inert CDR replacement method still requires confirmation that the antibody has retained its functionality. In particular, it must be determined that the antibody will still bind to its target and is still internalized into cells. If binding/internalization is abolished than the new antibody is of no use.

[0250] The first antibody selected for insertion of an immunogenic peptide was a DNA hydrolyzing antibody 3D8, also known as TMab4. The mouse antibody 3D8 was first disclosed in Kim et al., "Heavy and Light Chain Variable Single Domains of an Anti-DNA Binding Antibody Hydrolyze Both Double- and Single-stranded DNAs without Sequence Specificity", J Biol Chem., 2006, June 2; 281(22): 15287-9 and its humanized form was provided in International Patent Application Wo2019/244086. TMab4 was shown to bind to and penetrate into cancer cells and reach the cytoplasm via endosomal escape, thus it was selected for conversion into a Trojan antibody. It was found that CDRs 1, 2 and 3 of the heavy chain (CDRH1, CDRH2, CDRH3) and CDR 3 of the light chain (CDRL3) were inert CDRs.

[0251] Initially, the ability to replace CDRH1 of TMab4 was tested. Two peptides from CMV, two peptides from EBV and one peptide from influenza were inserted into various positions in CDRH1 (see Table 6). Penetration superior to that of the negative control (Adalimumab) was retained for all inserted peptides regardless of positioning within CDRH1. However, some insertions showed superior penetrance, while others diminished penetrance as compared to the parental TMab4. Several of the constructs included the replacement of a flanking amino acids next to the CDR. This was done as these additional replacements were predicted to reduce perturbation of the overall antibody conformation. Specifically, in construct T1, the "S" directly N-terminal to the CDR was also replaced. In constructs T 32, T_33 and T_34 the "CAAS" directly N-terminal to the CDR was also replaced. In constructs T 42 and T_43 the "AAS" directly N-terminal to the CDR was also replaced. One construct, T1_34, included a compensatory mutation (T30S) in the heavy chain that was predicted to reduce perturbation of the antibody. Thus, though overall alteration of the inert CDR did not abolish penetrance, as expected, it did have an impact on the overall ability to enter the cell.

TABLE 6

Trojan antibodies with insertion into CDRH1 of TMab4. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody; (The relative penetration of N1 is given as an average of all replicates.)

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
P1 (TMab4)	PC	—	—	—	—	100.00%
N1 (Adalimumab)	NC	—	—	—	—	50.72%
T1	TAb	CMV NLVPMVATV (1)	CDRH1	VH 25-33	SGYTFTSYV	104.54%

TABLE 6-continued

Trojan antibodies with insertion into CDRH1 of TMab4. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody; (The relative penetration of N1 is given as an average of all replicates.)

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
T2	TAb	CMV NLVPMVATV (1)	CDRH1	VH 26-33	GYTFTSYV	84.06%
T3	TAb	CMV NLVPMVATV (1)	CDRH1	VH 26-32	GYTFTSY	96.92%
T4	TAb	CMV NLVPMVATV (1)	CDRH1	VH 27-33	YTFTSYV	81.45%
T5	TAb	CMV NLVPMVATV (1)	CDRH1	VH 28-33	TFTSYV	83.25%
T1_32	TAb	EBV CLGGLLTMV (2)	CDRH1	VH 22-30	CAASGYTFT	89.85%
T1_33	TAb	EBV CLGGLLTMV (2)	CDRH1	VH 22-29	CAASGYTF	155.93%
T1_34	TAb	EBV CLGGLLTMV (2)	CDRH1	VH 22-29	CAASGYTF	106.10%
T1_35	TAb	FLU GILGFVFTL (3)	CDRH1	VH 26-31	GYTFTS	NA
T1_42	TAb	EBV AVFDRKSDAK (4)	CDRH1	VH 23-32	AASGYTFTSY	115.37%
T1_43	TAb	EBV AVFDRKSDAK (4)	CDRH1	VH 23-31	AASGYTFTS	101.66%
T1_46	TAb	CMV QYDFVAALF (5)	CDRH1	VH 26-32	GYTFTSY	81.46%

[0252] Several of the generated antibodies were tested for their ability to kill target cells in the presence of effector cells specific to the immunogenic peptide present in the Trojan antibody. As can be seen in FIG. **7**A, though all antibodies were still able to penetrate the cell, the ability to induce specific killing was highly variable. Of the five insertions of the NLVPMVATV (SEQ ID NO: i) peptide two produced no specific killing and while the other three did With respect to peptide CLGGLLTMV (SEQ ID NO: 2) the two insertions that produced superior penetration also produced superior killing.

[0253] Next, insertion of SEQ ID NO: 1 and SEQ ID NO: 3 into CDRH3 was tested (Table 7). SEQ ID NO: 3 showed some structural similarity to the CDR it is replacing, in particular the "G" near the beginning of the CDR was maintained, and so it was tested along with SEQ ID NO: 1. It had previously been reported that CDRH3 was completely dispensable for antibody binding and cell penetration (see Lee et al., "Functional Consequences of Complementarity-determining Region Deactivation in a Multifunctional Anti-nucleic Acid Antibody", J Biol Chem. 2013 Dec. 13; 288 (50):35877-85, hereby incorporated by reference in its entirety.). However, insertion of SEQ ID NO: 1 greatly impaired penetrance such that it was only slightly superior to the negative control antibody. In contrast, insertion of SEQ ID NO: 3 invariably produced penetration with two of the insertion positions as good if not better than the parental antibody. This all suggests that selection of the immunogenic peptide to match the insertion location is highly important.

TABLE 7

Trojan antibodies with insertion into CDRH3 of TMab4. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody; (The relative penetration of N1 is given as an average of all replicates.)

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
P1 (TMab4)	PC	—	—	—	—	100.00%
N1 (Adalimumab)	NC	—	—	—	—	50.72%
T7	TAb	CMV NLVPMVATV (1)	CDRH3	VH 100-108	AYKRGYAMD	84.45%
T8	TAb	CMV NLVPMVATV (1)	CDRH3	VH 99-106	GAYKRGYA	60.39%
T9	TAb	CMV NLVPMVATV (1)	CDRH3	VH 99-105	GAYKRGY	53.97%
T10	TAb	CMV NLVPMVATV (1)	CDRH3	VH 100-105	AYKRGY	59.90%
T11	TAb	CMV NLVPMVATV (1)	CDRH3	VH 100-106	AYKRGYA	62.05%
T12	TAb	CMV NLVPMVATV (1)	CDRH3	VH 101-105	YKRGY	51.82%
T13	TAb	CMV NLVPMVATV (1)	CDRH3	VH 101-106	YKRGYA	57.99%
T14	TAb	CMV NLVPMVATV (1)	CDRH3	VH 101-104	YKRG	63.08%
T1_39	TAb	FLU GILGFVFTL (3)	CDRH3	VH 99-107	GAYKRGYAM	75.15%
T1_40	TAb	FLU GILGFVFTL (3)	CDRH3	VH 99-106	GAYKRGYA	148.88%
T1_41	TAb	FLU GILGFVFTL (3)	CDRH3	VH 99-105	GAYKRGY	94.74%

[0254] Interestingly, when specific killing was tested with the Trojan antibodies containing SEQ ID NO: 1 inserted into CDRH3 are surprising result was observed. The two Tabs with the lowest measured penetrance demonstrated specific killing (FIG. **7**B). It may be that the low detection within the cell was due to a rapid antibody processing and display on the cell surface leading to effective killing.

[0255] Insertion of SEQ ID NO: 1 and SEQ ID NO: 5 into CDRL3 and insertion of SEQ ID NO: 1 into CDRH2 was also tested (Table 8). SEQ ID NO: 5 had very high sequence alignment with CDRL3 and so was selected for testing. Several of the constructs included the replacement of a flanking amino acids next to the CDR. This was done as these additional replacements were predicted to reduce perturbation of the overall antibody conformation. Specifically, in constructs T1_44 and T1_45, the "F" directly C-terminal to the CDR was also replaced. In constructs T18 the "Y" directly C-terminal to the CDR was also replaced. All of the tested insertions produced good penetrance essentially equivalent to the parental antibody. This result is highly important as CDRL3 has been reported to be important for cell penetration, and this function was not perturbed by replacement of this CDR with the tested immunogenic peptides.

TABLE 8

Trojan antibodies with insertion into CDRL3 and CDRH2 of TMab4. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody; (The relative penetration of N1 is given as an average of all replicates.)

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
P1 (TMab4)	PC	—	—	—	—	100.00%
N1 (Adalimumab)	NC	—	—	—	—	50.72%

TABLE 8-continued

Trojan antibodies with insertion into CDRL3 and CDRH2 of TMab4. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody; (The relative penetration of N1 is given as an average of all replicates.)

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
T15	TAb	CMV NLVPMVATV (1)	CDRL3	VL 97-103	YYYHMYT	103.87%
T16	TAb	CMV NLVPMVATV (1)	CDRL3	VL 98-103	YYHMYT	92.94%
T1_44	TAb	CMV QYDFVAALF (5)	CDRL3	VL 96-104	QYYYHMYTF	100.63%
T1_45	TAb	CMV QYDFVAALF (5)	CDRL3	VL 98-104	YYHMYTF	94.69%
T18	TAb	CMVNLVPMVATV (1)	CDRH2	VH 52-59	NPYNDGNY	111.90%

[0256] Specific killing was tested for the Trojan antibodies containing SEQ ID NO: 1 and in this case all of the antibodies were found to induce killing (FIG. **7**C). This indicates that this insertion produces highly measured penetrance and high levels of specific killing. Trojan antibodies are also generating containing a combination of inert CDR replacements. As 4 CDRs are inert, combinations of 2, 3 and 4 immunogenic peptides are generated. The inserted peptides can be repeats of the same peptide or different peptides. constructs included the replacement of a flanking amino acids next to the CDR. This was done as the additional replacements were predicted to reduce perturbation of the overall antibody conformation. Specifically, in construct T2_13, the "LLIK" directly N-terminal to the CDR and "YL" directly C-terminal to the CDR were also replaced. All of the SEQ ID NO: 1 insertions produced penetration above the negative control, although once again the levels of penetration varied.

TABLE 9

Trojan antibodies with insertion into CDRL1 and CDRL2 of 3E10. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody.

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
P2 (3E10)	PC	—	—	—	—	100.00%
N2 (Muromonab)	NC	—	—	—	—	54.70%
T2_6	TAb	CMV NLVPMVATV (1)	CDRL1	VL 27-35	KSVSTSSYS	80.61%
T2_11	TAb	CMV NLVPMVATV (1)	CDRL1	VL 28-36	SVSTSSYSY	98.50%
T2_12	TAb	FLU GILGFVFTL (3)	CDRL1	VL 28-36	SVSTSSYSY	X
T2_13	TAb	CMV NLVPMVATV (1)	CDRL2	VL 50-58	LLIKYASYL	72.17%

[0257] A second DNA binding antibody capable of penetrating into cells was also tested. Antibody 3E10 (see Weisbart et al., "DNA-dependent targeting of cell nuclei by a lupus autoantibody", Sci Rep. 2015 Jul. 9; 5:12022, hereby incorporated by reference in its entirety) was examined for inert CDRs and it was determined that CDRL1 and CDRL2 both did not engage the antigen during binding. SEQ ID NO: 1 was inserted into either CDRL1 or CDRL2 and SEQ ID NO: 3 was also inserted into CDRL1 (Table 9). One of the

[0258] Killing with peptide specific effector cells was also tested for cancer cells treated with the Trojan antibodies derived from 3E10 and including SEQ ID NO: 1. Both tested TAbs produced robust specific killing (FIG. **8**). These results demonstrate the universality of the Trojan system. Immunogenic peptides can be inserted into a variety of antibodies that can penetrate into cells and produce peptide specific killing.

[0259] All TAbs generated are cultured with cancer cells and penetrance is determined. Penetration is observed for all peptides which are determined to retain antibody conformation upon replacement of inert CDRs. All TAbs are tested for their ability to induce specific cancer cell killing in the presence of peptide specific effector cells. It will be understood by a skilled artisan that the specific type of cancer tested is not important as all cancer cells are able to bring HLA complex up to the cell surface and thereby display the immunogenic peptides of the TAbs. TAbs are able to produce enhanced specific cell killing above that of the parental antibody that does not have an immunogenic peptide. Trojan antibodies are also generating containing a combination of inert CDR replacements. As 2 CDRs are inert, combinations of two immunogenic peptides are generated. The inserted peptides can be repeats of the same peptide or different peptides.

Example 6: Trojan Antibody Functional Confirmation (Sequence Similarity)

[0260] Replacement based on sequence similarity was also performed for the TMab4 antibody. A screen of immunogenic peptides (see Table 3) found only 0.0057% of tested peptides were above the alignment score threshold (>25) for possible replacement. The three with the most significant similarity to the TMab4 antibody were selected for replacement. SEQ ID NO: 6 from EBV corresponded to amino acids 28-35 within the heavy chain of the antibody. This includes two amino acids ("MH") flanking the CDRH1 on its C-terminus. A compensatory mutation in the heavy chain (Y27D) was also made to reduce perturbation of the antibody. SEQ ID NO: 7 from SARS-CoV2 corresponded to amino acids 52-60 within the heavy chain of the antibody. This includes two amino acids ("YY") flanking the CDRH2 on its C-terminus. SEQ ID NO: 8 from EBV corresponds to amino acids 14-22 in the first framework region on the light chain of the antibody. These three TAbs were generated, and penetrance was tested as before (Table 10). Although all three showed penetrance that was above that of the negative control SEQ ID NO: 7 and SEQ ID NO: 8 produced penetrance that was as good or better than the parental antibody, while SEQ ID NO: 6 produced worse penetrance.

[0261] The sequence similarity method was also used to modify the 3E10 antibody. A screen of immunogenic peptides (see Table 3) found only 0.0093% of tested peptides were above the alignment score threshold (>25) for possible replacement. SEQ ID NO: 6 from EBV corresponded to amino acids 28-36 within CDRLS of the antibody. SEQ ID NO: 9 from SARS-CoV2 corresponded to amino acids 50-58 within the light chain of the antibody. This includes four amino acids ("LLIK") flanking the CDRL2 on its N-terminus and two amino acids ("YL") flanking the CDRL2 on its C-terminus. Both TAbs were generated and were found to have penetrance into cells that was comparable to the parental antibody (Table 11).

TABLE 10

Trojan antibodies with insertion based on sequence similarity into TMab4. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody; (The relative penetration of N1 is given as an average of all replicates.)

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
P1 (TMab4)	PC	—	—	—	—	100.00%
N1 (Adalimumab)	NC	—	—	—	—	50.72%
T19	TAb	EBV SVSSSISSL (6)	CDRH1	VH 28-35	TFTSYVMH	53.97%
T1_30	TAb	Cov2 LPFNDGVYF (7)	CDRH2	VH 52-60	NPYNDGNYY	117.01%
T1_31	TAb	EBV FLGERVTLT (8)	FW1L	VL 14-22	SVGDRVTIT	115.18%

TABLE 11

Trojan antibodies with insertion based on sequence similarity into 3E10. (PC)-positive control; (NC)-Negative control; (Tab)-Trojan antibody

Ab name	PC/ NC/ TAb	Peptide (SEQ ID NO:)	Location	Location of replaced fragment	Sequence of replaced fragment	Relative penetration
P2 (3E10)	PC	—	—	—	—	100.00%
N2 (Muromonab)	NC	—	—	—	—	54.70%
T2_20	TAb	EBV SVSSSISSL (6)	CDRL1	VL 28-36	SVSTSSYSY	99.64%
T2_23	TAb	COV2 LLALHRSYL (9)	CDRL2	VL 50-58	LLIKYASYL	98.32%

[0262] Finally, a third antibody DNA binding antibody, 71F12 (see Sakakibara et al., "Clonal evolution and antigen recognition of anti-nuclear antibodies in acute systemic lupus erythematosus", Sci Rep. 2017; 7: 16428, hereby incorporated by reference in its entirety), was analyzed for inert CDRs and it was determined that CDRL1 was inert. Substitutions were made based on sequence similarity and SEQ ID NO: 10 from Adenovirus corresponded to amino acids 26-34 within CDRL1 of the antibody (called T4_1). SEQ ID NO: 11 from HPV corresponds to amino acids 17-24 in the first framework region on the heavy chain of the antibody (called T4_3). Both TAbs are generated and are found to have penetrance into cells that was at least comparable to the parental antibody.

[0263] All generated TAbs are also tested for specific cell killing as described hereinabove. TAbs that successfully enter the cell are able to induce cell killing that is superior to the parental antibody that does not include killing.

Example 7: Further Confirmation of Trojan Antibody Killing

[0264] Killing by the Trojan antibodies was confirmed by a second method. An IncuCyte Imaging system was used to follow the cancer cells and quantify apoptosis by the presence of caspace-3/7 dye (see Materials and Methods). TAbs derived from both the TMab4 and 3E10 antibodies (T18 and T2_11) were selected for further investigation as both had demonstrated good killing. As can be seen in FIGS. **9A-9B** both TAbs produced specific cell killing well above that produced by the effector cells alone or by effector cells cocultured with cell treated with the parental antibody. This shows that the immunogenic peptides are not only transferred into the target cells, but are processed and displayed on the cell surface which enables specific killing by effector cells.

[0265] The other TAbs are also tested using the IncuCyte Imaging assay. Specific killing above that induced by the effector cells alone and/or the parental antibody is observed with the TAbs of the invention.

[0266] The sequences of the various TAbs produced, and the parental antibodies are summarized in Table 12. It will be understood that when a heavy chain contains the immunogenic peptide the light chain of the parent is used to make the TAb and when the light chain contains the immunogenic peptide the heavy chain of the parent is used to make the TAb. Notably, the 3E10 antibody has two variants (called P2 and P3) with different light chains. Either can be used for generating TAbs.

