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(54) Title: MAGEB2 BINDING CONSTRUCTS

FIGURE 1

MAGEB2 and similar peptides

	1	2	3	4	5	6	7	8	9	10	
MAGEB2	G	V	Y	D	G	E	E	H	S	V	(SEQ ID NO: 1)
MAGEA4	G	V	Y	D	G	R	E	H	T	V	(SEQ ID NO: 2)
MAGEA8	G	L	Y	D	G	R	E	H	S	V	(SEQ ID NO: 3)
KEA	G	V	I	D	G	H	I	Y	A	V	(SEQ ID NO: 18461)
MB	G	L	S	D	G	E	W	Q	L	V	(SEQ ID NO: 18462)
ADF	G	V	M	A	G	D	I	Y	S	V	(SEQ ID NO: 18463)
DPYSL4	G	L	Y	D	G	P	M	H	E	V	(SEQ ID NO: 18464)
CNP2	G	V	Y	G	G	S	V	H	E	A	(SEQ ID NO: 18465)
MYOF	F	V	Y	D	E	P	G	H	A	V	(SEQ ID NO: 18466)
COX14	T	V	Y	G	G	Y	L	C	S	V	(SEQ ID NO: 18467)
STXBP5	Y	T	Y	D	E	A	I	H	S	V	(SEQ ID NO: 18468)
SLK	F	I	V	D	G	V	E	V	S	V	(SEQ ID NO: 18469)

(57) Abstract: The present disclosure relates to antibody constructs comprising a domain which binds to a MAGEB2 peptide complexed with an HLA and optionally, another domain which binds to CD3. Moreover, the disclosure provides polynucleotides encoding the antibody constructs vectors comprising said polynucleotides and host cells transformed or transfected with said polynucleotides or vectors. Furthermore, the disclosure provides processes for producing the antibody constructs of the disclosure, medical uses of said antibody constructs, and kits comprising said antibody constructs.

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MAGEB2 BINDING CONSTRUCTS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 63/027,148, filed May 19, 2020 and U.S. Provisional Application No. 63/128,773, filed December 21, 2020. The above-identified applications are each hereby incorporated herein by reference for all purposes.

REFERENCE TO THE SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on May 14, 2021, is named A-2635-WO-PCT sequence listing.txt and is 7,139,825 bytes in size.

FIELD OF THE INVENTION

[0003] The field of this invention relates to compositions and methods related to biopharmaceuticals, including bispecific antibody constructs.

BACKGROUND OF THE INVENTION

[0004] The MAGE (melanoma antigen genes) family contains about 60 genes that are categorized into several subfamilies. The MAGE-A, -B, and -C subfamilies are expressed mainly in the testis and are aberrantly expressed in various cancer types. The MAGE-D, -E, -F, -G, -H, -L, and -N subfamilies are expressed in a wide variety of tissues. See, e.g., Lee and Potts, J. Mol. Biol., 2018. One of the MAGE family members, MAGEB2, is typically only expressed in normal testis. MAGEB2, which may function to enhance ubiquitin ligase activity of RING-type zinc finger containing E3 ubiquitin protein ligases, has been found to be aberrantly expressed in a variety of human tumors such as lung carcinoma, breast carcinoma, melanoma, and others. Given this aberrant expression, MAGEB2 is a potential target for therapeutic agents.

[0005] Many types of cancers, although having a variety of available treatments, still are considered to have a high unmet medical need, with patients needing improved, effective therapeutics.

[0006] Protein-based pharmaceuticals have a significant role in almost every field of medicine and account for many of the therapeutic agents in development and already commercially available. Compared to the more traditional small molecule pharmaceuticals, protein-based pharmaceuticals can have higher specificity and activity at relatively lower concentrations and can provide for treatment of

high impact diseases such as various cancers, auto-immune diseases, and metabolic disorders (Roberts, Trends Biotechnol. 2014 Jul;32(7):372-80, Wang, Int J Pharm. 1999 Aug 20;185(2):129-88).

[0007] One type of protein-based pharmaceutical is a bispecific antibody which typically can simultaneously bind to two different types of antigen. They are known in several structural formats, and current applications have been explored for cancer immunotherapy and drug delivery (Fan, Gaowei; Wang, Zujian; Hao, Mingju; Li, Jinming (2015). "Bispecific antibodies and their applications". Journal of Hematology & Oncology. 8: 130).

[0008] Bispecific antibodies can be made in several different formats. For example, they can be IgG-like, e.g., full length bispecific antibodies, or they can be non-IgG-like bispecific antibodies, which are not full-length antibody constructs. Full length bispecific antibodies typically retain the traditional monoclonal antibody (mAb) structure of two Fab arms and one Fc region, except the two Fab sites bind different antigens. Non full-length bispecific antibodies can lack an Fc region entirely. These include chemically linked Fabs, consisting of only the Fab regions, and various types of bivalent and trivalent single-chain variable fragments (scFvs). There are also fusion proteins mimicking the variable domains of two antibodies. An example of such a format is the bi-specific T-cell engager (BiTE®) (Yang, Fa; Wen, Weihong; Qin, Weijun (2016). "Bispecific Antibodies as a Development Platform for New Concepts and Treatment Strategies". International Journal of Molecular Sciences. 18 (1): 48).

[0009] Although treatments for various cancers exist, patients are still in need of more effective treatments. Accordingly, the invention provides bispecific antibody constructs that target tumor cells that express MAGEB2, and CD3 expressed by immune effector cells.

SUMMARY OF THE INVENTION

[0010] In one embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a MAGEB2 peptide-HLA complex on the surface of a target cell.

[0011] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a MAGEB2 peptide-HLA complex on the surface of a target cell, and a second domain that binds to human CD3 on the surface of a T cell.

[0012] In further embodiments, the invention provides isolated antibody constructs that bind to the same epitope as the antibody constructs provided herein.

[0013] In yet further embodiments, the invention provides isolated antibody constructs that bind to an epitope comprising a MAGEB2 peptide (e.g., SEQ ID NO: 1), wherein the antibody constructs bind to at least one of the following MAGEB2 peptide residues: Asp4, Gly5, Glu6, Glu7, His8, Ser9, or Val10.

[0014] In other embodiments, the invention provides isolated antibody constructs that bind to an epitope comprising both a MAGEB2 peptide (e.g., SEQ ID NO: 1) and an HLA-A2, wherein the antibody constructs bind to at least one of the following residues HLA-A2 residues: Arg65, Lys66, Ala69, Gln72,

Thr73, Val76, Lys146, Ala149, Ala150, His151, Glu154, Gln155, Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Lys68, Ser71, Arg75, Gly79, Thr80, Arg82, Gly83, or Glu89.

[0015] In another embodiment, the invention provides isolated antibody constructs that bind to an epitope comprising both a MAGEB2 peptide (e.g., SEQ ID NO: 1) and an HLA-A2/MHC, wherein the antibody constructs bind to at least one of the following MAGEB2 residues: Asp4, Gly5, Glu6, Glu7, His8, Ser9, or Val10, and wherein the antibody construct further binds to at least one of the following residues HLA-A2 residues: Arg65, Lys66, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Glu154, Gln155, Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Lys68, Ser71, Arg75, Gly79, Thr80, Arg82, Gly83, or Glu89.

[0016] In one embodiment, the invention provides isolated antibody constructs that bind to an epitope comprising both a MAGEB2 peptide (e.g., SEQ ID NO: 1) and an HLA-A2/MHC, wherein the antibody constructs comprise at least one of the following heavy chain amino acid residues: Ser30, Ser31, His32, Tyr32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, or Gly105.

[0017] In another embodiment the invention provides antibody constructs that further comprise at least one of the following light chain amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Phe66, Ser66, Gly67, Trp90, Tyr92, Arg93, Leu95, or Gln95.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018] Figure 1. This figure depicts the amino acid sequences for the MAGE-B2, MAGE-A4, and MAGE-A8 peptides, highlighting the differences in three sequences. This figure also depicts other similar peptides. SEQ ID NOs 1-3 and 18461-18469 are disclosed in their respective order of appearance.

[0019] Figures 2A-2F. Figure 2A depicts expression of the MAGEB2 peptide-HLA-A*02:01 complex in various cancer tissues and normal tissues, with the left panel, upper part, showing the median relative MS signal intensities from technical replicate measurements are plotted as colored dots for single HLA-A*02 positive normal (left part of figure) and tumor samples (right part of figure) on which the peptide was detected, and the right panel depicting results from the absolute quantitation analysis (AbsQuant) of MAGEB2 peptide on 12 different tumor tissues. Each data point on the logarithmic scale corresponds to replicate measurements of one tumor sample. The median peptide copy number per cell of 67 is indicated by a red line; Figure 2B depicts mRNA expression of MAGEB2 in various tumor tissues; Figure 2C depicts mRNA expression of MAGEA4 in various tumor tissues; Figure 2D depicts mRNA expression of MAGEB2 in various normal tissues; Figure 2E depicts mRNA expression of

MAGEA4 in various normal tissues; Figure 2F depicts mRNA expression of MAGEB2 in various normal tissues.