TABLE 12

Antibody sequences

Name	Chain	SEQ ID NO:	Name	Chain	SEQ ID NO:
TMab04- P1	VH	1021	T1_30	VH	1045
TMab04- P1	VL	1022	T1_31	VL	1046
3E10-P2/P3	VH	1023	T1_32	VH	1047
3E10-P2	VL	1024	T1_33	VH	1048
3E10-P3	VL	1025	T1_34	VH	1049
71F12-P4	VH	1026	T1_35	VH	1050
71F12-P4	VL	1027	T1_39	VH	1051
T1	VH	1028	T1_40	VH	1052
T2	VH	1029	T1_41	VH	1053
T3	VH	1030	T1_42	VH	1054
T4	VH	1031	T1_43	VH	1055
T5	VH	1032	T1_44	VL	1056
T7	VH	1033	T1_45	VL	1057
T8	VH	1034	T1_46	VH	1058
T9	VH	1035	T1_47	VH	1059
T10	VH	1036	T2_20	VL	1060
T11	VH	1037	T2_23	VL	1061
T12	VH	1038	T2_6	VL	1062
T13	VH	1039	T2_11	VL	1063
T14	VH	1040	T2_12	VL	1064
T15	VL	1041	T2_13	VL	1065
T16	VL	1042	T4_1	VL	1066
T18	VH	1043	T4_3	VH	1067
T19	VH	1044			

[0267] Various known therapeutic antibodies were examined for inert CDRs. Crystal structure analysis for each CDR in contact with its antigen was performed and the number of amino acids contacting the antigen was counted. A distance of less than 5 angstroms between an amino acid of the CDR and an amino acid of the antigen was considered contact. More than 2 amino acids in contact with the antigen indicates a CDR involved in binding. Fewer than 2 indicates a definitely inert CDR. Exactly 2 indicates a CDR that is unlikely to be involved in binding or lowly involved. For purposes of evaluation all such CDRs are considered inert. Numerous other antibodies were found that contained inert CDRs which could be replaced with immunogenic peptides such as those provided in Tables 1-3. The MBR is used to optimize positioning. Alternatively, TAbs are designed by identifying peptides from Table 3 with sequence homology to known antibodies and specifically those with inert CDRs.

Peptides with high homology are swapped into the antibody to produce TAbs. All produced Tabs are checked for cell penetrance and penetrance is retained. TAbs are also check for specific cell killing as described hereinabove and levels of killing above those produced by the parental antibody are observed.

Example 8: Trojan Antibody Combined with a Targeting Antibody (Bispecific Trojan, Bi-TAb)

[0268] The TAbs described hereinabove can be considered killing modules that they have been shown to enter into target cells and induce specific killing by effector cells primed against the immunogenic peptide. However, in order to increase the specificity of these molecules, target them to cancer cells and reduce off-target effects a targeting module was added. Three EGFR antibodies were selected to use as the targeting module: Cetuximab, Panitumumab and Necitumumab. All three are known to specifically bind to EGFR and to target to EGFR overexpressing cancers. Antibodies targeting to other cancer specific/overexpressed molecules are also possible. As this is merely the targeting module, and is distinct from the killing module, any known cancer targeting antibody can be used. EGFR is used merely as a proof of concept.

[0269] The T18 and T2_11 TAbs were used for the generation of bi-TAbs as a proof of principle. Control bi-functional antibodies were also generated using the TMab4 or 3E10 parental antibodies. The bispecific molecules were generated using the known knob-in-holes approach for restricting heavy chain homodimerization. The unique modifications are made in the constant region of the heavy chain of both the killing module and the targeting module (see Table 13, see the method provided in Shatz et al., "Knob-into-holes antibody production in mammalian cell lines reveals that asymmetric afucosylation is sufficient for full antibody-dependent cellular cytotoxicity", 2013, mAbs 5:6, 872-881, herein incorporated by reference in its entirety). This promotes heterodimerization between the different heavy chains and discourages homodimerization. The produced bi-Tabs were found to have at least 90% purity for the desired dual-function molecule. Schematics of the final bi-TAbs and their controls are shown in FIG. **10** and the full sequences are provided in Table 13.

TABLE 13

Sequences of targeting arms and bifunctional antibodies.

Name	Chain	SEQ ID NO:
cFTAb1_arm1_P2	LC	1077
cFTAb1_arm1_P2	HC	1078
cFTAb1_arm2_Cetuximab	LC	1079
cFTAb1_arm2_Cetuximab	HC	1080
cFTAb2_arm1_P2	LC	1077
cFTAb2_arm1_P2	HC	1078
cFTAb2_arm2_Panitumumab	LC	1081
cFTAb2_arm2_Panitumumab	HC	1082
cFTAb3_arm1_P1	LC	1083
cFTAb3_arm1_P1	HC	1084
cFTAb3_arm2_Cetuximab	LC	1079
cFTAb3_arm2_Cetuximab	HC	1080
cFTAb4_arm1_P1	LC	1083
cFTAb4_arm1_P1	HC	1084
cFTAb4_arm2_Panitumumab	LC	1081
cFTAb4_arm2_Panitumumab	HC	1082
cFTAb5_arm1_P2	LC	1077
cFTAb5_arm1_P2	HC	1078

TABLE 13-continued

Sequences of targeting arms and bifunctional antibodies.

Name	Chain	SEQ ID NO:
cFTAb5_arm2_Necitumumab	LC	1085
cFTAb5_arm2_Necitumumab	HC	1086
FTAb1_arm1_T2_11	LC	1087
FTAb1_arm1_T2_11	HC	1088
FTAb1_arm1_Cetuximab	LC	1079
FTAb1_arm1_Cetuximab	HC	1080
FTAb2_arm1_T2_11	LC	1087
FTAb2_arm1_T2_11	HC	1088
FTAb2_arm2_Panitumumab	LC	1081
FTAb2_arm2_Panitumumab	HC	1082
FTAb3_arm1_T18	LC	1089
FTAb3_arm1_T18	HC	1090
FTAb3_arm2_Cetuximab	LC	1079
FTAb3_arm2_Cetuximab	HC	1080
FTAb4_arm1_T18	LC	1089
FTAb4_arm1_T18	HC	1090
FTAb4_arm2_Panitumumab	LC	1081
FTAb4_arm2_Panitumumab	HC	1082
FTAb5_arm1_T2_11	LC	1087
FTAb5_arm1_T2_11	HC	1088
FTAb5_arm2_Necitumumab	LC	1085
FTAb5_arm2_Necitumumab	HC	1086

[0270] The bi-TAbs were tested for their ability to bind surface EGFR on breast cancer cells that express high levels of EGFR. It is predicted that the additional killing module should not impact surface binding of the targeting module and indeed that is what is observed (FIG. **11**). The bi-TAbs at either a concentration of 0.3 nM or 3 nM successfully bound surface EGFR and at a level comparable to the control original anti-EGFR antibody. Thus, the bi-TAbs can effectively target to cancer cells based on the targeting module selected.

[0271] Next, the bi-TAbs ability to bring the immunogenic peptide on to the surface of the cancer cells in complex with an HLA molecule was tested. HLA-peptide display was measured as described hereinabove (Materials and Methods). A time course experiment was performed to monitor surface display over time. All five of the bi-TAbs successfully brought the peptide to the cell surface by 10 hours of incubation (FIG. **12**). All bi-Tabs were superior to their control counterparts.

[0272] Finally, cancer cell killing was examined at various effector cell concentration. Bi-TAbs 3-5 each with a different targeting module were tested at effector:target cell (E:T) concentrations of 1:1, 3:1 and 6:1. At a ratio of 6:1 all three antibodies induced specific killing above what is observed with the control antibodies (FIG. **13**). Bi-TAbs 4 and 5 (one which contains the P1 derived TAb and one which contains the P2 derived TAb) also showed increased killing at ratios of 3:1 and even 1:1. A culture without effector cells was used as a control. These results demonstrate the high level of effectiveness of the bi-TAb as it combines cancer cell targeting with high levels of specific killing.

[0273] The three anti-EGFR antibodies used themselves contain inert CDRs. A summary of these inert CDRs is provided in Table 14. CDRH1, CDRL1 and CDRL2 of Cetuximab, CDRL1 and CDRL2 of Panitumumab and CDRL1 and CDRL2 of Necitumumab were all found to be inert. These CDRs are also replaced with immunogenic peptides. The targeting of the replaced antibodies is confirmed and the ability to bind to EGFR and target to EGFR overexpressing cancer cells is retained. The combination of the modified targeting module to the killing module increases the number of immunogenic peptides delivered. The peptide used in the killing module and the peptide used in the targeting module can be the same or different.

TABLE 14

Inert CDRs in anti-EGFR antibodies.

Antibody	CDRH1 score	CDRH2 score	CDRH3 score	CDRL1 score	CDRL2 score	CDRL3 score	Inert CDRs
Cetuximab	1	>2	>2	2	1	>2	H1, L1, L2
Panitumumab	>2	>2	>2	2	1	>2	L1, L2
Necitumumab	>2	>2	>2	2	0	>2	L1, L2

[0274] Bi-TAbs are generated with the other killing modules and various targeting modules. The bi-Tabs are evaluated as above to cancer cell targeting, HLA-peptide surface display and for specific killing. Bi-Tabs are superior to the control bi-functional molecule and are able to target to cancers, induce peptide display and ultimately enhance killing of the target cells by effector cells specific to the immunogenic peptide.

[0275] In vivo validation is also performed. The engineered bi-Tabs are injected into immune competent mice expressing a tumor targetable by the targeting module. Control bi-functional molecules lacking the immunogenic peptide and/or binding a non-cancer related target are also administered. Animal survival over time is monitored as is tumor size. The Trojan antibodies are found to shrink tumors and/or extend survival time in a statistically significant manner, indicating that they activate the immune system against the cancer. Mice may be vaccinated with the immunogenic peptide beforehand.

[0276] Although the invention has been described in conjunction with specific embodiments thereof, it is evident that many alternatives, modifications and variations will be apparent to those skilled in the art. Accordingly, it is intended to embrace all such alternatives, modifications and variations that fall within the spirit and broad scope of the appended claims.

SEQUENCE LISTING

```
Sequence total quantity: 1090
SEQ ID NO: 1            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 1
NLVPMVATV                                                           9

SEQ ID NO: 2            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 2
CLGGLLTMV                                                           9

SEQ ID NO: 3            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A
SEQUENCE: 3
GILGFVFTL                                                           9

SEQ ID NO: 4            moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Epstein-Barr virus
SEQUENCE: 4
AVFDRKSDAK                                                          10

SEQ ID NO: 5            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 5
QYDPVAALF                                                           9

SEQ ID NO: 6            moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
```

-continued

```
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 6
TPSVSSSISS L                                                    11

SEQ ID NO: 7            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 7
LPFNDGVYF                                                       9

SEQ ID NO: 8            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 8
FLGERVTLT                                                       9

SEQ ID NO: 9            moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 9
LLALHRSYL                                                       9

SEQ ID NO: 10           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human adenovirus 5
SEQUENCE: 10
STDVASLNY                                                       9

SEQ ID NO: 11           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human papillomavirus
SEQUENCE: 11
TLGIVCPI                                                        8

SEQ ID NO: 12           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 12
RYSIFFDY                                                        8

SEQ ID NO: 13           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 13
CPLSKILL                                                        8

SEQ ID NO: 14           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 14
SLGYITTV                                                        8

SEQ ID NO: 15           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 15
RAKFKQLL                                                        8
```

-continued

```
SEQ ID NO: 16           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 16
TNKIKEQL                                                        8

SEQ ID NO: 17           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 17
QTRQKFHL                                                        8

SEQ ID NO: 18           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 18
EMRLRMIL                                                        8

SEQ ID NO: 19           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 19
MAREKNDL                                                        8

SEQ ID NO: 20           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human papillomavirus
SEQUENCE: 20
CCKCDSTL                                                        8

SEQ ID NO: 21           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human papillomavirus
SEQUENCE: 21
HDIILECV                                                        8

SEQ ID NO: 22           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 22
LPQGFSAL                                                        8

SEQ ID NO: 23           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 23
NLTTRTQL                                                        8

SEQ ID NO: 24           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 24
AEHVNNSY                                                        8

SEQ ID NO: 25           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 25
AEVQIDRL                                                          8

SEQ ID NO: 26           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 26
EPLVDLPI                                                          8

SEQ ID NO: 27           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 27
FPREGVFV                                                          8

SEQ ID NO: 28           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 28
NITRFQTL                                                          8

SEQ ID NO: 29           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 29
QPYRVVVL                                                          8

SEQ ID NO: 30           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 30
RLQSLQTY                                                          8

SEQ ID NO: 31           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 31
SPRRARSV                                                          8

SEQ ID NO: 32           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 32
VYYPDKVF                                                          8

SEQ ID NO: 33           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 33
YAWNRKRI                                                          8

SEQ ID NO: 34           moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 34
FLPFFSNV                                                          8
```

-continued

```
SEQ ID NO: 35          moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 35
APHGVVFL                                                          8

SEQ ID NO: 36          moltype = AA  length = 8
FEATURE                Location/Qualifiers
source                 1..8
                       mol_type = protein
                       organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 36
GVYHKNNK                                                          8

SEQ ID NO: 37          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human adenovirus 11
SEQUENCE: 37
TYFNLGNKF                                                         9

SEQ ID NO: 38          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human adenovirus 5
SEQUENCE: 38
TDLGQNLLY                                                         9

SEQ ID NO: 39          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human adenovirus 5
SEQUENCE: 39
TLLYVLFEV                                                         9

SEQ ID NO: 40          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human adenovirus 5
SEQUENCE: 40
VLAWTRAFV                                                         9

SEQ ID NO: 41          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human alphaherpesvirus 1
SEQUENCE: 41
YVAGFLALY                                                         9

SEQ ID NO: 42          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human alphaherpesvirus 1
SEQUENCE: 42
ALMGAVTSL                                                         9

SEQ ID NO: 43          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
                       mol_type = protein
                       organism = Human alphaherpesvirus 1
SEQUENCE: 43
MMLRDRWSL                                                         9

SEQ ID NO: 44          moltype = AA  length = 9
FEATURE                Location/Qualifiers
source                 1..9
```

-continued

```
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 44
AVLCLYLLY                                                          9

SEQ ID NO: 45           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 45
FLWEDQTLL                                                          9

SEQ ID NO: 46           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 46
FIPQYLSAV                                                          9

SEQ ID NO: 47           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 47
FLIAYQPLL                                                          9

SEQ ID NO: 48           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 48
SVYPYDEFV                                                          9

SEQ ID NO: 49           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 49
VYMSPFYGY                                                          9

SEQ ID NO: 50           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 50
FLGDDPSPA                                                          9

SEQ ID NO: 51           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 51
RLTGYPAGI                                                          9

SEQ ID NO: 52           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 52
APASVYQPA                                                          9

SEQ ID NO: 53           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 53
CPRRPAVAF                                                          9
```

-continued

```
SEQ ID NO: 54           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 54
VVRGPTVSL                                                           9

SEQ ID NO: 55           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 55
LIDGIFLRY                                                           9

SEQ ID NO: 56           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 56
SQLAHLVYV                                                           9

SEQ ID NO: 57           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 57
FLGAGALAV                                                           9

SEQ ID NO: 58           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 58
FLGGHVAVA                                                           9

SEQ ID NO: 59           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 59
TLRGLFFSV                                                           9

SEQ ID NO: 60           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 60
KYFYCNSLF                                                           9

SEQ ID NO: 61           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 61
EYQRLYATF                                                           9

SEQ ID NO: 62           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 62
APRIGGRRA                                                           9

SEQ ID NO: 63           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 63
APRTWCRLL                                                          9

SEQ ID NO: 64           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 64
ALMLRLLRI                                                          9

SEQ ID NO: 65           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 65
RILGVLVHL                                                          9

SEQ ID NO: 66           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 66
YMESVFQMY                                                          9

SEQ ID NO: 67           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 67
ILIEGIFFA                                                          9

SEQ ID NO: 68           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 68
YMANQILRY                                                          9

SEQ ID NO: 69           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 69
VPRPDDPVL                                                          9

SEQ ID NO: 70           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 70
VYTPSPYVF                                                          9

SEQ ID NO: 71           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 71
AYLPRPVEF                                                          9

SEQ ID NO: 72           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 72
AILTQYWKY                                                          9
```

-continued

```
SEQ ID NO: 73           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 73
ATDSLNNEY                                                           9

SEQ ID NO: 74           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 74
AYVSVLYRW                                                           9

SEQ ID NO: 75           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 75
LASDPHYEY                                                           9

SEQ ID NO: 76           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 76
LLAYVSVLY                                                           9

SEQ ID NO: 77           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 77
RLNELLAYV                                                           9

SEQ ID NO: 78           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 78
SIVHHHAQY                                                           9

SEQ ID NO: 79           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 79
ALATVTLKY                                                           9

SEQ ID NO: 80           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 80
ALLDRDCRV                                                           9

SEQ ID NO: 81           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 81
FLADAVVRL                                                           9

SEQ ID NO: 82           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 82
FTAPEVGTY                                                          9

SEQ ID NO: 83           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 83
RLLGFADTV                                                          9

SEQ ID NO: 84           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 84
RSSLGSLLY                                                          9

SEQ ID NO: 85           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 85
ALHTALATV                                                          9

SEQ ID NO: 86           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 86
TLLELVVSV                                                          9

SEQ ID NO: 87           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 87
VPGWSRRTL                                                          9

SEQ ID NO: 88           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 88
ALLAKMLFY                                                          9

SEQ ID NO: 89           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 89
RMLGDVMAV                                                          9

SEQ ID NO: 90           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 90
TMLEDHEFV                                                          9

SEQ ID NO: 91           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 91
ALLGLTLGV                                                          9
```

-continued

```
SEQ ID NO: 92           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 92
FVLATGDFV                                                           9

SEQ ID NO: 93           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 93
GIFEDRAPV                                                           9

SEQ ID NO: 94           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 94
LLTTPKFTV                                                           9

SEQ ID NO: 95           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 95
NLLTTPKFT                                                           9

SEQ ID NO: 96           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 96
TMYYKDVTV                                                           9

SEQ ID NO: 97           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 97
YLANGGFLI                                                           9

SEQ ID NO: 98           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 98
ALSALLTKL                                                           9

SEQ ID NO: 99           moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 99
FLTCTDRSV                                                           9

SEQ ID NO: 100          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 100
DRLDNRLQL                                                           9

SEQ ID NO: 101          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 101
KSRRPLTTF                                                          9

SEQ ID NO: 102          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 102
RRAQMAPKR                                                          9

SEQ ID NO: 103          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 103
GPHETITAL                                                          9

SEQ ID NO: 104          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 104
PAWSRRTLL                                                          9

SEQ ID NO: 105          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 105
ASDSLNNEY                                                          9

SEQ ID NO: 106          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 106
FLVDAIVRV                                                          9

SEQ ID NO: 107          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 107
GLADTVVAC                                                          9

SEQ ID NO: 108          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 108
RPRGEVRFL                                                          9

SEQ ID NO: 109          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 109
SAPLPSNRV                                                          9

SEQ ID NO: 110          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 110
SLPRSRTPI                                                          9
```