[0020] Figures 3A-3B. Figure 3A is a visual representation of the preparation of the multivalent peptide-MHC (pMHC) immunogen used to immunize XenoMouse; Figure 3B depicts the results of a titer analysis of immunized XenoMouse, with the y-axis representing GeoMean fold over a control peptide (soluble) and the x-axis having the various different groups of immunized mice.

[0021] Figure 4A-4B. Figure 4A depicts the results of cell-based affinity determination by fluorescence cytometry and nonlinear regression (one site - specific binding) analysis on T2 cells loaded with MAGEB2 peptide. Tested MAGEB2 pMHC HLE bispecific antibody constructs are the following (with sequences provided in Table 22 herein:

- 1 = MA_03-E11_AS_CC_x_I2C0_x_scFc_(G2B);
- 2 = MA_09-E2_CC_x_I2C0_x_scFc_(V8T);
- 3 = MA_09-F12_CC_x_I2C0_x_scFc_(D1U);
- 4 = MA_09-G10_CC_x_I2C0_x_scFc_(C4K);
- 5 = MA_09-H7_CC_x_I2C0_x_scFc_(T3S);
- 6 = MA_09-H10_CC_x_I2C0_x_scFc_(B6N); and
- 7 = MA_10-B5_CC_x_I2C0_x_scFc_(H6H).

[0022] Figure 4B depicts the results of a cytotoxicity assay on the MAGEB2 pMHC bearing cell line DAN-G. Tested MAGEB2 pMHC HLE BiTE® molecules are the following (with sequences provided in Table 22 herein):

- 1 = MA_03-G10_AS_CC_x_I2C0_x_scFc_(N3H);
- 2 = MA_98-C7_CC_x_I2C0_x_scFc_(Y8P);
- 3 = MA_03-G11_AS_CC_x_I2C0_x_scFc_(O4R);
- 4 = MA_98-G12_AS_CC_x_I2C0_x_scFc_(Q4Z); and
- 5 = MA_03-E7_AS_CC_x_I2C0_x_scFc_(L6M).

[0023] Figure 5A-5B. Figure 5A depicts the response of the BiTE® molecule MA_10-B5_CC_x_I2C0_x_scFc_(H6H) against 112 MAGE-B2 similar peptides, MAGE-B2 and relevant controls in 2 different T-cell donors, with % T2Luc viability (Donor RG1198) on the y-axis and % T2Luc viability (Donor 330) on the x-axis; Figure 5B depicts the response of the BiTE® molecule MA_03-G10_AS_CC_x_I2C0_x_scFc_(N3H) against 112 MAGE-B2 similar peptides, MAGE-B2 and relevant controls in 2 different T-cell donors, with % T2Luc viability (Donor RG1198) on the y-axis and % T2Luc viability (Donor 330) on the x-axis.

[0024] Figure 6A-6B. Figure 6A depicts the potency of the MA_10-B5_CC_x_I2C0_x_scFc_(H6H) BiTE® molecule against MAGE-B2 and various reactive similar peptides, with % T2Luc viability on the x-axis and the log concentration [nM] on the x-axis; Figure 6B depicts the potency of the MA_03-G10_AS

CC_x_I2C0_x_scFc_(N3H) BiTE[®] molecule against MAGE-B2 and various reactive similar peptides, with % T2Luc viability on the y-axis and the log concentration [nM] on the x-axis.

[0025] Figure 7. This figure depicts the potency of two different BiTE[®] molecules against the full length 10-mer MAGEB2 peptide as compared to 9-mer deletion variants of the MAGEB2 peptide.

[0026] Figure 8. This figure summarizes in table format the TDCC activity of ten BiTE[®] molecules on four different cell lines with known MAGEB2 pMHC copies per cell. Note that the BiTE[®] molecule 3-character name is a shortened version of the full BiTE[®] molecule nomenclature as seen in Table 22 herein, where the 3-character name is in parentheses.

[0027] Figure 9. This figure depicts TDCC plots of three different BiTE[®] molecules on cell lines with intermediate-low expression of MAGEB2, with % specific cytotoxicity on the y-axis and log BiTE[®] molecule concentration (pM) on the x-axis. Note that the BiTE[®] molecule 3-character name is a shortened version of the full BiTE[®] molecule nomenclature as seen in Table 22 herein, where the 3-character name is in parentheses.