-continued

```
SEQ ID NO: 111          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 111
ALWALPHAA                                                           9

SEQ ID NO: 112          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 112
ILIEGIFFV                                                           9

SEQ ID NO: 113          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 113
VTEHDTLLY                                                           9

SEQ ID NO: 114          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 114
ELNRKMIYM                                                           9

SEQ ID NO: 115          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 115
IPSINVHHY                                                           9

SEQ ID NO: 116          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 116
TRATKMQVI                                                           9

SEQ ID NO: 117          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 117
QIKVRVKMV                                                           9

SEQ ID NO: 118          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 118
DELRRKMMY                                                           9

SEQ ID NO: 119          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 119
EEAIVAYTL                                                           9

SEQ ID NO: 120          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 120
ELKRKMMYM                                                           9

SEQ ID NO: 121          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 121
QIKVRVDMV                                                           9

SEQ ID NO: 122          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 122
VLEETSVML                                                           9

SEQ ID NO: 123          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 123
ARAKKDELK                                                           9

SEQ ID NO: 124          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 124
ARAKKDELR                                                           9

SEQ ID NO: 125          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 125
DELKRKMIY                                                           9

SEQ ID NO: 126          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 126
FMDILTTCV                                                           9

SEQ ID NO: 127          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human coronavirus 229E
SEQUENCE: 127
KEWAYCVEM                                                           9

SEQ ID NO: 128          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human coronavirus 229E
SEQUENCE: 128
LITGRLAAL                                                           9

SEQ ID NO: 129          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human coronavirus 229E
SEQUENCE: 129
LLLNCLWSV                                                           9
```

-continued

```
SEQ ID NO: 130          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human coronavirus OC43
SEQUENCE: 130
TMLDIQPED                                                           9

SEQ ID NO: 131          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human coronavirus OC43
SEQUENCE: 131
LPRWYFYYL                                                           9

SEQ ID NO: 132          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human coronavirus OC43
SEQUENCE: 132
KLWHYCSTL                                                           9

SEQ ID NO: 133          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 133
LLIEGIFFI                                                           9

SEQ ID NO: 134          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 134
AFLGERVTL                                                           9

SEQ ID NO: 135          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 135
KLGPGEEQV                                                           9

SEQ ID NO: 136          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 136
RFIAQLLLL                                                           9

SEQ ID NO: 137          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 137
TLTSYWRRV                                                           9

SEQ ID NO: 138          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 138
VEDLFGANL                                                           9

SEQ ID NO: 139          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 139
WQWEHIPPA                                                    9

SEQ ID NO: 140      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 140
LPCVLWPVL                                                    9

SEQ ID NO: 141      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 141
RAKFKQLLQ                                                    9

SEQ ID NO: 142      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 142
SENDRLRLL                                                    9

SEQ ID NO: 143      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 143
TLDTKPLSV                                                    9

SEQ ID NO: 144      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 144
FMVFLQTHI                                                    9

SEQ ID NO: 145      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 145
HPVGEADYF                                                    9

SEQ ID NO: 146      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 146
VLKDAIKDL                                                    9

SEQ ID NO: 147      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 147
AYSSWMYSY                                                    9

SEQ ID NO: 148      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human gammaherpesvirus 4
SEQUENCE: 148
QAKWRLQTL                                                    9
```

-continued

```
SEQ ID NO: 149          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 149
RLRAEAQVK                                                           9

SEQ ID NO: 150          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 150
SVRDRLARL                                                           9

SEQ ID NO: 151          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 151
IVTDFSVIK                                                           9

SEQ ID NO: 152          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 152
VSFIEFVGW                                                           9

SEQ ID NO: 153          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 153
EGGVGWRHW                                                           9

SEQ ID NO: 154          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 154
QPRAPIRPI                                                           9

SEQ ID NO: 155          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 155
RRIYDLIEL                                                           9

SEQ ID NO: 156          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 156
RPPIFIRLL                                                           9

SEQ ID NO: 157          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 157
YPLHEQHGM                                                           9

SEQ ID NO: 158          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 158
LMIIPLINV                                                           9

SEQ ID NO: 159          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 159
SLVIVTTFV                                                           9

SEQ ID NO: 160          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 160
TLFIGSHVV                                                           9

SEQ ID NO: 161          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 161
YLQQNWWTL                                                           9

SEQ ID NO: 162          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 162
ALLVLYSFA                                                           9

SEQ ID NO: 163          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 163
GLGTLGAAL                                                           9

SEQ ID NO: 164          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 164
LLSAWILTA                                                           9

SEQ ID NO: 165          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 165
LLWTLVVLL                                                           9

SEQ ID NO: 166          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 166
MGSLEMVPM                                                           9

SEQ ID NO: 167          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 167
YLLEMLWRL                                                           9
```

-continued

```
SEQ ID NO: 168          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 168
VLQWASLAV                                                           9

SEQ ID NO: 169          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 169
FLYALALLL                                                           9

SEQ ID NO: 170          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 170
IEDPPFNSL                                                           9

SEQ ID NO: 171          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 171
RRRWRRLTV                                                           9

SEQ ID NO: 172          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 172
TYGPVFMCL                                                           9

SEQ ID NO: 173          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 173
FLRGRAYGL                                                           9

SEQ ID NO: 174          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 8
SEQUENCE: 174
LVLILYLCV                                                           9

SEQ ID NO: 175          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 8
SEQUENCE: 175
LLNGWRWRL                                                           9

SEQ ID NO: 176          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human gammaherpesvirus 8
SEQUENCE: 176
IGLITVLFL                                                           9

SEQ ID NO: 177          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 177
DAAPAIQHI                                                    9

SEQ ID NO: 178          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 178
KQYLGVYIW                                                    9

SEQ ID NO: 179          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 179
TYATFLVTW                                                    9

SEQ ID NO: 180          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 180
KENIAAYKF                                                    9

SEQ ID NO: 181          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 181
KTNNWHAGW                                                    9

SEQ ID NO: 182          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 182
APKTATSSW                                                    9

SEQ ID NO: 183          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 183
QTTGRITNR                                                    9

SEQ ID NO: 184          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 184
VEDINRVFL                                                    9

SEQ ID NO: 185          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 185
CYDHAQTHL                                                    9

SEQ ID NO: 186          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 186
TLDYKPLSV                                                    9
```

-continued

```
SEQ ID NO: 187          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 187
YRSGIIAVV                                                           9

SEQ ID NO: 188          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 188
RPPIFIRRL                                                           9

SEQ ID NO: 189          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 189
FLDKGTYTL                                                           9

SEQ ID NO: 190          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 190
ARYAYYLQF                                                           9

SEQ ID NO: 191          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 191
RRRKGWIPL                                                           9

SEQ ID NO: 192          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 192
LQHYREVAA                                                           9

SEQ ID NO: 193          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 193
AENAGNDAC                                                           9

SEQ ID NO: 194          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 194
RVRAYTYSK                                                           9

SEQ ID NO: 195          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 4
SEQUENCE: 195
YVLDHLIVV                                                           9

SEQ ID NO: 196          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                    mol_type = protein
                    organism = Human herpesvirus 4
SEQUENCE: 196
DEVEFLGHY                                                    9

SEQ ID NO: 197      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 4
SEQUENCE: 197
GLCTLVAML                                                    9

SEQ ID NO: 198      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 4
SEQUENCE: 198
KDTWLDARM                                                    9

SEQ ID NO: 199      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 4
SEQUENCE: 199
VLFGLLCLL                                                    9

SEQ ID NO: 200      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 5
SEQUENCE: 200
ELRRKMMYM                                                    9

SEQ ID NO: 201      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 5
SEQUENCE: 201
ELKRKMIYM                                                    9

SEQ ID NO: 202      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 6
SEQUENCE: 202
EFKSKFSTL                                                    9

SEQ ID NO: 203      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 6
SEQUENCE: 203
EGRDRILTV                                                    9

SEQ ID NO: 204      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 6
SEQUENCE: 204
FEKERFLFL                                                    9

SEQ ID NO: 205      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Human herpesvirus 6
SEQUENCE: 205
EGRERILTV                                                    9
```

-continued

```
SEQ ID NO: 206          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 206
NVKHKKNPL                                                           9

SEQ ID NO: 207          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 207
VVKGKVLSI                                                           9

SEQ ID NO: 208          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 208
EARRRLAEM                                                           9

SEQ ID NO: 209          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 209
RSKPRHMCV                                                           9

SEQ ID NO: 210          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 210
DFKSKYLTL                                                           9

SEQ ID NO: 211          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human herpesvirus 6
SEQUENCE: 211
SPRSRLQQL                                                           9

SEQ ID NO: 212          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 212
VLATAVREL                                                           9

SEQ ID NO: 213          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 213
FQANTPPAV                                                           9

SEQ ID NO: 214          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 214
IPYTAAVQV                                                           9

SEQ ID NO: 215          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 215
KLAKLIIDL                                                          9

SEQ ID NO: 216          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 216
RLPREKLKK                                                          9

SEQ ID NO: 217          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 217
SPKAGLLSL                                                          9

SEQ ID NO: 218          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 218
SLQQEITLL                                                          9

SEQ ID NO: 219          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human orthopneumovirus
SEQUENCE: 219
ISDYFHNTY                                                          9

SEQ ID NO: 220          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = human papillomavirus 11
SEQUENCE: 220
KVLIRCYLC                                                          9

SEQ ID NO: 221          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = human papillomavirus 11
SEQUENCE: 221
SIDQLCKTF                                                          9

SEQ ID NO: 222          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = human papillomavirus 44
SEQUENCE: 222
HNNGICWGN                                                          9

SEQ ID NO: 223          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 223
CYEQLGDSS                                                          9

SEQ ID NO: 224          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 224
ITIRCIICQ                                                          9
```

-continued

```
SEQ ID NO: 225          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 225
KTLEERVKK                                                           9

SEQ ID NO: 226          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 226
MRGDKATIK                                                           9

SEQ ID NO: 227          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 227
PYGVCIMCL                                                           9

SEQ ID NO: 228          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 228
QLGDSSDEE                                                           9

SEQ ID NO: 229          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 229
RLQCVQCKK                                                           9

SEQ ID NO: 230          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 230
VYKFLFTDL                                                           9

SEQ ID NO: 231          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 231
YYYAGSSRL                                                           9

SEQ ID NO: 232          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 232
LQFIFQLCK                                                           9

SEQ ID NO: 233          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 233
MTLCAEVKK                                                           9

SEQ ID NO: 234          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 234
QYRVFRIKL                                                           9

SEQ ID NO: 235          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 52
SEQUENCE: 235
RIKLPDPNK                                                           9

SEQ ID NO: 236          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 236
ILIRCIICQ                                                           9

SEQ ID NO: 237          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 237
KCLNEILIR                                                           9

SEQ ID NO: 238          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 238
KVCLRLLSK                                                           9

SEQ ID NO: 239          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 239
ATEVRTLQQ                                                           9

SEQ ID NO: 240          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 240
CTIVCPSCA                                                           9

SEQ ID NO: 241          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 241
LCINSTATE                                                           9

SEQ ID NO: 242          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 242
AVPDDLYIK                                                           9

SEQ ID NO: 243          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 243
KYTFWEVNL                                                           9
```

-continued

```
SEQ ID NO: 244          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 244
RVRLPDPNK                                                           9

SEQ ID NO: 245          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 245
TSESQLFNK                                                           9

SEQ ID NO: 246          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus 58
SEQUENCE: 246
YTFWEVNLK                                                           9

SEQ ID NO: 247          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 247
YLTAPTGCI                                                           9

SEQ ID NO: 248          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 248
DSAPILTAF                                                           9

SEQ ID NO: 249          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 249
KSAIVTLTY                                                           9

SEQ ID NO: 250          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 250
LAVSKNKAL                                                           9

SEQ ID NO: 251          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 251
LQDVSLEVY                                                           9

SEQ ID NO: 252          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 252
NPCHTTKLL                                                           9

SEQ ID NO: 253          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 253
NTTPIVHLK                                                           9

SEQ ID NO: 254          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 254
QVILCPTSV                                                           9

SEQ ID NO: 255          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 255
RLECAIYYK                                                           9

SEQ ID NO: 256          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 256
SPEIIRQHL                                                           9

SEQ ID NO: 257          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 257
TLYTAVSST                                                           9

SEQ ID NO: 258          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 258
VVEGQVDYY                                                           9

SEQ ID NO: 259          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 259
YRFKKHCTL                                                           9

SEQ ID NO: 260          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 260
ALQAIELQL                                                           9

SEQ ID NO: 261          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 261
TLQDVSLEV                                                           9

SEQ ID NO: 262          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 262
YIIFVYIPL                                                           9
```

-continued

```
SEQ ID NO: 263          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 263
FAFRDLCIV                                                           9

SEQ ID NO: 264          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 264
IILECVYCK                                                           9

SEQ ID NO: 265          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 265
TTLEQQYNK                                                           9

SEQ ID NO: 266          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 266
VCDKCLKFY                                                           9

SEQ ID NO: 267          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 267
CPEEKQRHL                                                           9

SEQ ID NO: 268          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 268
YGTTLEQQY                                                           9

SEQ ID NO: 269          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 269
EYRHYCYSL                                                           9

SEQ ID NO: 270          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 270
VYDFAFQDL                                                           9

SEQ ID NO: 271          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 271
GTLGIVCPI                                                           9

SEQ ID NO: 272          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 272
IVCPICSQK                                                           9

SEQ ID NO: 273          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 273
QAEPDRAHY                                                           9

SEQ ID NO: 274          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 274
RAHYNIVTF                                                           9

SEQ ID NO: 275          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 275
TLHEYMLDL                                                           9

SEQ ID NO: 276          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 276
LQPETTDLY                                                           9

SEQ ID NO: 277          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 277
TPTLHEYML                                                           9

SEQ ID NO: 278          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 278
LLMGTLGIV                                                           9

SEQ ID NO: 279          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 279
TLGIVCPIC                                                           9

SEQ ID NO: 280          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 280
IHSMNSTIL                                                           9

SEQ ID NO: 281          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 281
ISEYRHYCY                                                           9
```

-continued

```
SEQ ID NO: 282          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 282
KFYSKISEY                                                           9

SEQ ID NO: 283          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 283
KLPQLCTEL                                                           9

SEQ ID NO: 284          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 284
VYDFAFRDL                                                           9

SEQ ID NO: 285          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 285
TIHDIILEC                                                           9

SEQ ID NO: 286          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 286
YMLDLQPET                                                           9

SEQ ID NO: 287          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 18
SEQUENCE: 287
IHSMNSSIL                                                           9

SEQ ID NO: 288          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 18
SEQUENCE: 288
NVFPIFLQM                                                           9

SEQ ID NO: 289          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 18
SEQUENCE: 289
KLPDLCTEL                                                           9

SEQ ID NO: 290          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 18
SEQUENCE: 290
NLLIRCLRC                                                           9

SEQ ID NO: 291          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human papillomavirus type 18
SEQUENCE: 291
FQQLFLNTL                                                           9

SEQ ID NO: 292          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 18
SEQUENCE: 292
LFLNTLSFV                                                           9

SEQ ID NO: 293          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 6
SEQUENCE: 293
LLLGTLNIV                                                           9

SEQ ID NO: 294          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 6b
SEQUENCE: 294
TIDQLCKTF                                                           9

SEQ ID NO: 295          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 295
EADVQQWLT                                                           9

SEQ ID NO: 296          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 296
FYTPLADQF                                                           9

SEQ ID NO: 297          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 297
GLCPHCINV                                                           9

SEQ ID NO: 298          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 298
GLFNNVLYH                                                           9

SEQ ID NO: 299          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 299
LHTDFEQVM                                                           9

SEQ ID NO: 300          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 300
LLHTDFEQV                                                           9
```

-continued

```
SEQ ID NO: 301          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 301
SESSFFNLI                                                           9

SEQ ID NO: 302          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 302
SSHSGSFQI                                                           9

SEQ ID NO: 303          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 303
TEADVQQWL                                                           9

SEQ ID NO: 304          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 304
VQQWLTWCN                                                           9

SEQ ID NO: 305          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 305
TAKSRVHPL                                                           9

SEQ ID NO: 306          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human polyomavirus 1
SEQUENCE: 306
LLLIWFRPV                                                           9

SEQ ID NO: 307          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human polyomavirus 1
SEQUENCE: 307
AVDTVLAKK                                                           9

SEQ ID NO: 308          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human polyomavirus 1
SEQUENCE: 308
EPLVWIDCY                                                           9

SEQ ID NO: 309          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human polyomavirus 1
SEQUENCE: 309
AITEVECFL                                                           9

SEQ ID NO: 310          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human polyomavirus 1
SEQUENCE: 310
LLMWEAVTV                                                           9

SEQ ID NO: 311          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human respiratory syncytial virus A2
SEQUENCE: 311
RARRELPRF                                                           9

SEQ ID NO: 312          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human respiratory syncytial virus A2
SEQUENCE: 312
YLEKESIYY                                                           9

SEQ ID NO: 313          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human respiratory syncytial virus A2
SEQUENCE: 313
NPKASLLSL                                                           9

SEQ ID NO: 314          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human respiratory syncytial virus A2
SEQUENCE: 314
QVMLRWGVL                                                           9

SEQ ID NO: 315          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 315
GILGFVFTL                                                           9

SEQ ID NO: 316          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 316
SRYWAIRTR                                                           9

SEQ ID NO: 317          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 317
NMLSTVLGV                                                           9

SEQ ID NO: 318          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 318
LPFERATVM                                                           9

SEQ ID NO: 319          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 319
LPFERATIM                                                           9
```

-continued

```
SEQ ID NO: 320          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 320
LPFDKSTVM                                                           9

SEQ ID NO: 321          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 321
LPFEKSTIM                                                           9

SEQ ID NO: 322          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 322
LPFDKPTIM                                                           9

SEQ ID NO: 323          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 323
LPFEKSTVM                                                           9

SEQ ID NO: 324          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 324
CVNGSCFTV                                                           9

SEQ ID NO: 325          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 325
LPFDRTTIM                                                           9

SEQ ID NO: 326          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 326
KTGGPIYRR                                                           9

SEQ ID NO: 327          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 327
LPFDRPTIM                                                           9

SEQ ID NO: 328          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza B virus
SEQUENCE: 328
GLDNHTILL                                                           9

SEQ ID NO: 329          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                    mol_type = protein
                    organism = JC polyomavirus
SEQUENCE: 329
ILMWEAVTL                                                    9

SEQ ID NO: 330      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = JC polyomavirus
SEQUENCE: 330
SITEVECFL                                                    9

SEQ ID NO: 331      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 331
NLNESLIDL                                                    9

SEQ ID NO: 332      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 332
RLDKVEAEV                                                    9

SEQ ID NO: 333      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 333
VYDPLQPEL                                                    9

SEQ ID NO: 334      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 334
TLKSFTVEK                                                    9

SEQ ID NO: 335      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 335
HADQLTPTW                                                    9

SEQ ID NO: 336      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 336
NATNVVIKV                                                    9

SEQ ID NO: 337      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 337
VGYLQPRTF                                                    9

SEQ ID NO: 338      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 338
YFQPRTFLL                                                    9
```

-continued

```
SEQ ID NO: 339          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 339
FQFCNDPFL                                                           9

SEQ ID NO: 340          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 340
ASVYAWNRK                                                           9

SEQ ID NO: 341          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 341
GYLQPRTFL                                                           9

SEQ ID NO: 342          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 342
YLQLRTFLL                                                           9

SEQ ID NO: 343          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 343
YLQPRIFLL                                                           9

SEQ ID NO: 344          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 344
AEVQIDRLI                                                           9

SEQ ID NO: 345          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 345
ALNTLVKQL                                                           9

SEQ ID NO: 346          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 346
CVADYSVLY                                                           9

SEQ ID NO: 347          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 347
GSFCTQLNR                                                           9

SEQ ID NO: 348          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 348
GVVFLHVTY                                                           9

SEQ ID NO: 349      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 349
LLFNKVTLA                                                           9

SEQ ID NO: 350      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 350
LLQYGSFCT                                                           9

SEQ ID NO: 351      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 351
RLQSLQTYV                                                           9

SEQ ID NO: 352      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 352
RVDFCGKGY                                                           9

SEQ ID NO: 353      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 353
SVLNDILSR                                                           9

SEQ ID NO: 354      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 354
VLNDILSRL                                                           9

SEQ ID NO: 355      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 355
FVFKNIDGY                                                           9

SEQ ID NO: 356      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 356
GTHWFVTQR                                                           9

SEQ ID NO: 357      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 357
GTITSGWTF                                                           9
```

-continued

```
SEQ ID NO: 358          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 358
KEIDRLNEV                                                           9

SEQ ID NO: 359          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 359
LEPLVDLPI                                                           9

SEQ ID NO: 360          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 360
LPPAYTNSF                                                           9

SEQ ID NO: 361          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 361
NGVEGFNCY                                                           9

SEQ ID NO: 362          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 362
NQKLIANQF                                                           9

SEQ ID NO: 363          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 363
RISNCVADY                                                           9

SEQ ID NO: 364          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 364
RLFRKSNLK                                                           9

SEQ ID NO: 365          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 365
TLDSKTQSL                                                           9

SEQ ID NO: 366          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 366
TPINLVRDL                                                           9

SEQ ID NO: 367          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 367
YFPLQSYGF                                                           9

SEQ ID NO: 368          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 368
FQPTNGVGY                                                           9

SEQ ID NO: 369          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 369
RFDNPVLPF                                                           9

SEQ ID NO: 370          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 370
TSNQVAVLY                                                           9

SEQ ID NO: 371          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 371
GLTVLPPLL                                                           9

SEQ ID NO: 372          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 372
SIIAYTMSL                                                           9

SEQ ID NO: 373          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 373
YLQPRTFLL                                                           9

SEQ ID NO: 374          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 374
EPVLKGVKL                                                           9

SEQ ID NO: 375          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 375
LTDEMIAQY                                                           9

SEQ ID NO: 376          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 376
QYIKWPWYI                                                           9
```

-continued

```
SEQ ID NO: 377          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 377
VLKGVKLHY                                                           9

SEQ ID NO: 378          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 378
VTYVPAQEK                                                           9

SEQ ID NO: 379          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 379
KCYGVSPTK                                                           9

SEQ ID NO: 380          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 380
SPRRARSVA                                                           9

SEQ ID NO: 381          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 381
YEQYIKWPW                                                           9

SEQ ID NO: 382          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 382
AEIRASANL                                                           9

SEQ ID NO: 383          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 383
GVYFASTEK                                                           9

SEQ ID NO: 384          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 384
GVYYHKNNK                                                           9

SEQ ID NO: 385          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 385
MIAQYTSAL                                                           9

SEQ ID NO: 386          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 386
NSASFSTFK                                                           9

SEQ ID NO: 387      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 387
NYNYLYRLF                                                           9

SEQ ID NO: 388      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 388
ADAGFIKQY                                                           9

SEQ ID NO: 389      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 389
ALDPLSETK                                                           9

SEQ ID NO: 390      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 390
AYSNNSIAI                                                           9

SEQ ID NO: 391      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 391
DAVRDPQTL                                                           9

SEQ ID NO: 392      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 392
EILPVSMTK                                                           9

SEQ ID NO: 393      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 393
ETKCTLKSF                                                           9

SEQ ID NO: 394      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 394
EVFAQVKQI                                                           9

SEQ ID NO: 395      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 395
EYVSQPFLM                                                           9
```

-continued

```
SEQ ID NO: 396          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 396
FAMQMAYRF                                                           9

SEQ ID NO: 397          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 397
FASVYAWNR                                                           9

SEQ ID NO: 398          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 398
FERDISTEI                                                           9

SEQ ID NO: 399          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 399
FPQSAPHGV                                                           9

SEQ ID NO: 400          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 400
FTISVTTEI                                                           9

SEQ ID NO: 401          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 401
FVIRGDEVR                                                           9

SEQ ID NO: 402          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 402
FVSNGTHWF                                                           9

SEQ ID NO: 403          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 403
GAAAYYVGY                                                           9

SEQ ID NO: 404          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 404
GEVFNATRF                                                           9

SEQ ID NO: 405          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 405
HLMSFPQSA                                                           9

SEQ ID NO: 406          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 406
HVSGTNGTK                                                           9

SEQ ID NO: 407          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 407
HWFVTQRNF                                                           9

SEQ ID NO: 408          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 408
IAIPTNFTI                                                           9

SEQ ID NO: 409          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 409
IANQFNSAI                                                           9

SEQ ID NO: 410          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 410
INITRFQTL                                                           9

SEQ ID NO: 411          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 411
IPFAMQMAY                                                           9

SEQ ID NO: 412          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 412
IPTNFTISV                                                           9

SEQ ID NO: 413          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 413
IYQTSNFRV                                                           9

SEQ ID NO: 414          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 414
KIADYNYKL                                                           9
```

-continued

```
SEQ ID NO: 415          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 415
KIYSKHTPI                                                           9

SEQ ID NO: 416          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 416
KSNLKPFER                                                           9

SEQ ID NO: 417          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 417
KVFRSSVLH                                                           9

SEQ ID NO: 418          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 418
LGAENSVAY                                                           9

SEQ ID NO: 419          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 419
LPFNDGVYF                                                           9

SEQ ID NO: 420          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 420
LPLVSSQCV                                                           9

SEQ ID NO: 421          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 421
LPPLLTDEM                                                           9

SEQ ID NO: 422          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 422
NASVVNIQK                                                           9

SEQ ID NO: 423          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 423
NATRFASVY                                                           9

SEQ ID NO: 424          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 424
NSFTRGVYY                                                           9

SEQ ID NO: 425          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 425
NSIAIPTNF                                                           9

SEQ ID NO: 426          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 426
QELGKYEQY                                                           9

SEQ ID NO: 427          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 427
QIAPGQTGK                                                           9

SEQ ID NO: 428          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 428
QLTPTWRVY                                                           9

SEQ ID NO: 429          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 429
QPTESIVRF                                                           9

SEQ ID NO: 430          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 430
QTNSPRRAR                                                           9

SEQ ID NO: 431          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 431
RSVASQSII                                                           9

SEQ ID NO: 432          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 432
RVYSTGSNV                                                           9

SEQ ID NO: 433          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 433
SANNCTFEY                                                           9
```

-continued

```
SEQ ID NO: 434          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 434
SFKEELDKY                                                           9

SEQ ID NO: 435          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 435
SVYAWNRKR                                                           9

SEQ ID NO: 436          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 436
TLADAGFIK                                                           9

SEQ ID NO: 437          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 437
VASQSIIAY                                                           9

SEQ ID NO: 438          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 438
VFAQVKQIY                                                           9

SEQ ID NO: 439          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 439
VFKNIDGYF                                                           9

SEQ ID NO: 440          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 440
VGGNYNYLY                                                           9

SEQ ID NO: 441          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 441
WFVTQRNFY                                                           9

SEQ ID NO: 442          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 442
WTAGAAAYY                                                           9

SEQ ID NO: 443          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 443
WTFGAGAAL                                                          9

SEQ ID NO: 444          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 444
YGFQPTNGV                                                          9

SEQ ID NO: 445          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 445
YNYLYRLFR                                                          9

SEQ ID NO: 446          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 446
YQDVNCTEV                                                          9

SEQ ID NO: 447          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 447
YYHKNNKSW                                                          9

SEQ ID NO: 448          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 448
TQDLFLPFF                                                          9

SEQ ID NO: 449          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 449
FVFLVLLPL                                                          9

SEQ ID NO: 450          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 450
LVKNKCVNF                                                          9

SEQ ID NO: 451          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 451
STQDLFLPF                                                          9

SEQ ID NO: 452          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 452
NIADYNYKL                                                          9
```

-continued

```
SEQ ID NO: 453          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 453
NYNYRYRLF                                                           9

SEQ ID NO: 454          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 454
TIADYNYKL                                                           9

SEQ ID NO: 455          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human adenovirus 5
SEQUENCE: 455
LLYANSAHAL                                                          10

SEQ ID NO: 456          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 456
SSGVVFGTWY                                                          10

SEQ ID NO: 457          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 457
EYVHARWAAF                                                          10

SEQ ID NO: 458          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 458
HTDLHPNNTY                                                          10

SEQ ID NO: 459          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 459
AYLGAFLSVL                                                          10

SEQ ID NO: 460          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 460
FVYTPSPYVF                                                          10

SEQ ID NO: 461          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 461
AYSLLFPAPF                                                          10

SEQ ID NO: 462          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 462
RPTERPRAPA                                                          10

SEQ ID NO: 463          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 463
FTDALGIDEY                                                          10

SEQ ID NO: 464          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 464
SALPTNADLY                                                          10

SEQ ID NO: 465          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 1
SEQUENCE: 465
LYPDAPPLRL                                                          10

SEQ ID NO: 466          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 466
GFLIAYQPLL                                                          10

SEQ ID NO: 467          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 2
SEQUENCE: 467
FLVDAIVRVA                                                          10

SEQ ID NO: 468          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 468
PHSVVNPFVK                                                          10

SEQ ID NO: 469          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 469
MILIEGIFFV                                                          10

SEQ ID NO: 470          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 470
TPRVTGGGAM                                                          10

SEQ ID NO: 471          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 471
AYAQKIFKIL                                                          10
```

-continued

```
SEQ ID NO: 472          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 472
YILEETSVML                                                          10

SEQ ID NO: 473          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 473
RRKMMYMCYR                                                          10

SEQ ID NO: 474          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 474
TYSQKIFKIL                                                          10

SEQ ID NO: 475          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 475
RPPIFIRRLH                                                          10

SEQ ID NO: 476          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 476
VEITPYKPTW                                                          10

SEQ ID NO: 477          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 477
EENLLDFVRF                                                          10

SEQ ID NO: 478          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 478
LLDFVRFMGV                                                          10

SEQ ID NO: 479          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 479
PYLFWLAAIA                                                          10

SEQ ID NO: 480          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 480
VMSNTLLSAW                                                          10

SEQ ID NO: 481          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 481
QNGALAINTF                                                          10

SEQ ID NO: 482          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 482
DTPLIPLTIF                                                          10

SEQ ID NO: 483          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human gammaherpesvirus 8
SEQUENCE: 483
ATVKTGNIKL                                                          10

SEQ ID NO: 484          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human herpesvirus 2
SEQUENCE: 484
AERQGSPTPA                                                          10

SEQ ID NO: 485          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 485
KPQGQRLIEV                                                          10

SEQ ID NO: 486          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 486
QTDTYTLLGY                                                          10

SEQ ID NO: 487          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 487
ILIEGIFFVS                                                          10

SEQ ID NO: 488          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 488
HVFPHRFISF                                                          10

SEQ ID NO: 489          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 489
RIRLVVPSAL                                                          10

SEQ ID NO: 490          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 490
SLILIGITTL                                                          10
```

-continued

```
SEQ ID NO: 491          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 491
KVEGEQHVIK                                                          10

SEQ ID NO: 492          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 492
IAPYAGLIMI                                                          10

SEQ ID NO: 493          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human metapneumovirus
SEQUENCE: 493
KPAVGVYHIV                                                          10

SEQ ID NO: 494          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human orthopneumovirus
SEQUENCE: 494
FSECNALGSY                                                          10

SEQ ID NO: 495          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human orthopneumovirus
SEQUENCE: 495
STELNYNHLY                                                          10

SEQ ID NO: 496          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human orthopneumovirus
SEQUENCE: 496
FLTEAIVHSV                                                          10

SEQ ID NO: 497          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 31
SEQUENCE: 497
YVLDLQPEAT                                                          10

SEQ ID NO: 498          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 35
SEQUENCE: 498
FACYDLCIVY                                                          10

SEQ ID NO: 499          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 39
SEQUENCE: 499
FAFSDLYVVY                                                          10

SEQ ID NO: 500          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = human papillomavirus 45
SEQUENCE: 500
FAFKDLCIVY                                                          10

SEQ ID NO: 501          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 51
SEQUENCE: 501
VAFTEIKIVY                                                          10

SEQ ID NO: 502          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 52
SEQUENCE: 502
YILDLQPETT                                                          10

SEQ ID NO: 503          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 58
SEQUENCE: 503
FVFADLRIVY                                                          10

SEQ ID NO: 504          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = human papillomavirus 73
SEQUENCE: 504
FAFSDLCIVY                                                          10

SEQ ID NO: 505          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 505
ILTAFNSSHK                                                          10

SEQ ID NO: 506          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 506
LTAPTGCIKK                                                          10

SEQ ID NO: 507          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 507
TLKCLRYRFK                                                          10

SEQ ID NO: 508          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 508
YYVHEGIRTY                                                          10

SEQ ID NO: 509          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 509
YICEEASVTV                                                          10
```

-continued

```
SEQ ID NO: 510          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 510
LLIRCINCQK                                                          10

SEQ ID NO: 511          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 511
AVCDKCLKFY                                                          10

SEQ ID NO: 512          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 512
CVYCKQQLLR                                                          10

SEQ ID NO: 513          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 513
NPYAVCDKCL                                                          10

SEQ ID NO: 514          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 514
RPRKLPQLCT                                                          10

SEQ ID NO: 515          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 515
YAVCDKCLKF                                                          10

SEQ ID NO: 516          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 516
QYNKPLCDLL                                                          10

SEQ ID NO: 517          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 517
GIVCPICSQK                                                          10

SEQ ID NO: 518          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 518
HGDTPTLHEY                                                          10

SEQ ID NO: 519          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 519
HYNIVTFCCK                                                          10

SEQ ID NO: 520          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 520
YMLDLQPETT                                                          10

SEQ ID NO: 521          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 521
TIHDIILECV                                                          10

SEQ ID NO: 522          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 522
HNIRGRWTGR                                                          10

SEQ ID NO: 523          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 523
FAFRDLCIVY                                                          10

SEQ ID NO: 524          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 524
QERPRKLPQL                                                          10

SEQ ID NO: 525          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 525
RWTGRCMSCC                                                          10

SEQ ID NO: 526          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 526
SSRTRRETQL                                                          10

SEQ ID NO: 527          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 527
HPAATHTKAV                                                          10

SEQ ID NO: 528          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 528
TLLQQYCLYL                                                          10
```

-continued

```
SEQ ID NO: 529          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 529
GLCPHCINVG                                                          10

SEQ ID NO: 530          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 530
HAKALKERMV                                                          10

SEQ ID NO: 531          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 531
IDTCISATFR                                                          10

SEQ ID NO: 532          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 532
LLHTDFEQVM                                                          10

SEQ ID NO: 533          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 533
QSALKLAIYK                                                          10

SEQ ID NO: 534          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 534
SALKLAIYKA                                                          10

SEQ ID NO: 535          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 535
KLYQNPTTYI                                                          10

SEQ ID NO: 536          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 536
RLYQNPTTYI                                                          10

SEQ ID NO: 537          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 537
KFLPDLYDYK                                                          10

SEQ ID NO: 538          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 538
VLRGFLILGK                                                          10

SEQ ID NO: 539          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 539
GILGFVFTLT                                                          10

SEQ ID NO: 540          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 540
RMVLASTTAK                                                          10

SEQ ID NO: 541          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 541
SFSFGGFTFK                                                          10

SEQ ID NO: 542          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 542
KNIDGYFKIY                                                          10

SEQ ID NO: 543          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 543
CMTSCCSCLK                                                          10

SEQ ID NO: 544          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 544
DSFKEELDKY                                                          10

SEQ ID NO: 545          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 545
QPYRVVVLSF                                                          10

SEQ ID NO: 546          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 546
SEPVLKGVKL                                                          10

SEQ ID NO: 547          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 547
CALDPLSETK                                                          10
```