[0028] Figure 10. This figure depicts TDCC plots of three different BiTE[®] molecules on the DAN-G MAGEB2 (-) cell line, with % specific cytotoxicity on the y-axis and log BiTE[®] molecule concentration (pM) on the x-axis. Note that the BiTE[®] molecule 3-character name is a shortened version of the full BiTE[®] molecule nomenclature as seen in Table 22 herein, where the 3-character name is in parentheses.

[0029] Figures 11A-B. Figure 11A depicts TDCC plots of two different BiTE[®] molecules on human primary cells (cardiac myocytes, endothelial cells, and epithelial cells), with % specific lysis (cytotoxicity) on the y-axis and BiTE[®] molecule concentration (nM) on the x-axis; Figure 11B depicts BiTE[®] molecule induced target cell lysis on MAGEB2 negative cells, with % cytotoxicity on the y-axis and log BiTE[®] molecule concentration (pM) on the x-axis. Note that the BiTE[®] molecule 3-character name is a shortened version of the full BiTE[®] molecule nomenclature as seen in Table 22 herein, where the 3-character name is in parentheses.

[0030] Figures 12A and 12B. Figure 12A depicts TDCC plots of varying BiTE[®] molecules on MAGEA4(+) / MAGEB2(-) cell lines (NCI-H1703 and SCaBER), with % specific cytotoxicity on the y-axis and log BiTE[®] molecule concentration (pM) on the x-axis. Note that the BiTE[®] molecule 3-character name is a shortened version of the full BiTE[®] molecule nomenclature as seen in Table 22 herein, where the 3-character name is in parentheses. Figure 12B is a table form of the data from Figure 12A and highlights the differences in activity between Family 4 molecules and Family 7 molecules, where only Family 7 molecules show activity against MAGE-A4 expressing cells.

[0031] Figures 13A and 13B. Figure 13A depicts the structure of the MAGEB2 peptide interactions with MHC. The left structure is a protein structure representation of the peptide-MHC complex

(pMHC) and the right structure is a representation of the electrostatic surface of the pMHC; Figure 13B depicts the structure of the MAGEB2 peptide interactions with other HLA-A*02 serotypes.

[0032] Figure 14. This figure depicts the structure of the Family 4 L7E scFv SEQ115734 bound mage-b2 HLA-A: overall structure at 1.9 Å.

[0033] Figure 15. This figure depicts the structure of the Family 4 L7E scFv SEQ115734 bound mage-b2 HLA-A: overall structure at 1.9 Å, with the left panel highlighting CDR interactions with the MAGEB2 peptide and MHC, and the right panel highlighting light chain (LC) and heavy chain (HC) interactions with the MHC.

[0034] Figure 16. This figure depicts the structure of the Family 4 L7E scFv SEQ115734 bound MAGEB2 HLA-A: overall structure at 1.9 Å and certain water-mediated interactions.

[0035] Figure 17. This figure depicts the structure of the H6N scFv heavy chain (HC) interactions with the MAGEB2 peptide, and H6N scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0036] Figure 18. This figure depicts the structure of the H6N scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the H6N scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0037] Figure 19. This figure depicts the structure of the H6N scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the H6N scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0038] Figure 20. This figure depicts the structure of the H6N scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the H6N scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0039] Figure 21. This figure depicts the structure of the N3H scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the N3H scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0040] Figure 22. This figure depicts the structure of the N3H scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the N3H scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0041] Figure 23. This figure depicts the structure of the N3H scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the N3H scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0042] Figure 24. This figure depicts the structure of the N3H scFv heavy chain (HC) interactions with the MAGEB2 peptide, and the N3H scFv light chain (LC) interactions with the HLA and the MAGEB2 peptide.

[0043] Figure 25. This figure summarizes sequence alignments of three different Family 4 BiTE[®] molecules. SEQ ID NOs 18470-18472, 556, 556, and 576, are disclosed in their respective order of appearance.

[0044] Figure 26. This figure summarizes sequence alignments of three different Family 7 BiTE[®] molecules. SEQ ID NOs 18473-18478 are disclosed in their respective order of appearance.

[0045] Figure 27. This figure summarizes the results—activity as measured by IL-2 production—of three different BiTE[®] molecules binding to cell lines expressing different HLA-A serotypes and exogenously loaded with the MAGEB2 peptide of SEQ ID NO: 1.

[0046] Figure 28. This figure depicts the overall structure of the Family 7 10B5 (H6H) bound MAGEB2 HLA-A at 2.02 Å.

[0047] Figure 29. This figure depicts the structure of Family 7 10B5 (H6H) in the right panel as compared to the structure of Family 4 molecule N3H in the left panel, highlighting the different interactions observed and described in Example 10 herein.