-continued

```
SEQ ID NO: 548          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 548
EILDITPCSF                                                          10

SEQ ID NO: 549          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 549
FTISVTTEIL                                                          10

SEQ ID NO: 550          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 550
IGAEHVNNSY                                                          10

SEQ ID NO: 551          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 551
ILPDPSKPSK                                                          10

SEQ ID NO: 552          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 552
IYSKHTPINL                                                          10

SEQ ID NO: 553          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 553
KLPDDFTGCV                                                          10

SEQ ID NO: 554          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 554
KTSVDCTMYI                                                          10

SEQ ID NO: 555          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 555
LSSTASALGK                                                          10

SEQ ID NO: 556          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 556
STQDLFLPFF                                                          10

SEQ ID NO: 557          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 557
SVLNDILSRL                                                          10

SEQ ID NO: 558      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 558
TEKSNIIRGW                                                          10

SEQ ID NO: 559      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 559
WIFGTTLDSK                                                          10

SEQ ID NO: 560      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 560
YHLMSFPQSA                                                          10

SEQ ID NO: 561      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 561
TQLNRALTGI                                                          10

SEQ ID NO: 562      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 562
NESLIDLQEL                                                          10

SEQ ID NO: 563      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 563
DGVYFASTEK                                                          10

SEQ ID NO: 564      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 564
DSKVGGNYNY                                                          10

SEQ ID NO: 565      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 565
EVFAQVKQIY                                                          10

SEQ ID NO: 566      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 566
FDEDDSEPVL                                                          10
```

-continued

```
SEQ ID NO: 567          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 567
FERDISTEIY                                                          10

SEQ ID NO: 568          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 568
FEYVSQPFLM                                                          10

SEQ ID NO: 569          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 569
FLPFFSNVTW                                                          10

SEQ ID NO: 570          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 570
GVFVSNGTHW                                                          10

SEQ ID NO: 571          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 571
GVYYPDKVFR                                                          10

SEQ ID NO: 572          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 572
GYLQPRTFLL                                                          10

SEQ ID NO: 573          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 573
HVTYVPAQEK                                                          10

SEQ ID NO: 574          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 574
IHADQLTPTW                                                          10

SEQ ID NO: 575          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 575
KFLPFQQFGR                                                          10

SEQ ID NO: 576          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 576
KVGGNYNYLY                                                          10

SEQ ID NO: 577          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 577
LPIGINITRF                                                          10

SEQ ID NO: 578          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 578
NTSNQVAVLY                                                          10

SEQ ID NO: 579          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 579
NVYADSFVIR                                                          10

SEQ ID NO: 580          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 580
QIPFAMQMAY                                                          10

SEQ ID NO: 581          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 581
QYIKWPWYIW                                                          10

SEQ ID NO: 582          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 582
RASANLAATK                                                          10

SEQ ID NO: 583          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 583
RFASVYAWNR                                                          10

SEQ ID NO: 584          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 584
RVYSTGSNVF                                                          10

SEQ ID NO: 585          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 585
SETKCTLKSF                                                          10
```

-continued

```
SEQ ID NO: 586          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 586
STGSNVFQTR                                                          10

SEQ ID NO: 587          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 587
SVASQSIIAY                                                          10

SEQ ID NO: 588          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 588
SWMESEFRVY                                                          10

SEQ ID NO: 589          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 589
TECSNLLLQY                                                          10

SEQ ID NO: 590          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 590
TPCSFGGVSV                                                          10

SEQ ID NO: 591          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 591
VFVSNGTHWF                                                          10

SEQ ID NO: 592          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 592
VYSSANNCTF                                                          10

SEQ ID NO: 593          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 593
YTNSFTRGVY                                                          10

SEQ ID NO: 594          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 594
IYKTPPIKDF                                                          10

SEQ ID NO: 595          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 595
LLTDEMIAQY                                                          10

SEQ ID NO: 596          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 596
SYFIASFRLF                                                          10

SEQ ID NO: 597          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 597
EITDTIDKFG K                                                        11

SEQ ID NO: 598          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 598
LPEGMDPFAE K                                                        11

SEQ ID NO: 599          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human alphaherpesvirus 3
SEQUENCE: 599
ARLCDLPATP K                                                        11

SEQ ID NO: 600          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 600
LQRGPQYSEH P                                                        11

SEQ ID NO: 601          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 601
PSQEPMSIYV Y                                                        11

SEQ ID NO: 602          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 602
QEFFWDANDI Y                                                        11

SEQ ID NO: 603          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 603
QYDPVAALFF F                                                        11

SEQ ID NO: 604          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 604
RLTVSGLAWT R                                                        11
```

-continued

```
SEQ ID NO: 605          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 605
RNLVPMVATV Q                                                        11

SEQ ID NO: 606          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 606
TPRVTGGGAM A                                                        11

SEQ ID NO: 607          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 607
VFPTKDVALR H                                                        11

SEQ ID NO: 608          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 608
VLCPKNMIIK P                                                        11

SEQ ID NO: 609          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 609
YSEHPTFTSQ Y                                                        11

SEQ ID NO: 610          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 610
YYTSAFVFPT K                                                        11

SEQ ID NO: 611          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 611
QYTPDSTPCH R                                                        11

SEQ ID NO: 612          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 612
RPHERNGFTV L                                                        11

SEQ ID NO: 613          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 613
AKARAKKDEL R                                                        11

SEQ ID NO: 614          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
```

-continued

```
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 614
CYVLEETSVM L                                                        11

SEQ ID NO: 615          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 615
EFCRVLCCYV L                                                        11

SEQ ID NO: 616          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 616
EQVTEDCNEN P                                                        11

SEQ ID NO: 617          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 617
ESLKTFEQVT E                                                        11

SEQ ID NO: 618          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 618
FPKTTNGCSQ A                                                        11

SEQ ID NO: 619          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 619
GKSTHPMVTR S                                                        11

SEQ ID NO: 620          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 620
KDELRRKMMY M                                                        11

SEQ ID NO: 621          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 621
KNSAFPKTTN G                                                        11

SEQ ID NO: 622          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 622
KQIKVRVDMV R                                                        11

SEQ ID NO: 623          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 623
MAYAQKIFKI L                                                        11
```

-continued

```
SEQ ID NO: 624          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 624
NIEFFTKNSA F                                                        11

SEQ ID NO: 625          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 625
SVMKRRIEEI C                                                        11

SEQ ID NO: 626          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 626
YPRNPTEQGN I                                                        11

SEQ ID NO: 627          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 627
HPVGEADYFE Y                                                        11

SEQ ID NO: 628          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 628
QPRAPIRPIP T                                                        11

SEQ ID NO: 629          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 629
SSCSSCPLSK I                                                        11

SEQ ID NO: 630          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human gammaherpesvirus 4
SEQUENCE: 630
EPLPQGQLTA Y                                                        11

SEQ ID NO: 631          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human herpesvirus 3
SEQUENCE: 631
AVYENPLSVE K                                                        11

SEQ ID NO: 632          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Human parvovirus B19
SEQUENCE: 632
TEADVQQWLT W                                                        11

SEQ ID NO: 633          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
```

-continued

```
                    mol_type = protein
                    organism = Human polyomavirus 1
SEQUENCE: 633
FFAVGGDPLE M                                                    11

SEQ ID NO: 634      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Human respiratory syncytial virus A2
SEQUENCE: 634
IAVGLLLYCK A                                                    11

SEQ ID NO: 635      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Influenza A virus
SEQUENCE: 635
TIAMELIRMI K                                                    11

SEQ ID NO: 636      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 636
EILDITPCSF G                                                    11

SEQ ID NO: 637      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 637
AQALNTLVKQ L                                                    11

SEQ ID NO: 638      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 638
FCNDPFLGVY Y                                                    11

SEQ ID NO: 639      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 639
FPQSAPHGVV F                                                    11

SEQ ID NO: 640      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 640
KSWMESEFRV Y                                                    11

SEQ ID NO: 641      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 641
LQIPFAMQMA Y                                                    11

SEQ ID NO: 642      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 642
NYNYLYRLFR K                                                    11
```

-continued

```
SEQ ID NO: 643          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 643
YEQYIKWPWY I                                                        11

SEQ ID NO: 644          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 644
IPIGAGICAS Y                                                        11

SEQ ID NO: 645          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 645
KPFERDISTE I                                                        11

SEQ ID NO: 646          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 646
QEVFAQVKQI Y                                                        11

SEQ ID NO: 647          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 647
RFPNITNLCP F                                                        11

SEQ ID NO: 648          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 648
YECDIPIGAG I                                                        11

SEQ ID NO: 649          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 649
YENQKLIANQ F                                                        11

SEQ ID NO: 650          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 650
YYVGYLQPRT F                                                        11

SEQ ID NO: 651          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 651
SFELLHAPAT V                                                        11

SEQ ID NO: 652          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 652
TYVPAQEKNF T                                                        11

SEQ ID NO: 653          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Epstein Barr Virus
SEQUENCE: 653
HPVGDADYFE Y                                                        11

SEQ ID NO: 654          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Epstein Barr Virus
SEQUENCE: 654
HPVGQADYFE Y                                                        11

SEQ ID NO: 655          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 655
RVAGDSGFAA Y                                                        11

SEQ ID NO: 656          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 656
EFFWDANDIY                                                          10

SEQ ID NO: 657          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 657
RPHERNGFTV                                                          10

SEQ ID NO: 658          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 658
LPRRSGAAGA                                                          10

SEQ ID NO: 659          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 659
ALQIPFAMQM                                                          10

SEQ ID NO: 660          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 660
QELIRQGTDY                                                          10

SEQ ID NO: 661          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 661
RARSVASQSI                                                          10
```

-continued

```
SEQ ID NO: 662          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 662
RLITGRLQSL                                                          10

SEQ ID NO: 663          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 663
TLATHGLAAV                                                          10

SEQ ID NO: 664          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 664
TTDPSFLGRY                                                          10

SEQ ID NO: 665          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 665
VENPHLMGWD                                                          10

SEQ ID NO: 666          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 666
YPDKVFRSSV                                                          10

SEQ ID NO: 667          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 667
AYAQKIFKI                                                           9

SEQ ID NO: 668          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 668
CRVLCCYVL                                                           9

SEQ ID NO: 669          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 669
CVETMCNEY                                                           9

SEQ ID NO: 670          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 670
DEEDAIAAY                                                           9

SEQ ID NO: 671          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 671
FRCPRRFCF                                                          9

SEQ ID NO: 672          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 672
KLGGALQAK                                                          9

SEQ ID NO: 673          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 673
MLNIPSINV                                                          9

SEQ ID NO: 674          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 674
VMAPRTLIL                                                          9

SEQ ID NO: 675          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 675
YILEETSVM                                                          9

SEQ ID NO: 676          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human papillomavirus type 16
SEQUENCE: 676
MLDLQPETT                                                          9

SEQ ID NO: 677          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 677
CTELKLSDY                                                          9

SEQ ID NO: 678          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Influenza A virus
SEQUENCE: 678
FEDLRVLSF                                                          9

SEQ ID NO: 679          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 679
ALSKGVHFV                                                          9

SEQ ID NO: 680          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 680
ALWEIQQVV                                                          9
```

-continued

```
SEQ ID NO: 681          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 681
DTDFVNEFY                                                           9

SEQ ID NO: 682          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 682
FIAGLIAIV                                                           9

SEQ ID NO: 683          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 683
FTSDYYQLY                                                           9

SEQ ID NO: 684          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 684
KQIYKTPPI                                                           9

SEQ ID NO: 685          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 685
KTFPPTEPK                                                           9

SEQ ID NO: 686          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 686
LLLDRLNQL                                                           9

SEQ ID NO: 687          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 687
LLYDANYFL                                                           9

SEQ ID NO: 688          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 688
MLAKALRKV                                                           9

SEQ ID NO: 689          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 689
MQLFFSYFA                                                           9

SEQ ID NO: 690          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 690
PTDNYITTY                                                           9

SEQ ID NO: 691          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 691
SPRWYFYYL                                                           9

SEQ ID NO: 692          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 692
VYFLQSINF                                                           9

SEQ ID NO: 693          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Severe acute respiratory syndrome coronavirus 2
SEQUENCE: 693
VYIGDPAQL                                                           9

SEQ ID NO: 694          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 694
FPTKDVAL                                                            8

SEQ ID NO: 695          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 695
NEGVKAAW                                                            8

SEQ ID NO: 696          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 696
DYNFVKQLF                                                           9

SEQ ID NO: 697          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 697
TYPVLEEMF                                                           9

SEQ ID NO: 698          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 698
RYSIFFDYM                                                           9

SEQ ID NO: 699          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 699
TYSAGIVQI                                                           9
```

-continued

```
SEQ ID NO: 700          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 700
VYALPLKML                                                           9

SEQ ID NO: 701          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Human betaherpesvirus 5
SEQUENCE: 701
GPISGHVLK                                                           9

SEQ ID NO: 702          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 702
SQKTYQGSY                                                           9

SEQ ID NO: 703          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 703
KEFTVSGNIL TI                                                       12

SEQ ID NO: 704          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 704
MVKISGGPR                                                           9

SEQ ID NO: 705          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 705
AEEAAGIGIL T                                                        11

SEQ ID NO: 706          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 706
DPARYEFLW                                                           9

SEQ ID NO: 707          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 707
DPARYEFLW                                                           9

SEQ ID NO: 708          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 708
REPVTKAEML                                                          10

SEQ ID NO: 709          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 709
REPVTKAEML                                                          10

SEQ ID NO: 710          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 710
REPVTKAEML                                                          10

SEQ ID NO: 711          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 711
SESLKMIF                                                            8

SEQ ID NO: 712          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 712
REPVTKAEML                                                          10

SEQ ID NO: 713          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 713
CTACRWKKAC QR                                                       12

SEQ ID NO: 714          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 714
CYMEAVAL                                                            8

SEQ ID NO: 715          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 715
LAAQERRVPR                                                          10

SEQ ID NO: 716          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 716
LAAQERRVPR                                                          10

SEQ ID NO: 717          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 717
ASGPGGGAPR                                                          10

SEQ ID NO: 718          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 718
LAAQERRVPR                                                          10
```

-continued

```
SEQ ID NO: 719          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 719
LAAQERRVPR                                                      10

SEQ ID NO: 720          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 720
MSLQRQFLR                                                       9

SEQ ID NO: 721          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 721
LLGPGRPYR                                                       9

SEQ ID NO: 722          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 722
LLGPGRPYR                                                       9

SEQ ID NO: 723          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 723
LLGPGRPYR                                                       9

SEQ ID NO: 724          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 724
SHETVIIEL                                                       9

SEQ ID NO: 725          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 725
LHHAFVDSIF                                                      10

SEQ ID NO: 726          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 726
QQITKTEV                                                        8

SEQ ID NO: 727          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 727
WQYFFPVIF                                                       9

SEQ ID NO: 728          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 728
FATPMEAEL                                                    9

SEQ ID NO: 729          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 729
YYWPRPRRY                                                    9

SEQ ID NO: 730          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 730
QGQHFLQKV                                                    9

SEQ ID NO: 731          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 731
MEVDPIGHLY                                                   10

SEQ ID NO: 732          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 732
AELVHFLLL                                                    9

SEQ ID NO: 733          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 733
SRFGGAVVR                                                    9

SEQ ID NO: 734          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 734
AARAVFLAL                                                    9

SEQ ID NO: 735          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 735
SAYGEPRKL                                                    9

SEQ ID NO: 736          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 736
ISGGPRISY                                                    9

SEQ ID NO: 737          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 737
GADGVGKSA                                                    9
```

-continued

```
SEQ ID NO: 738          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 738
GADGVGKSAL                                                          10

SEQ ID NO: 739          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 739
SNDGPTLI                                                            8

SEQ ID NO: 740          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 740
ANDPIFVVL                                                           9

SEQ ID NO: 741          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 741
QCSGNFMGF                                                           9

SEQ ID NO: 742          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 742
RTKQLYPEW                                                           9

SEQ ID NO: 743          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 743
ETVSEQSNV                                                           9

SEQ ID NO: 744          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 744
EAFIQPITR                                                           9

SEQ ID NO: 745          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 745
ELVRRILSR                                                           9

SEQ ID NO: 746          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 746
EVYDGREHSA                                                          10

SEQ ID NO: 747          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 747
TVSGNILTIR                                                          10

SEQ ID NO: 748          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 748
EVISCKLIKR                                                          10

SEQ ID NO: 749          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 749
HTMEVTVYHR                                                          10

SEQ ID NO: 750          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 750
ITKKVADLVG F                                                        11

SEQ ID NO: 751          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 751
ASSTLYLVF                                                           9

SEQ ID NO: 752          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 752
SAFPTTINF                                                           9

SEQ ID NO: 753          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 753
MPFATPMEA                                                           9

SEQ ID NO: 754          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 754
FATPMEAELA R                                                        11

SEQ ID NO: 755          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 755
CILGKLFTK                                                           9

SEQ ID NO: 756          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 756
AVCPWTWLR                                                           9
```

-continued

```
SEQ ID NO: 757          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 757
KTLTSVFQK                                                          9

SEQ ID NO: 758          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 758
ATFLGSLTWK                                                         10

SEQ ID NO: 759          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 759
ALNFPGSQK                                                          9

SEQ ID NO: 760          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 760
RQKRILVNL                                                          9

SEQ ID NO: 761          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 761
GFKQSSKAL                                                          9

SEQ ID NO: 762          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 762
LSRLSNRLL                                                          9

SEQ ID NO: 763          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 763
LSRLSNRLL                                                          9

SEQ ID NO: 764          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 764
RPHVPESAF                                                          9

SEQ ID NO: 765          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 765
QRPYGYDQIM                                                         10

SEQ ID NO: 766          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 766
APRGVRMAV                                                   9

SEQ ID NO: 767          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 767
APRGVRMAV                                                   9

SEQ ID NO: 768          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 768
RVRFFFPSL                                                   9

SEQ ID NO: 769          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
source                  1..13
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 769
APRGPHGGAA SGL                                              13

SEQ ID NO: 770          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 770
SSPGCQPPA                                                   9

SEQ ID NO: 771          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 771
SPRWWPTCL                                                   9

SEQ ID NO: 772          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 772
SPSSNRIRNT                                                  10

SEQ ID NO: 773          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 773
LPRWPPPQL                                                   9

SEQ ID NO: 774          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 774
SAYGEPRKL                                                   9

SEQ ID NO: 775          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 775
LAMPFATPM                                                   9
```