[0048] Figure 30. This figure depicts some of the water mediated bonding network elucidated by the crystal structure of the 10B5 (H6H) and MAGEB2 pMHC interaction, where water is represented as black spheres, and as further described in Example 10 herein.

[0049] Figure 31. This figure depicts the complementary surface of the heavy chain to the pMHC surface that facilitates this unique recognition. The figure panels show the vacuum electrostatic surfaces, pMHC (left panel) and the HC CDR's (right panel) in grayscale, and is further described in Example 10 herein.

[0050] Figure 32. This figure is a graphical summary of data from an *in vivo* tumor study, where animals with HCT-116 were treated with the N3H molecule on three different time points over the course of the study and as further detailed in Example 11 herein.

[0051] Figure 33. This figure is a graphical summary of data from two treatment groups receiving different doses in an *in vivo* tumor study, where animals with HCT-116 were treated with the N3H molecule on three different time points over the course of the study and as further detailed in Example 11 herein. The upper panel has results from the 2.0 mg/kg treatment group and the lower panel has results from the 0.2 mg/kg treatment group.

[0052] Figure 34. This figure is a graphical summary of data from an *in vivo* tumor study, where animals with HCT-116 were treated with the H6H molecule on three different time points over the course of the study and as further detailed in Example 11 herein.

[0053] Figure 35. This figure is a graphical summary of data from two treatment groups receiving different doses in an *in vivo* tumor study, where animals with HCT-116 were treated with the H6H molecule on three different time points over the course of the study and as further detailed in

Example 11 herein. The upper panel has results from the 2.0 mg/kg treatment group and the lower panel has results from the 0.2 mg/kg treatment group.

[0054] Figure 36. This figure is a graphical summary of data from a pharmacokinetic (pK) study performed on samples taken from the animal studies summarized in Figures 32-34 and further detailed in Example 11 herein. The left panel summarizes pK data from the 2.0 mg/kg and 0.2 mg/kg doses in the N3H molecule treatment groups, and the right panel summarizes pK data from the 2.0 mg/kg and 0.2 mg/kg doses in the H6H molecule treatment groups.

[0055] Figure 37. This figure contains six different graphical summaries of TDCC assays using the N3H molecule to target cells expressing various different HLAs, demonstrating effective cell targeting and killing against cells expressing HLA A*02:01, HLA A*02:05, HLA A*02:06, and HLA A*02:07 and as further detailed in Example 13 herein. The y-axis shows % specific cytotoxicity and the x-axis shows the log MAGEB2 peptide concentration (M).

[0056] Figure 38. This figure summarizes FACS analyses performed on cells expressing various different HLAs and pulsed with the MAGEB2 peptide at 50 μ M and 0.05 μ M (and unpulsed controls), demonstrating effective loading with peptide of HLA A*02:01, HLA A*02:05, HLA A*02:06, and HLA A*02:07 and as further detailed in Example 13 herein.

[0057] Figure 39. This figure summarizes FACS analyses performed on cells expressing various different HLAs and pulsed with the MAGEB2 peptide at 50 μ M and 0.05 μ M (and unpulsed controls), but where FACS gating was set on D5 cells for each concentration to better illustrate loading, and demonstrating effective loading with peptide of HLA A*02:01, HLA A*02:05, HLA A*02:06, and HLA A*02:07 and as further detailed in Example 13 herein.

[0058] Figure 40. This figure summarizes the structural *in silico* modeling workflow for the Family 4 molecules.

[0059] Figure 41. This figure provides an overview structure of both the L7E molecule crystal structure and the N3H molecule crystal structure overlayed with the N3H *in silico* homology model, and is further described in Example 14 herein.

[0060] Figure 42. This figure provides a comparison between the L7E crystal structure and homology *in silico* models for WT, L6A, N3H, and Y8P, and is further described in Example 14 herein.

[0061] Figure 43. This figure provides an *in silico* model comparison between WT and L7E at light chain positions 92, 95, 96, and 97, and is further described in Example 14 herein.

[0062] Figure 44. This figure provides an *in silico* model comparison between WT and L6A at light chain positions 92, 95, 96, and 97, and is further described in Example 14 herein.

[0063] Figure 45. This figure provides an *in silico* model comparison between WT and N3H at light chain positions 92, 95, 96, and 97, and is further described in Example 14 herein.

[0064] Figure 46. This figure provides an *in silico* model comparison between WT and Y8P at light chain positions 92, 95, 96, and 97, and is further described in Example 14 herein.

[0065] Figure 47. This figure provides *in silico* model predicted alternate residues at light chain positions 92, 95, 96, and 97 in the parental molecule, and is further described in Example 14 herein.

[0066] Figure 48. This figure provides *in silico* model predicted alternate residues at light chain positions 92, 95, 96, and 97 in the L6A molecule, and is further described in Example 14 herein.

[0067] Figure 49. This figure provides *in silico* model predicted alternate residues at light chain positions 92, 95, 96, and 97 in the N3H molecule, and is further described in Example 14 herein.

[0068] Figure 50. This figure provides *in silico* model predicted alternate residues at light chain positions 92, 95, 96, and 97 in the Y8P molecule, and is further described in Example 14 herein.

[0069] Figures 51A and 51B. These figures provide in graph format summaries of results of the N3H, H6H, and control molecules against tumor organoids using two different T-cell donors. The y-axis is IFNg concentration in pg/ml and the x-axis is each different molecule tested.

[0070] Figures 52A and 52B. These figures provide in graph format summaries of results of the N3H (Figure 52A) and H6H (Figure 52B) molecules in TDCC assays using Dan-G target cells. The x-axis is log BiTE[®] molecule concentration (nM) and the y-axis is % cytotoxicity.

DETAILED DESCRIPTION

[0071] HLA class I and HLA class II (alternatively called MHC class I and MHC class II) molecules on the cell surface present antigens to the immune system. In some cases, endogenously produced proteins, such as MAGEB2, are proteolytically cleaved into peptides within the cell and presented on the cell surface via the MHC class I molecule. Typically, these peptides are 8-13 amino acid residues long and also comprise “anchor residues” that help bind the peptide to the MHC molecule’s binding groove.

[0072] As discussed above, MAGEB2 is aberrantly expressed in a variety of human cancer types. MAGEB2 is not typically expressed on the surface of cells. MAGEB2 peptides, however, are displayed on the surface of tumor cells by the MHC class I molecule. In particular, the MAGEB2 peptide GGYDGEHSV (SEQ ID NO: 1) is displayed on the surface of tumor cells by the MHC class I molecule as a peptide-MHC (“pMHC”) complex. See, for example, U.S. Patent Appl. Publ. No. US2016/0250307A1 (U.S. Patent Appl. No. 14/975,952) and US2017/0080070A1 (U.S. Patent Appl. No. 15/357,757).

[0073] Given that this MAGEB2 peptide is displayed on the surface of a cell (e.g., a cancer cell), albeit in the context of a peptide-MHC complex, it is potentially targetable by specific binding agents such as monoclonal antibodies or bispecific antibody constructs. Generating an antibody or bispecific antibody construct or other binding construct that targets this peptide-MHC complex poses a unique and difficult challenge due to expression of the MHC on nearly all cells in the body and the possibility

of detrimental binding to MHC not presenting the MAGEB2 peptide. This is compounded by the peptide being so relatively small in comparison to the MHC complex. As will be described herein, the binding constructs of the invention overcome those challenges.

[0074] The term “pMAGE-HLA” as used herein refers to the MAGEB2 peptide GGYDGEHVS (SEQ ID NO: 1), the MAGEA4 peptide GGYDGREHTV (SEQ ID NO: 2) and/or the MAGEA8 peptide GGYDGREHVS (SEQ ID NO: 3) when complexed with an HLA (e.g., HLA-A*02:01). Alternatively, the term “pMHC” as used herein can refer to the same and be used interchangeably, or it can refer to simply a peptide-MHC (HLA) complex in more general terms.

[0075] Bispecific antibody constructs comprising one domain that binds to CD3 expressed on a T-cell surface and one domain that binds to a target protein expressed on a target cell directly connect T-cells to target cells to induce T-cell redirected lysis. This mechanism of action is distinct from chemotherapies, other types of targeted therapies, and other immunotherapies in that it can work with any CD3-positive T-cell, independent of a costimulatory activating signal (Klinger et al., Immunol Reviews 2016). The presence of the pMAGE-HLA on the cell surface of cancer cells such as non-small cell lung carcinoma, hepatocellular carcinoma, or head and neck carcinoma provides a basis for targeting these cancers with a bispecific antibody construct that binds to a pMAGE-HLA (e.g., the MAGEB2 peptide of SEQ ID NO: 1 complexed with an HLA) and CD3.

[0076] In certain embodiments of the present invention, antibody constructs, including bispecific antibody constructs, targeting specifically a pMAGE-HLA derived from MAGEB2 associated with a malignancy are provided. To further this invention, MAGEB2 may be identified as a gene that is upregulated and/or aberrantly expressed in tumors relative to normal tissue expression of MAGEB2. In this regard, it may be shown that the MAGEB2 protein or a specific MAGEB2 peptide is expressed in particular tumors, or displayed on the cell surface, according to methods known in the art, for example, genetic analyses, immunohistochemistry, or mass spectrometry.