-continued

```
SEQ ID NO: 776          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 776
FRSGLDSYV                                                          9

SEQ ID NO: 777          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 777
YRPRPRRY                                                           8

SEQ ID NO: 778          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 778
ARGPESRLL                                                          9

SEQ ID NO: 779          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 779
SYLDSGIHF                                                          9

SEQ ID NO: 780          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 780
NYNNFYRFL                                                          9

SEQ ID NO: 781          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 781
EYSKECLKEF                                                         10

SEQ ID NO: 782          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 782
EYLSLSDKI                                                          9

SEQ ID NO: 783          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 783
RYCNLEGPPI                                                         10

SEQ ID NO: 784          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 784
EYLQLVFGI                                                          9

SEQ ID NO: 785          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 785
TFPDLESEF                                                    9

SEQ ID NO: 786          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 786
VAELVHFLL                                                    9

SEQ ID NO: 787          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 787
NYKRCFPVI                                                    9

SEQ ID NO: 788          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 788
NYKRCFPVI                                                    9

SEQ ID NO: 789          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 789
YLAMPFATPM E                                                 11

SEQ ID NO: 790          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 790
LYATVIHDI                                                    9

SEQ ID NO: 791          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 791
TYACFVSNL                                                    9

SEQ ID NO: 792          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 792
QYSWFVNGTF                                                   10

SEQ ID NO: 793          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 793
VYFFLPDHL                                                    9

SEQ ID NO: 794          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 794
LYSACFWWL                                                    9
```

-continued

```
SEQ ID NO: 795          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 795
IYMDGTADFS F                                                    11

SEQ ID NO: 796          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 796
AFLPWHRLF                                                       9

SEQ ID NO: 797          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 797
KFLDALISL                                                       9

SEQ ID NO: 798          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 798
RYQLDPKFI                                                       9

SEQ ID NO: 799          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 799
KYDCFLHPF                                                       9

SEQ ID NO: 800          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 800
KYVGIEREM                                                       9

SEQ ID NO: 801          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 801
EYILSLEEL                                                       9

SEQ ID NO: 802          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 802
TYLPTNASL                                                       9

SEQ ID NO: 803          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 803
NYGIYKQDL                                                       9

SEQ ID NO: 804          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 804
TCQPTCRSL                                                       9

SEQ ID NO: 805          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 805
LYVDSLFFLC                                                      10

SEQ ID NO: 806          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 806
NYARTEDFF                                                       9

SEQ ID NO: 807          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 807
NSQPVWLCL                                                       9

SEQ ID NO: 808          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 808
CMTWNQMNL                                                       9

SEQ ID NO: 809          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 809
FPSDSWCYF                                                       9

SEQ ID NO: 810          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 810
VVVGAVGVG                                                       9

SEQ ID NO: 811          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 811
EADPTGHSY                                                       9

SEQ ID NO: 812          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 812
EVDPIGHLY                                                       9

SEQ ID NO: 813          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 813
EVDPIGHVY                                                       9
```

-continued

```
SEQ ID NO: 814          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 814
MPFATPMEAE L                                                        11

SEQ ID NO: 815          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 815
VPLDCVLYRY                                                          10

SEQ ID NO: 816          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 816
LPHSSSHWL                                                           9

SEQ ID NO: 817          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 817
EAAGIGILTV                                                          10

SEQ ID NO: 818          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 818
LPSSADVEF                                                           9

SEQ ID NO: 819          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 819
TPRLPSSADV EF                                                       12

SEQ ID NO: 820          moltype = AA  length = 14
FEATURE                 Location/Qualifiers
source                  1..14
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 820
LPAVVGLSPG EQEY                                                     14

SEQ ID NO: 821          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 821
AEPINIQTW                                                           9

SEQ ID NO: 822          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 822
EEKLIVVLF                                                           9

SEQ ID NO: 823          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 823
SELFRSGLDS Y                                                    11

SEQ ID NO: 824          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 824
KELEGILLL                                                       9

SEQ ID NO: 825          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 825
KEADPTGHSY                                                      10

SEQ ID NO: 826          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 826
MEVDPIGHLY                                                      10

SEQ ID NO: 827          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 827
SESIKKKVL                                                       9

SEQ ID NO: 828          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 828
SEIWRDIDFD                                                      10

SEQ ID NO: 829          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 829
KILDAVVAQK                                                      10

SEQ ID NO: 830          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 830
TLDWLLQTPK                                                      10

SEQ ID NO: 831          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 831
KINKNPKYK                                                       9

SEQ ID NO: 832          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 832
KIFSEVTLK                                                       9
```

-continued

```
SEQ ID NO: 833          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 833
SLFRAVITK                                                       9

SEQ ID NO: 834          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 834
HLFGYSWYK                                                       9

SEQ ID NO: 835          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 835
LIYRRRLMK                                                       9

SEQ ID NO: 836          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 836
IALNFPGSQK                                                      10

SEQ ID NO: 837          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 837
ALLAVGATK                                                       9

SEQ ID NO: 838          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 838
RSYVPLAHR                                                       9

SEQ ID NO: 839          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 839
ALNFPGSQK                                                       9

SEQ ID NO: 840          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 840
PLLENVISK                                                       9

SEQ ID NO: 841          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 841
NTYASPRFKF                                                      10

SEQ ID NO: 842          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 842
VLRENTSPK                                                    9

SEQ ID NO: 843          moltype = AA  length = 12
FEATURE                 Location/Qualifiers
source                  1..12
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 843
SLFPNSPKWT SK                                                12

SEQ ID NO: 844          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 844
GLASFKSFLK                                                   10

SEQ ID NO: 845          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 845
RAGLQVRKNK                                                   10

SEQ ID NO: 846          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 846
YVDFREYEYY                                                   10

SEQ ID NO: 847          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 847
FLEGNEVGKT Y                                                 11

SEQ ID NO: 848          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 848
ILDTAGREEY                                                   10

SEQ ID NO: 849          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 849
YTDFHCQYV                                                    9

SEQ ID NO: 850          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 850
EADPTGHSY                                                    9

SEQ ID NO: 851          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 851
EVDPIGHLY                                                    9
```

-continued

```
SEQ ID NO: 852          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 852
EVDPASNTY                                                           9

SEQ ID NO: 853          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 853
ILDSSEEDK                                                           9

SEQ ID NO: 854          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 854
KCDICTDEY                                                           9

SEQ ID NO: 855          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 855
SSDYVIPIGT Y                                                        11

SEQ ID NO: 856          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 856
RSDSGQQARY                                                          10

SEQ ID NO: 857          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 857
TSEKRPFMCA Y                                                        11

SEQ ID NO: 858          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 858
RVRFFFPSL                                                           9

SEQ ID NO: 859          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 859
VRIGHLYIL                                                           9

SEQ ID NO: 860          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 860
VRIGHLYIL                                                           9

SEQ ID NO: 861          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 861
EGDCAPEEK                                                       9

SEQ ID NO: 862          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 862
EGDCAPEEK                                                       9

SEQ ID NO: 863          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 863
EGDCAPEEK                                                       9

SEQ ID NO: 864          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 864
EGDCAPEEK                                                       9

SEQ ID NO: 865          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 865
RNGYRALMDK S                                                    11

SEQ ID NO: 866          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 866
FIASNGVKLV                                                      10

SEQ ID NO: 867          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 867
SSKALQRPV                                                       9

SEQ ID NO: 868          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 868
FLIIWQNTM                                                       9

SEQ ID NO: 869          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 869
ACDPHSGHFV                                                      10

SEQ ID NO: 870          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 870
ILDKVLVHL                                                       9
```

-continued

```
SEQ ID NO: 871          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 871
GLFGDIYLA                                                       9

SEQ ID NO: 872          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 872
RIAECILGM                                                       9

SEQ ID NO: 873          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 873
VVMSWAPPV                                                       9

SEQ ID NO: 874          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 874
SLADEAEVYL                                                      10

SEQ ID NO: 875          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 875
ILNAMIAKI                                                       9

SEQ ID NO: 876          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 876
SLFEGIDIYT                                                      10

SEQ ID NO: 877          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 877
FLDEFMEGV                                                       9

SEQ ID NO: 878          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 878
SLYKFSPFPL                                                      10

SEQ ID NO: 879          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 879
VVPCEPPEV                                                       9

SEQ ID NO: 880          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 880
LLLDDLLVSI                                                          10

SEQ ID NO: 881          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 881
RLSSCVPVA                                                           9

SEQ ID NO: 882          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 882
VVPCEPPEV                                                           9

SEQ ID NO: 883          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 883
YLCSGSSYFV                                                          10

SEQ ID NO: 884          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 884
SLIAAAAFCL A                                                        11

SEQ ID NO: 885          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 885
FLDRFLSCM                                                           9

SEQ ID NO: 886          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 886
VLPDVFIRCV                                                          10

SEQ ID NO: 887          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 887
MLAVISCAV                                                           9

SEQ ID NO: 888          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 888
MLMAQEALAF L                                                        11

SEQ ID NO: 889          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 889
MLMAQEALAF L                                                        11
```

-continued

```
SEQ ID NO: 890          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 890
SLLMWITQC                                                       9

SEQ ID NO: 891          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 891
FLGPWAAS                                                        8

SEQ ID NO: 892          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 892
KVLEYVIKV                                                       9

SEQ ID NO: 893          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 893
KVLEYVIKV                                                       9

SEQ ID NO: 894          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 894
GLYDGMEHL                                                       9

SEQ ID NO: 895          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 895
FLWGPRALV                                                       9

SEQ ID NO: 896          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 896
YLQLVFGIEV                                                      10

SEQ ID NO: 897          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 897
KVAELVHFL                                                       9

SEQ ID NO: 898          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 898
FLWGPRALV                                                       9

SEQ ID NO: 899          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 899
GVYDGREHTV                                                          10

SEQ ID NO: 900      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 900
ALSVMGVYV                                                           9

SEQ ID NO: 901      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 901
ILFGISLREV                                                          10

SEQ ID NO: 902      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 902
KVVEFLAML                                                           9

SEQ ID NO: 903      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 903
ALKDVEERV                                                           9

SEQ ID NO: 904      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 904
LLFGLALIEV                                                          10

SEQ ID NO: 905      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 905
SLLMWITQC                                                           9

SEQ ID NO: 906      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 906
SLLMWITQC                                                           9

SEQ ID NO: 907      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 907
SLLMWITQC                                                           9

SEQ ID NO: 908      moltype = AA  length = 11
FEATURE             Location/Qualifiers
source              1..11
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 908
MLMAQEALAF L                                                        11
```

-continued

```
SEQ ID NO: 909          moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 909
MLMAQEALAF L                                                    11

SEQ ID NO: 910          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 910
KASEKIFYV                                                       9

SEQ ID NO: 911          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 911
SLGWLFLLL                                                       9

SEQ ID NO: 912          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 912
RQKKIRIQL                                                       9

SEQ ID NO: 913          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 913
YLSGANLNL                                                       9

SEQ ID NO: 914          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 914
GVLVGVALI                                                       9

SEQ ID NO: 915          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 915
IMIGVLVGV                                                       9

SEQ ID NO: 916          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 916
KTWGQYWQV                                                       9

SEQ ID NO: 917          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 917
AMLGTHTMEV                                                      10

SEQ ID NO: 918          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 918
KTWGQYWQV                                                       9

SEQ ID NO: 919          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 919
ITDQVPFSV                                                       9

SEQ ID NO: 920          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 920
YLEPGPVTA                                                       9

SEQ ID NO: 921          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 921
VLYRYGSFSV                                                      10

SEQ ID NO: 922          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 922
LLDGTATLRL                                                      10

SEQ ID NO: 923          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 923
RLMKQDFSV                                                       9

SEQ ID NO: 924          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 924
SLADTNSLAV                                                      10

SEQ ID NO: 925          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 925
RLPRIFCSC                                                       9

SEQ ID NO: 926          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 926
ILTVILGVL                                                       9

SEQ ID NO: 927          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 927
EAAGIGILTV                                                      10
```

-continued

```
SEQ ID NO: 928          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 928
SLSKILDTV                                                          9

SEQ ID NO: 929          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 929
TLMSAMTNL                                                          9

SEQ ID NO: 930          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 930
ALDVYNGLL                                                          9

SEQ ID NO: 931          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 931
FLFLLFFWL                                                          9

SEQ ID NO: 932          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 932
FLTPKKLQCV                                                         10

SEQ ID NO: 933          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 933
VISNDVCAQV                                                         10

SEQ ID NO: 934          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 934
VLHWDPETV                                                          9

SEQ ID NO: 935          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 935
SVYDFFVWL                                                          9

SEQ ID NO: 936          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 936
TLDSQVMSL                                                          9

SEQ ID NO: 937          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 937
MLLAVLYCL                                                    9

SEQ ID NO: 938      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 938
CLLWSFQTSA                                                   10

SEQ ID NO: 939      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 939
YMDGTMSQV                                                    9

SEQ ID NO: 940      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 940
YMDGTMSQV                                                    9

SEQ ID NO: 941      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 941
SVASTITGV                                                    9

SEQ ID NO: 942      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 942
LLYKLADLI                                                    9

SEQ ID NO: 943      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 943
GVALQTMKQ                                                    9

SEQ ID NO: 944      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 944
FMNKFIYEI                                                    9

SEQ ID NO: 945      moltype = AA  length = 10
FEATURE             Location/Qualifiers
source              1..10
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 945
YLNDHLEPWI                                                   10

SEQ ID NO: 946      moltype = AA  length = 9
FEATURE             Location/Qualifiers
source              1..9
                    mol_type = protein
                    organism = Homo sapiens
SEQUENCE: 946
CQWGRLWQL                                                    9
```

-continued

```
SEQ ID NO: 947          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 947
VLLQAGSLHA                                                      10

SEQ ID NO: 948          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 948
FLALSILVL                                                       9

SEQ ID NO: 949          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 949
LLAALVQDYL                                                      10

SEQ ID NO: 950          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 950
CMLGTYTQDF                                                      10

SEQ ID NO: 951          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 951
LLNAFTVTV                                                       9

SEQ ID NO: 952          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 952
LMLQNALTTM                                                      10

SEQ ID NO: 953          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 953
KVHPVIWSL                                                       9

SEQ ID NO: 954          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 954
LLGATCMFV                                                       9

SEQ ID NO: 955          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 955
ALGGHPLLGV                                                      10

SEQ ID NO: 956          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 956
ALGGHPLLGV                                                          10

SEQ ID NO: 957          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 957
TMNGSKSPV                                                           9

SEQ ID NO: 958          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 958
FMVEDETVL                                                           9

SEQ ID NO: 959          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 959
FINDEIFVEL                                                          10

SEQ ID NO: 960          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 960
HLSTAFARV                                                           9

SEQ ID NO: 961          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 961
FVGEFFTDV                                                           9

SEQ ID NO: 962          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 962
TIHDSIQYV                                                           9

SEQ ID NO: 963          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 963
RLAPFVYLL                                                           9

SEQ ID NO: 964          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 964
SLLSGDWVL                                                           9

SEQ ID NO: 965          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 965
GLQLGVQAV                                                           9
```

-continued

```
SEQ ID NO: 966          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 966
PLTEYIQPV                                                       9

SEQ ID NO: 967          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 967
KIFGSLAFL                                                       9

SEQ ID NO: 968          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 968
IISAVVGIL                                                       9

SEQ ID NO: 969          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 969
ALCRWGLLL                                                       9

SEQ ID NO: 970          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 970
ILHNGAYSL                                                       9

SEQ ID NO: 971          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 971
VVLGVVFGI                                                       9

SEQ ID NO: 972          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 972
YMIMVKCWMI                                                      10

SEQ ID NO: 973          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 973
YLVPQQGFFC                                                      10

SEQ ID NO: 974          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 974
RLLQETELV                                                       9

SEQ ID NO: 975          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 975
HLYQGCQVV                                                           9

SEQ ID NO: 976          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 976
PLQPEQLQV                                                           9

SEQ ID NO: 977          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 977
ALIHHNTHL                                                           9

SEQ ID NO: 978          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 978
TLEEITGYL                                                           9

SEQ ID NO: 979          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 979
PLTSIISAV                                                           9

SEQ ID NO: 980          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 980
FLLGLIFLL                                                           9

SEQ ID NO: 981          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 981
RLMNDMTAV                                                           9

SEQ ID NO: 982          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 982
ALLEIASCL                                                           9

SEQ ID NO: 983          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 983
NLSSAEVVV                                                           9

SEQ ID NO: 984          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 984
WLPFGFILI                                                           9
```

-continued

```
SEQ ID NO: 985          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 985
FLGYLILGV                                                          9

SEQ ID NO: 986          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 986
AQPDTAPLPV                                                         10

SEQ ID NO: 987          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 987
LLSDDDVVV                                                          9

SEQ ID NO: 988          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 988
CIAEQYHTV                                                          9

SEQ ID NO: 989          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 989
FLPEFGISSA                                                         10

SEQ ID NO: 990          moltype = AA  length = 8
FEATURE                 Location/Qualifiers
source                  1..8
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 990
VLFYLGQY                                                           8

SEQ ID NO: 991          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 991
TLNDECWPA                                                          9

SEQ ID NO: 992          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 992
ALLALTSAV                                                          9

SEQ ID NO: 993          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 993
AQCQETIRV                                                          9

SEQ ID NO: 994          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 994
GLPPDVQRVH                                                          10

SEQ ID NO: 995          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 995
STAPPVHNV                                                           9

SEQ ID NO: 996          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 996
LLLLTVLTV                                                           9

SEQ ID NO: 997          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 997
VLVPPLPSL                                                           9

SEQ ID NO: 998          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 998
RMPEAAPPV                                                           9

SEQ ID NO: 999          moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 999
LLGRNSFEV                                                           9

SEQ ID NO: 1000         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1000
TLPGYPPHV                                                           9

SEQ ID NO: 1001         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1001
VLCSIDWFM                                                           9

SEQ ID NO: 1002         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1002
VLDGLDVLL                                                           9

SEQ ID NO: 1003         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1003
ALYVDSLFFL                                                          10
```