[0077] In an embodiment, the present disclosure provides for methods of initiating a T cell-mediated immune response to a target cell or tissue in a subject. The method, in some embodiments, includes administering an effective amount of a binding domain or antibody construct, e.g. a bispecific antibody, described herein, specifically targeting pMAGE-HLA (e.g., with a MAGEB2 peptide) and/or a modified T cell, e.g. a CAR-T cell, that contains a nucleic acid encoding the binding domain or antibody construct, e.g. a bispecific antibody, to a subject in need thereof. In another embodiment, the modified T cell expresses a binding domain or antibody construct, e.g. a bispecific antibody, that may be anchored on a cell surface of the modified T cell or may be secreted from the modified T cell.

[0078] One particular example of mass spectrometry that can be used to show MAGEB2 expression by a cell is a high-throughput platform that is based on ultra-sensitive mass spectrometry, known as XPRESIDENT® (www.immatics.com/x-president.html). This high throughput platform identifies HLA-

bound peptides presented on tumor cells and has very high sensitivity allowing detection of these HLA-bound peptides at attomolar levels. All XPRESIDENT® peptides are sourced from native tumors (in 20 major cancer indications) including primary tissues and metastatic biopsies as well as tissues derived from healthy organs (40 most relevant organs of the human body). This target database comprises over 2000 tissue samples. Peptides are analyzed and identified through a combination of quantitative HLA peptidomics (mass spectrometry) complemented by quantitative transcriptomics (mRNA sequencing), enabling the analysis of differential expression and presentation of these potential drug targets between tumor and normal tissue. All HLA-restricted targets discovered by XPRESIDENT® on any allele are proven to be present on patients' cancer tissues in contrast to those predicted by *in silico* techniques. See also, U.S. Patent No. 10,545,154, U.S. Patent No. 9,791,443, and U.S. Patent No. 7,811,828.

[0079] It may also be demonstrated by flow cytometry that the pMAGE-HLA is present on the cell surface of particular cancer cell lines. Accordingly, MAGEB2, and in particular the MAGEB2 peptide GGYDGEHVS (SEQ ID NO: 1) complexed with an HLA, may be identified as a valid target associated with particular cancer types.

[0080] It is a surprising finding in the context of the present invention that the bispecific antibody constructs according to the present invention target the MAGEB2 peptide GGYDGEHVS (SEQ ID NO: 1) that is presented on a cancer cell surface by an MHC class I molecule with very high specificity, as will be discussed further herein. Lack of killing of non-cancer cells by the bispecific antibody constructs according to the present invention can likewise be confirmed *in vitro* and *in vivo*.

[0081] It is envisaged in the context of the present invention, that preferred bispecific antibody constructs do not only show a favorable ratio of cytotoxicity to affinity, but additionally show sufficient stability characteristics in order to facilitate practical handling in formulating, storing and administering said constructs. Sufficient stability is, for example, characterized by a high monomer content (i.e. non-aggregated and/or non-associated, native molecule) after standard preparation, such as at least 65% as determined by preparative size exclusion chromatography (SEC), more preferably at least 70% and even more preferably at least 75%. Also, the turbidity measured, e.g., at 340 nm as optical absorption at a concentration of 2.5 mg/ml should, preferably, be equal to or lower than 0.025, more preferably 0.020, e.g., in order to conclude to the essential absence of undesired aggregates. Advantageously, high monomer content is maintained after incubation in stress conditions such as freeze/thaw or incubation at 37 or 40°C.

pMAGE-HLA Binding Molecules

[0082] The invention provides antibody construct comprising a domain which binds to a pMAGE-HLA and optionally, another domain which binds to CD3.

[0083] Table 1 below provides amino acid sequences of exemplary MAGEB2 binding molecules VH-CDRs and VL-CDRs. Table 2 below provides amino acid sequences of exemplary MAGEB2 binding molecule VH and VL domains.

[0084] In certain embodiments, in addition to binding the MAGEB2 peptide (SEQ ID NO: 1) complexed with an MHC molecule, the binding molecules may bind to a MAGEA4 peptide (e.g., SEQ ID NO: 2) complexed with an MHC molecule and/or a MAGEA8 peptide (e.g., SEQ ID NO: 3) complexed with an MHC molecule.

Table 1.