-continued

```
SEQ ID NO: 1004         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1004
SLYSFPEPEA                                                          10

SEQ ID NO: 1005         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1005
SLLQHLIGL                                                           9

SEQ ID NO: 1006         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1006
LKLSGVVRL                                                           9

SEQ ID NO: 1007         moltype = AA  length = 11
FEATURE                 Location/Qualifiers
source                  1..11
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1007
PLPPARNGGL G                                                        11

SEQ ID NO: 1008         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1008
LAALPHSCL                                                           9

SEQ ID NO: 1009         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1009
ALWPWLLMAT                                                          10

SEQ ID NO: 1010         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1010
KMDAEHPEL                                                           9

SEQ ID NO: 1011         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1011
AWISKPPGV                                                           9

SEQ ID NO: 1012         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1012
SAWISKPPGV                                                          10

SEQ ID NO: 1013         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
```

-continued

```
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1013
MIAVFLPIV                                                           9

SEQ ID NO: 1014         moltype = AA  length = 15
FEATURE                 Location/Qualifiers
source                  1..15
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1014
HQQYFYKIPI LVINK                                                    15

SEQ ID NO: 1015         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1015
ELTLGEFLKL                                                          10

SEQ ID NO: 1016         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1016
ELTLGEFLKL                                                          10

SEQ ID NO: 1017         moltype = AA  length = 10
FEATURE                 Location/Qualifiers
source                  1..10
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1017
ILAKFLHWLE                                                          10

SEQ ID NO: 1018         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1018
RLVDDFLLV                                                           9

SEQ ID NO: 1019         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1019
RLARLALVL                                                           9

SEQ ID NO: 1020         moltype = AA  length = 9
FEATURE                 Location/Qualifiers
source                  1..9
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 1020
RLLVPTQFV                                                           9

SEQ ID NO: 1021         moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1021
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA YKRGYAMDYW GQGTTVTVSS  120

SEQ ID NO: 1022         moltype = AA  length = 113
FEATURE                 Location/Qualifiers
REGION                  1..113
                        note = Synthetic
```

-continued

```
source                  1..113
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1022
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYYYH MYTFGQGTKV EIK        113

SEQ ID NO: 1023         moltype = AA  length = 116
FEATURE                 Location/Qualifiers
REGION                  1..116
                        note = Synthetic
source                  1..116
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1023
EVQLVESGGG LVKPGGSRKL SCAASGFTFS NYGMHWVRQA PEKGLEWVAY ISSGSSTIYY  60
ADTVKGRFTI SRDNAKNTLF LQMTSLRSED TAMYYCARRG LLLDYWGQGT TLTVSS      116

SEQ ID NO: 1024         moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1024
DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSSYSYMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K           111

SEQ ID NO: 1025         moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1025
SIVMTQTPKF LPVSAGDRVT MTCKASQSVG NNVAWYQQKP GQSPKLLIYY ASNRYTGVPD  60
RFTGSGSGTD FTFTISSVQV EDLAVYFCQQ HYSSPWTFGG GTKLEIK                107

SEQ ID NO: 1026         moltype = AA  length = 116
FEATURE                 Location/Qualifiers
REGION                  1..116
                        note = Synthetic
source                  1..116
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1026
QVQLQESGPG LVKSSETLSL TCTVSGGSIS SYFWSWIRQP PGKGLEWIGY IYYSGSTNYN  60
PSLKSRVTIS LHTSKNQFSL KLSSVTAADT AVYYCARHRN WLFDYWGQGT LVTVSS      116

SEQ ID NO: 1027         moltype = AA  length = 110
FEATURE                 Location/Qualifiers
REGION                  1..110
                        note = Synthetic
source                  1..110
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1027
QSALTQPRSV SGSPGQSVTI SCTGTSSDVG GYNYVSWYQQ HPGKAPKVMI YDVSKRPSGV  60
PDRFSGSKSG NTASLTISGL QAEDEADYYC CSYAGSYTYV FGTGTKVTVL             110

SEQ ID NO: 1028         moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1028
EVQLVESGGG LVQPGGSLRL SCAANLVPMV ATVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA YKRGYAMDYW GQGTTVTVSS  120

SEQ ID NO: 1029         moltype = AA  length = 121
FEATURE                 Location/Qualifiers
REGION                  1..121
```

-continued

```
                        note = Synthetic
source                  1..121
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1029
EVQLVESGGG LVQPGGSLRL SCAASNLVPM VATVMHWVRQ APGKGLEWVS AINPYNDGNY  60
YADSVKGRFT ISRDNSRKTL YLQMNSLRAE DTAVYYCARG AYKRGYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1030         moltype = AA  length = 122
FEATURE                 Location/Qualifiers
REGION                  1..122
                        note = Synthetic
source                  1..122
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1030
EVQLVESGGG LVQPGGSLRL SCAASNLVPM VATVVMHWVR QAPGKGLEWV SAINPYNDGN  60
YYADSVKGRF TISRDNSRKT LYLQMNSLRA EDTAVYYCAR GAYKRGYAMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1031         moltype = AA  length = 122
FEATURE                 Location/Qualifiers
REGION                  1..122
                        note = Synthetic
source                  1..122
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1031
EVQLVESGGG LVQPGGSLRL SCAASGNLVP MVATVMHWVR QAPGKGLEWV SAINPYNDGN  60
YYADSVKGRF TISRDNSRKT LYLQMNSLRA EDTAVYYCAR GAYKRGYAMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1032         moltype = AA  length = 123
FEATURE                 Location/Qualifiers
REGION                  1..123
                        note = Synthetic
source                  1..123
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1032
EVQLVESGGG LVQPGGSLRL SCAASGYNLV PMVATVMHWV RQAPGKGLEW VSAINPYNDG  60
NYYADSVKGR FTISRDNSRK TLYLQMNSLR AEDTAVYYCA RGAYKRGYAM DYWGQGTTVT  120
VSS                                                                123

SEQ ID NO: 1033         moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1033
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGN LVPMVATVYW GQGTTVTVSS  120

SEQ ID NO: 1034         moltype = AA  length = 121
FEATURE                 Location/Qualifiers
REGION                  1..121
                        note = Synthetic
source                  1..121
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1034
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARNL VPMVATVMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1035         moltype = AA  length = 122
FEATURE                 Location/Qualifiers
REGION                  1..122
                        note = Synthetic
source                  1..122
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1035
```

-continued

```
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARNL VPMVATVAMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1036        moltype = AA  length = 123
FEATURE                Location/Qualifiers
REGION                 1..123
                       note = Synthetic
source                 1..123
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1036
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGN LVPMVATVAM DYWGQGTTVT  120
VSS                                                                123

SEQ ID NO: 1037        moltype = AA  length = 122
FEATURE                Location/Qualifiers
REGION                 1..122
                       note = Synthetic
source                 1..122
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1037
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGN LVPMVATVMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1038        moltype = AA  length = 124
FEATURE                Location/Qualifiers
REGION                 1..124
                       note = Synthetic
source                 1..124
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1038
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA NLVPMVATVA MDYWGQGTTV  120
TVSS                                                               124

SEQ ID NO: 1039        moltype = AA  length = 123
FEATURE                Location/Qualifiers
REGION                 1..123
                       note = Synthetic
source                 1..123
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1039
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA NLVPMVATVM DYWGQGTTVT  120
VSS                                                                123

SEQ ID NO: 1040        moltype = AA  length = 125
FEATURE                Location/Qualifiers
REGION                 1..125
                       note = Synthetic
source                 1..125
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1040
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA NLVPMVATVY AMDYWGQGTT  120
VTVSS                                                              125

SEQ ID NO: 1041        moltype = AA  length = 115
FEATURE                Location/Qualifiers
REGION                 1..115
                       note = Synthetic
source                 1..115
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1041
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQNLVP MVATVFGQGT KVEIK       115

SEQ ID NO: 1042        moltype = AA  length = 116
```

-continued

```
FEATURE                 Location/Qualifiers
REGION                  1..116
                        note = Synthetic
source                  1..116
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1042
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYNLV PMVATVFGQG TKVEIK      116

SEQ ID NO: 1043         moltype = AA  length = 121
FEATURE                 Location/Qualifiers
REGION                  1..121
                        note = Synthetic
source                  1..121
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1043
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INLVPMVATV  60
YADSVKGRFT ISRDNSRKTL YLQMNSLRAE DTAVYYCARG AYKRGYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1044         moltype = AA  length = 122
FEATURE                 Location/Qualifiers
REGION                  1..122
                        note = Synthetic
source                  1..122
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1044
EVQLVESGGG LVQPGGSLRL SCAASGDSVS SSISSLSWVR QAPGKGLEWV SAINPYNDGN  60
YYADSVKGRF TISRDNSRKT LYLQMNSLRA EDTAVYYCAR GAYKRGYAMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1045         moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1045
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA ILPFNDGVYF  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA YKRGYAMDYW GQGTTVTVSS  120

SEQ ID NO: 1046         moltype = AA  length = 113
FEATURE                 Location/Qualifiers
REGION                  1..113
                        note = Synthetic
source                  1..113
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1046
DLVMTQSPSS LSAFLGERVT LTCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYYYH MYTFGQGTKV EIK        113

SEQ ID NO: 1047         moltype = AA  length = 120
FEATURE                 Location/Qualifiers
REGION                  1..120
                        note = Synthetic
source                  1..120
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1047
EVQLVESGGG LVQPGGSLRL SCLGGLLTMV SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA YKRGYAMDYW GQGTTVTVSS  120

SEQ ID NO: 1048         moltype = AA  length = 121
FEATURE                 Location/Qualifiers
REGION                  1..121
                        note = Synthetic
source                  1..121
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1048
EVQLVESGGG LVQPGGSLRL SCLGGLLTMV TSYVMHWVRQ APGKGLEWVS AINPYNDGNY  60
```

-continued

```
YADSVKGRFT ISRDNSRKTL YLQMNSLRAE DTAVYYCARG AYKRGYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1049        moltype = AA  length = 121
FEATURE                Location/Qualifiers
REGION                 1..121
                       note = Synthetic
source                 1..121
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1049
EVQLVESGGG LVQPGGSLRL SCLGGLLTMV SSYVMHWVRQ APGKGLEWVS AINPYNDGNY  60
YADSVKGRFT ISRDNSRKTL YLQMNSLRAE DTAVYYCARG AYKRGYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1050        moltype = AA  length = 123
FEATURE                Location/Qualifiers
REGION                 1..123
                       note = Synthetic
source                 1..123
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1050
EVQLVESGGG LVQPGGSLRL SCAASGILGF VFTLYVMHWV RQAPGKGLEW VSAINPYNDG  60
NYYADSVKGR FTISRDNSRK TLYLQMNSLR AEDTAVYYCA RGAYKRGYAM DYWGQGTTVT  120
VSS                                                                123

SEQ ID NO: 1051        moltype = AA  length = 120
FEATURE                Location/Qualifiers
REGION                 1..120
                       note = Synthetic
source                 1..120
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1051
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGI LGFVFTLDYW GQGTTVTVSS  120

SEQ ID NO: 1052        moltype = AA  length = 121
FEATURE                Location/Qualifiers
REGION                 1..121
                       note = Synthetic
source                 1..121
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1052
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGI LGFVFTLMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1053        moltype = AA  length = 122
FEATURE                Location/Qualifiers
REGION                 1..122
                       note = Synthetic
source                 1..122
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1053
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGI LGFVFTLAMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1054        moltype = AA  length = 120
FEATURE                Location/Qualifiers
REGION                 1..120
                       note = Synthetic
source                 1..120
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1054
EVQLVESGGG LVQPGGSLRL SCAVFDRKSD AKVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA YKRGYAMDYW GQGTTVTVSS  120

SEQ ID NO: 1055        moltype = AA  length = 121
FEATURE                Location/Qualifiers
REGION                 1..121
```

-continued

```
                        note = Synthetic
source                  1..121
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1055
EVQLVESGGG LVQPGGSLRL SCAVFDRKSD AKYVMHWVRQ APGKGLEWVS AINPYNDGNY  60
YADSVKGRFT ISRDNSRKTL YLQMNSLRAE DTAVYYCARG AYKRGYAMDY WGQGTTVTVS  120
S                                                                  121

SEQ ID NO: 1056         moltype = AA  length = 113
FEATURE                 Location/Qualifiers
REGION                  1..113
                        note = Synthetic
source                  1..113
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1056
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYDPV AALFGQGTKV EIK         113

SEQ ID NO: 1057         moltype = AA  length = 115
FEATURE                 Location/Qualifiers
REGION                  1..115
                        note = Synthetic
source                  1..115
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1057
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYQYD PVAALFGQGT KVEIK       115

SEQ ID NO: 1058         moltype = AA  length = 122
FEATURE                 Location/Qualifiers
REGION                  1..122
                        note = Synthetic
source                  1..122
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1058
EVQLVESGGG LVQPGGSLRL SCAASQYDPV AALFVMHWVR QAPGKGLEWV SAINPYNDGN  60
YYADSVKGRF TISRDNSRKT LYLQMNSLRA EDTAVYYCAR GAYKRGYAMD YWGQGTTVTV  120
SS                                                                 122

SEQ ID NO: 1059         moltype = AA  length = 123
FEATURE                 Location/Qualifiers
REGION                  1..123
                        note = Synthetic
source                  1..123
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1059
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGQ YDPVAALFAM DYWGQGTTVT  120
VSS                                                                123

SEQ ID NO: 1060         moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1060
DIVLTQSPAS LAVSLGQRAT ISCRASKSVS SSISSLMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K           111

SEQ ID NO: 1061         moltype = AA  length = 111
FEATURE                 Location/Qualifiers
REGION                  1..111
                        note = Synthetic
source                  1..111
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1061
DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSSYSYMHWY QQKPGQPPKL LALHRSYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K           111
```

-continued

```
SEQ ID NO: 1062        moltype = AA  length = 111
FEATURE                Location/Qualifiers
REGION                 1..111
                       note = Synthetic
source                 1..111
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1062
DIVLTQSPAS LAVSLGQRAT ISCRASNLVP MVATVYMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K          111

SEQ ID NO: 1063        moltype = AA  length = 111
FEATURE                Location/Qualifiers
REGION                 1..111
                       note = Synthetic
source                 1..111
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1063
DIVLTQSPAS LAVSLGQRAT ISCRASKNLV PMVATVMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K          111

SEQ ID NO: 1064        moltype = AA  length = 111
FEATURE                Location/Qualifiers
REGION                 1..111
                       note = Synthetic
source                 1..111
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1064
DIVLTQSPAS LAVSLGQRAT ISCRASKGIL GFVFTLMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K          111

SEQ ID NO: 1065        moltype = AA  length = 111
FEATURE                Location/Qualifiers
REGION                 1..111
                       note = Synthetic
source                 1..111
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1065
DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSSYSYMHWY QQKPGQPPKN LVPMVATVES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI K          111

SEQ ID NO: 1066        moltype = AA  length = 110
FEATURE                Location/Qualifiers
REGION                 1..110
                       note = Synthetic
source                 1..110
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1066
QSALTQPRSV SGSPGQSVTI SCTGTSTDVA SLNYVSWYQQ HPGKAPKVMI YDVSKRPSGV  60
PDRFSGSKSG NTASLTISGL QAEDEADYYC CSYAGSYTYV FGTGTKVTVL            110

SEQ ID NO: 1067        moltype = AA  length = 116
FEATURE                Location/Qualifiers
REGION                 1..116
                       note = Synthetic
source                 1..116
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1067
QVQLQESGPG LVKSSETLGI VCPISGGSIS SYFWSWIRQP PGKGLEWIGY IYYSGSTNYN  60
PSLKSRVTIS LHTSKNQFSL KLSSVTAADT AVYYCARHRN WLFDYWGQGT LVTVSS     116

SEQ ID NO: 1068        moltype = AA  length = 107
FEATURE                Location/Qualifiers
REGION                 1..107
                       note = Synthetic
source                 1..107
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1068
DILLTQSPVI LSVSPGERVS FSCRASQSIG TNIHWYQQRT NGSPRLLIKY ASESISGIPS  60
```

-continued

```
RFSGSGSGTD FTLSINSVES EDIADYYCQQ NNNWPTTFGA GTKLELK                107

SEQ ID NO: 1069        moltype = AA  length = 119
FEATURE                Location/Qualifiers
REGION                 1..119
                       note = Synthetic
source                 1..119
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1069
QVQLKQSGPG LVQPSQSLSI TCTVSGFSLT NYGVHWVRQS PGKGLEWLGV IWSGGNTDYN  60
TPFTSRLSIN KDNSKSQVFF KMNSLQSNDT AIYYCARALT YYDYEFAYWG QGTLVTVSA   119

SEQ ID NO: 1070        moltype = AA  length = 107
FEATURE                Location/Qualifiers
REGION                 1..107
                       note = Synthetic
source                 1..107
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1070
DIQMTQSPSS LSASVGDRVT ITCQASQDIS NYLNWYQQKP GKAPKLLIYD ASNLETGVPS  60
RFSGSGSGTD FTFTISSLQP EDIATYFCQH FDHLPLAFGG GTKVEIK                107

SEQ ID NO: 1071        moltype = AA  length = 119
FEATURE                Location/Qualifiers
REGION                 1..119
                       note = Synthetic
source                 1..119
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1071
QVQLQESGPG LVKPSETLSL TCTVSGGSVS SGDYYWTWIR QSPGKGLEWI GHIYYSGNTN  60
YNPSLKSRLT ISIDTSKTQF SLKLSSVTAA DTAIYYCVRD RVTGAFDIWG QGTMVTVSS   119

SEQ ID NO: 1072        moltype = AA  length = 107
FEATURE                Location/Qualifiers
REGION                 1..107
                       note = Synthetic
source                 1..107
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1072
EIVMTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA  60
RFSGSGSGTD FTLTISSLEP EDFAVYYCHQ YGSTPLTFGG GTKAEIK                107

SEQ ID NO: 1073        moltype = AA  length = 121
FEATURE                Location/Qualifiers
REGION                 1..121
                       note = Synthetic
source                 1..121
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1073
QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SGDYYWSWIR QPPGKGLEWI GYIYYSGSTD  60
YNPSLKSRVT MSVDTSKNQF SLKVNSVTAA DTAVYYCARV SIFGVGTFDY WGQGTLVTVS  120
S                                                                  121

SEQ ID NO: 1074        moltype = AA  length = 330
FEATURE                Location/Qualifiers
REGION                 1..330
                       note = Synthetic
source                 1..330
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1074
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLWC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 1075        moltype = AA  length = 330
FEATURE                Location/Qualifiers
REGION                 1..330
```

-continued

```
                        note = Synthetic
source                  1..330
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1075
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  60
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  120
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  180
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  240
LTKNQVSLSC AVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLV SKLTVDKSRW  300
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   330

SEQ ID NO: 1076         moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Synthetic
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1076
RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD  60
SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC                107

SEQ ID NO: 1077         moltype = AA  length = 218
FEATURE                 Location/Qualifiers
REGION                  1..218
                        note = Synthetic
source                  1..218
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1077
DIVLTQSPAS LAVSLGQRAT ISCRASKSVS TSSYSYMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 1078         moltype = AA  length = 446
FEATURE                 Location/Qualifiers
REGION                  1..446
                        note = Synthetic
source                  1..446
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1078
EVQLVESGGG LVKPGGSRKL SCAASGFTFS NYGMHWVRQA PEKGLEWVAY ISSGSSTIYY  60
ADTVKGRFTI SRDNAKNTLF LQMTSLRSED TAMYYCARRG LLLDYWGQGT TLTVSSASTK  120
GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS  180
LSSVVTVPSS SLGTQTYICN VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSRDELTKN  360
QVSLSCAVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLVSKLT VDKSRWQQGN  420
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       446

SEQ ID NO: 1079         moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = Synthetic
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1079
DILLTQSPVI LSVSPGERVS FSCRASQSIG TNIHWYQQRT NGSPRLLIKY ASESISGIPS  60
RFSGSGSGTD FTLSINSVES EDIADYYCQQ NNNWPTTFGA GTKLELKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 1080         moltype = AA  length = 449
FEATURE                 Location/Qualifiers
REGION                  1..449
                        note = Synthetic
source                  1..449
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 1080
QVQLKQSGPG LVQPSQSLSI TCTVSGFSLT NYGVHWVRQS PGKGLEWLGV IWSGGNTDYN  60
TPFTSRLSIN KDNSKSQVFF KMNSLQSNDT AIYYCARALT YYDYEFAYWG QGTLVTVSAA  120
```

-continued

```
STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL  360
TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ  420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGK                                    449

SEQ ID NO: 1081        moltype = AA  length = 214
FEATURE                Location/Qualifiers
REGION                 1..214
                       note = Synthetic
source                 1..214
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1081
DIQMTQSPSS LSASVGDRVT ITCQASQDIS NYLNWYQQKP GKAPKLLIYD ASNLETGVPS  60
RFSGSGSGTD FTFTISSLQP EDIATYFCQH FDHLPLAFGG GTKVEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 1082        moltype = AA  length = 449
FEATURE                Location/Qualifiers
REGION                 1..449
                       note = Synthetic
source                 1..449
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1082
QVQLQESGPG LVKPSETLSL TCTVSGGSVS SGDYYWTWIR QSPGKGLEWI GHIYYSGNTN  60
YNPSLKSRLT ISIDTSKTQF SLKLSSVTAA DTAIYYCVRD RVTGAFDIWG QGTMVTVSSA  120
STKGPSVFPL APSSKSTSGG TAALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG  180
LYSLSSVVTV PSSSLGTQTY ICNVNHKPSN TKVDKKVEPK SCDKTHTCPP CPAPELLGGP  240
SVFLFPPKPK DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS  300
TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV YTLPPSRDEL  360
TKNQVSLWCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL DSDGSFFLYS KLTVDKSRWQ  420
QGNVFSCSVM HEALHNHYTQ KSLSLSPGK                                    449

SEQ ID NO: 1083        moltype = AA  length = 220
FEATURE                Location/Qualifiers
REGION                 1..220
                       note = Synthetic
source                 1..220
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1083
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYYYH MYTFGQGTKV EIKRTVAAPS  120
VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAL QSGNSQESVT EQDSKDSTYS  180
LSSTLTLSKA DYEKHKVYAC EVTHQGLSSP VTKSFNRGEC                        220

SEQ ID NO: 1084        moltype = AA  length = 450
FEATURE                Location/Qualifiers
REGION                 1..450
                       note = Synthetic
source                 1..450
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1084
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INPYNDGNYY  60
ADSVKGRFTI SRDNSRKTLY LQMNSLRAED TAVYYCARGA YKRGYAMDYW GQGTTVTVSS  120
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS  180
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG  240
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN  300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE  360
LTKNQVSLSC AVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLV SKLTVDKSRW  420
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK                                   450

SEQ ID NO: 1085        moltype = AA  length = 214
FEATURE                Location/Qualifiers
REGION                 1..214
                       note = Synthetic
source                 1..214
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1085
EIVMTQSPAT LSLSPGERAT LSCRASQSVS SYLAWYQQKP GQAPRLLIYD ASNRATGIPA  60
```

-continued

```
RFSGSGSGTD FTLTISSLEP EDFAVYYCHQ YGSTPLTFGG GTKAEIKRTV AAPSVFIFPP  120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSTLT  180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC                              214

SEQ ID NO: 1086        moltype = AA  length = 451
FEATURE                Location/Qualifiers
REGION                 1..451
                       note = Synthetic
source                 1..451
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1086
QVQLQESGPG LVKPSQTLSL TCTVSGGSIS SGDYYWSWIR QPPGKGLEWI GYIYYSGSTD  60
YNPSLKSRVT MSVDTSKNQF SLKVNSVTAA DTAVYYCARV SIFGVGTFDY WGQGTLVTVS  120
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG  240
GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY  300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRD  360
ELTKNQVSLW CLVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL YSKLTVDKSR  420
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K                                 451

SEQ ID NO: 1087        moltype = AA  length = 218
FEATURE                Location/Qualifiers
REGION                 1..218
                       note = Synthetic
source                 1..218
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1087
DIVLTQSPAS LAVSLGQRAT ISCRASKNLV PMVATVMHWY QQKPGQPPKL LIKYASYLES  60
GVPARFSGSG SGTDFTLNIH PVEEEDAATY YCQHSREFPW TFGGGTKLEI KRTVAAPSVF  120
IFPPSDEQLK SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLS  180
STLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGEC                          218

SEQ ID NO: 1088        moltype = AA  length = 446
FEATURE                Location/Qualifiers
REGION                 1..446
                       note = Synthetic
source                 1..446
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1088
EVQLVESGGG LVKPGGSRKL SCAASGFTFS NYGMHWVRQA PEKGLEWVAY ISSGSSTIYY  60
ADTVKGRFTI SRDNAKNTLF LQMTSLRSED TAMYYCARRG LLLDYWGQGT TLTVSSASTK  120
GPSVFPLAPS SKSTSGGTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP AVLQSSGLYS  180
LSSVVTVPSS SLGTQTYICN VNHKPSNTKV DKKVEPKSCD KTHTCPPCPA PELLGGPSVF  240
LFPPKPKDTL MISRTPEVTC VVVDVSHEDP EVKFNWYVDG VEVHNAKTKP REEQYNSTYR  300
VVSVLTVLHQ DWLNGKEYKC KVSNKALPAP IEKTISKAKG QPREPQVYTL PPSRDELTKN  360
QVSLSCAVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLVSKLT VDKSRWQQGN  420
VFSCSVMHEA LHNHYTQKSL SLSPGK                                       446

SEQ ID NO: 1089        moltype = AA  length = 220
FEATURE                Location/Qualifiers
REGION                 1..220
                       note = Synthetic
source                 1..220
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1089
DLVMTQSPSS LSASVGDRVT ITCKSSQSLF NSRTRKNYLA WYQQKPGKAP KLLIYWASTR  60
ESGVPSRFSG SGSGTDFTLT ISSLQPEDFA TYYCQQYYYH MYTFGQGTKV EIKRTVAAPS  120
VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAL QSGNSQESVT EQDSKDSTYS  180
LSSTLTLSKA DYEKHKVYAC EVTHQGLSSP VTKSFNRGEC                        220

SEQ ID NO: 1090        moltype = AA  length = 451
FEATURE                Location/Qualifiers
REGION                 1..451
                       note = Synthetic
source                 1..451
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 1090
EVQLVESGGG LVQPGGSLRL SCAASGYTFT SYVMHWVRQA PGKGLEWVSA INLVPMVATV  60
YADSVKGRFT ISRDNSRKTL YLQMNSLRAE DTAVYYCARG AYKRGYAMDY WGQGTTVTVS  120
SASTKGPSVF PLAPSSKSTS GGTAALGCLV KDYFPEPVTV SWNSGALTSG VHTFPAVLQS  180
SGLYSLSSVV TVPSSSLGTQ TYICNVNHKP SNTKVDKKVE PKSCDKTHTC PPCPAPELLG  240
```

-continued

```
GPSVFLFPPK PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY  300
NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP QVYTLPPSRD  360
ELTKNQVSLS CAVKGFYPSD IAVEWESNGQ PENNYKTTPP VLDSDGSFFL VSKLTVDKSR  420
WQQGNVFSCS VMHEALHNHY TQKSLSLSPG K                                 451
```

1. A dual-function antigen binding molecule comprising:

a. a first antibody or antigen binding fragment thereof comprising at least one immunogenic peptide inserted into a CDR of said antibody or antigen binding fragment thereof, and where said insertion comprises removal of CDR sequence; and

b. a second antibody capable of binding epidermal growth factor receptor (EGFR), wherein said antibody is selected from cetuximab, panitumumab and necitumumab or antibody comprising at least 85% sequence identity thereto.

2. The dual function antigen binding molecule of claim **1**, wherein said first antibody or antigen binding fragment thereof and said second antibody comprise at least one modification that promotes heterodimerization and inhibit homodimerization, and wherein one of said first and second antibody comprises a heavy chain constant region comprising SEQ ID NO: 1074 and the other antibody comprises a heavy chain constant region comprising SEQ ID NO: 1075.

3. (canceled)

4. The dual function antigen binding molecule of claim **1**, wherein said first antibody or antigen binding fragment thereof binds to a target cell, and wherein said target cell is a cancer cell and a cancer cell antigen is selected from HER2, EGFR, EpCAM, PSMA, BCMA, CD123, CD33, CD38, CTLA, LAG-3, ICOS, 4-1BB and PD-L1, a dendritic cell and a dendritic cell antigen is selected from CD40, CD205, CD206, CLEC9A, CLEC12A, CD209, and CD207 or both.

5. The dual function antigen binding molecule of claim **1**, wherein said immunogenic peptide is a cancer specific peptide, is a viral peptide, is a peptide recognized by CD4 T cells, CD8 T cells or a combination thereof.

6. The dual function antigen binding molecule of claim **5**, wherein said peptide is a cancer specific peptide and is selected from a peptide sequence provided in Table 1.

7. (canceled)

8. The dual function antigen binding molecule of claim **5**, wherein said peptide is a viral peptide is-derived from Cytomegalovirus (CMV), Epstein-Barr virus (EBV), Severe acute respiratory syndrome coronavirus 2 (SARS-CoV2), Adenovirus, Human papilloma virus (HPV) or Influenza virus (FLU) and is selected from a peptide sequence provided in Table 2 or Table 3.

9. (canceled)

10. The dual function antigen binding molecule of claim **1**, further comprising a cell penetration sequence that targets said first antibody or antigen binding fragment thereof to a cytoplasm of a cell bound by said first antibody or antigen binding fragment thereof and wherein said cell penetration sequence is an endosomal escape domain (EED).

11. (canceled)

12. (canceled)

13. The dual function antigen binding molecule of claim **1**, wherein said CDR is an inert CDR having little or no contribution to binding to a target antigen.

14. The dual function antigen binding molecule of claim **13**, wherein an inert CDR comprises two or fewer amino acids that contact said target antigen and wherein contact comprises a distance of not more than 5 angstroms between an amino acid of a CDR and an amino acid of said target antigen.

15. (canceled)

16. The dual function antigen binding molecule of claim **1**, wherein said insertion and removal produces no change or minimal change in the overall conformation of said first antibody or antigen binding fragment thereof such that said first antibody or antigen binding fragment thereof binds its target antigen at an equivalent affinity to said first antibody or antigen binding fragment devoid of said immunogenic peptide.

17. The dual function antigen binding molecule of claim **1**, wherein at least one inert CDR of an antigen binding region is replaced with a cell penetration sequence.

18. (canceled)

19. (canceled)

20. (canceled)

21. (canceled)

22. The dual function antigen binding molecule of claim **1**, wherein within said first antibody or antigen binding fragment thereof said antigen binding region, said immunogenic peptide and said cell penetrating sequence are each separated by a linker, wherein said dual function antigen binding molecule is devoid of a chemical linker, or both.

23. (canceled)

24. The dual function antigen binding molecule of claim **1**, wherein said first antibody before said immunogenic peptide is inserted is selected from:

a. antibody TMab4 comprising a heavy chain variable region of SEQ ID NO: 1021 and a light chain variable region of SEQ ID NO: 1022;

b. antibody 3E10 comprising a heavy chain variable region of SEQ ID NO: 1023 and a light chain variable region of SEQ ID NO: 1024; and

c. antibody 71F12 comprising a heavy chain variable region of SEQ ID NO: 1026 and a light chain variable region of SEQ ID NO: 1027; and

d. said immunogenic peptide is inserted into CDRH1, CDRH2, CDRH3 or CDRL3 of said TMab4, CDRL1 or CDRL2 of said 3E10 or CDRL1 of said 71F12.

25. (canceled)

26. The dual function antigen binding molecule of claim **24**, wherein said first antibody comprises at least one of:

a. a light chain variable region of SEQ ID NO: 1022 and a heavy chain variable region selected from SEQ ID NO: 1028-1040, 1043-1045, 1047-1055, and 1058-1059;

b. a heavy chain variable region of SEQ ID NO: 1021 and a light chain variable region selected from SEQ ID NO: 1041-1042, 1046, and 1056-1057;

c. a heavy chain variable region of SEQ ID NO: 1023 and a light chain variable region selected from SEQ ID NO: 1060-1065;

d. a heavy chain variable region of SEQ ID NO: 1026 and a light chain variable region of SEQ ID NO: 1066; and
e. a light chain variable region of SEQ ID NO: 1027 and a heavy chain variable region of SEQ ID NO: 1067;

said dual function antigen binding molecule comprises two heavy chains and two light chains and wherein:

a. said two heavy chains are SEQ ID NO: 1088 and 1080 and said two light chains are SEQ ID NO: 1087 and 1079;
b. said two heavy chains are SEQ ID NO: 1088 and 1082 and said two light chains are SEQ ID NO: 1087 and 1081;
c. said two heavy chains are SEQ ID NO: 1090 and 1080 and said two light chains are SEQ ID NO: 1089 and 1079;
d. said two heavy chains are SEQ ID NO: 1090 and 1082 and said two light chains are SEQ ID NO: 1089 and 1081; or
e. said two heavy chains are SEQ ID NO: 1088 and 1086 and said two light chains are SEQ ID NO: 1087 and 1085; or

both.

27. (canceled)

28. An antibody or antigen binding fragment thereof comprising at least one immunogenic peptide inserted into a variable region of said antibody or antigen binding fragment thereof, and where said insertion comprises removal of antibody or antigen binding fragment sequence.

29. A pharmaceutical composition comprising a dual-function antigen binding molecule of claim **1** and a pharmaceutically acceptable carrier excipient or adjuvant.

30. A nucleic acid molecule comprising at least one open reading frame, wherein said open reading frame encodes a dual-function antigen binding molecule of claim **1**, optionally wherein said nucleic acid molecule is an expression vector and comprises at least one regulatory element operatively linked to said open reading frame.

31. (canceled)

32. A method of treating EGFR positive cancer in a subject in need thereof, the method comprising administering to said subject a pharmaceutical composition of claim **29**, thereby treating cancer in a subject.

33. (canceled)

34. A method of engineering an antibody or antigen binding fragment thereof, the method comprising:

a. selecting an antibody or antigen binding fragment thereof of interest;
b. receiving structural analysis of said selected antibody or antigen binding domain bound to its target;
c. determining at least one CDR of said selected antibody or antigen binding domain that is not required for binding to said target based on said structural analysis;
d. replacing said determined at least one CDR or a portion thereof with an immunogenic peptide; or
a. selecting an antibody or antigen binding fragment thereof of interest;
b. receiving a database of immunogenic peptides;
c. performing pairwise alignment of peptides of a variable region of said selected antibody or antigen binding fragment thereof of interest with immunogenic peptides of said database;
d. determining a peptide from said selected antibody or antigen binding fragment thereof and an immunogenic peptide with an alignment score above a predetermined threshold; and
e. replacing said determined peptide from said selected antibody or antigen binding fragment thereof with said determined immunogenic peptide;

thereby engineering an antibody or antigen binding fragment thereof.

35. (canceled)

36. The method of claim **34**, where at least one of.

a. said method further comprises optimizing said replacing to produce as little perturbation in the structure of said selected antibody or antigen binding fragment thereof of interest as possible,
b. said engineered antibody or antigen binding fragment thereof is an immunogenic peptide delivery antibody;
c. step (a) comprises selecting an antibody or antigen binding fragment thereof that binds to a surface of a target cell;
d. step (a) comprises selecting an antibody or antigen binding fragment thereof that binds to a surface of a target cell and upon binding to a surface is internalized and delivered to a cytosol of said target cell;
e. said method further comprises confirming at least one of: delivery of said immunogenic peptide to a cytosol of said target cell, delivery of said immunogenic peptide in complex with an HLA molecule to a surface of said target cell and specific killing of said target cell by an effector cell specific to said immunogenic peptide; and
f. wherein said method further comprises selecting a targeting antibody that binds to a protein on a surface of a target cell and producing a dual-function antigen binding molecule by combining said engineered antibody and said targeting antibody, optionally wherein combining comprises engineering a heavy chain constant region of said targeting antibody and a heavy chain constant region of said engineered antibody to promote heterodimerization and inhibit homodimerization.

37. (canceled)
38. (canceled)
39. (canceled)
40. (canceled)
41. (canceled)
42. (canceled)

* * * * *