Molecule	CDR-L1	CDR-L2	CDR-L3	CDR-H1	CDR-H2	CDR-H3
H6H	RTSQSISSYLN (SEQ ID NO: 223)	AASSLQG (SEQ ID NO: 224)	QQTYSMPFT (SEQ ID NO: 225)	NAWMS (SEQ ID NO: 439)	RIRSRSYGGTTDYA APVKG (SEQ ID NO: 440)	PSYSGSYNYFSVMDV (SEQ ID NO: 441)
N3H	GGNNIGSKSVH (SEQ ID NO: 145)	DDNDRPS (SEQ ID NO: 146)	QVWDYSGQRQV (SEQ ID NO: 147)	SYAMS (SEQ ID NO: 361)	AISGSGGGTYAAS VKG (SEQ ID NO: 362)	GKGVHLGFDY (SEQ ID NO: 363)
Y8P	GGNNIGSKSVH (SEQ ID NO: 307)	DDNDRPS (SEQ ID NO: 308)	QVWDYSPLRHV (SEQ ID NO: 309)	SHAMS (SEQ ID NO: 523)	SISGSGGGTYAAS VKG (SEQ ID NO: 524)	GKGVHLGFDY (SEQ ID NO: 525)
L7E	GGNNIGSKSVH (SEQ ID NO: 115)	DDNDRPS (SEQ ID NO: 116)	QVWDYRTLDWV (SEQ ID NO: 117)	SHAMS (SEQ ID NO: 331)	TISGSGGGTYAAS VKG (SEQ ID NO: 332)	GKGVHLGFDY (SEQ ID NO: 333)
H6N	GGNNIGSKSVH (SEQ ID NO: 121)	DDNDRPS (SEQ ID NO: 122)	QVWDYRTLDWV (SEQ ID NO: 123)	SHAMS (SEQ ID NO: 337)	TISGSGGGTYADS VKG (SEQ ID NO: 338)	GKGVHLGFDY (SEQ ID NO: 339)

Table 2.

Molecule	VL	VH
H6H	DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQ KPGRAPKLLIFAASSLQGGVPSRFSGSGSDFTLTISL QPEDFATYYCQQTYSMPFTFGCGTKVEIK (SEQ ID NO: 628)	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPG KCLEWVGRIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFLQMN SLKTEDTAVYYCTTPSYSGSYNYFSVMDVWGQGTTLTVSS (SEQ ID NO: 629)
N3H	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQ KPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSGQRQVFGCGTKLTVL (SEQ ID NO: 576)	EVQLLESGLLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGK CLEWVSAISGSGGGTYAASVKGRFTISRDNKNTLYLQMSSLR AEDTAVYYCATGKGVHLGFDYWGQGTTLTVSS (SEQ ID NO: 577)
Y8P	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQ KPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTI SRVEAGDEADYYCQVWDYSPLRHVFGCGTKLTVL (SEQ ID NO: 684)	EVQLLESGLLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGK CLEWVSSISGSGGGTYAASVKGRFTISRDNKNTLYLQMNSLR AEDTAVYYCATGKGVHLGFDYWGQGTTLTVSS (SEQ ID NO: 685)
L7E	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQ KPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS RVEAGDEADYYCQVWDYRTLDWVFGCGTKLTVL (SEQ ID NO: 556)	EVQLLESGLLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGK CLEWVSTISGSGGGTYAASVKGRFTISRDNKNTLYLQMNSLR AEDTAVYYCATGKGVHLGFDYWGQGTTLTVSS (SEQ ID NO: 557)
H6N	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQ KPGQAPVMVYDDNDRPSGIPERFSGSNFGNTATLIIS RVEAGDEADYYCQVWDYRTLDWVFGCGTKLTVL (SEQ ID NO: 560)	EVQLLESGLLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGK CLEWVSTISGSGGGTYADSVKGRFTISRDNKNTLYLQMNSLR AEDTAVYYCATGKGVHLGFDYWGQGTTLTVSS (SEQ ID NO: 561)

[0085] In one embodiment, the invention provides an isolated binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises:

- a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region

comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or

b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or

c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or

d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or

e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or

f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or

g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or

h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or

i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or

j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

[0086] In one embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises:

a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or

- b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or
- c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or
- d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or
- f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or
- g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or
- h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or
- i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

[0087] In one embodiment, the invention provides a T-cell receptor (TCR) comprising an isolated binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises:

- a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or
- b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region

comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or

c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or

d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or

e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or

f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or

g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or

h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or

i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or

j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

[0088] In one embodiment, the invention provides an isolated binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain binds to the same epitope as an antibody or antibody construct that comprises:

a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or

b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or

- c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or
- d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or
- f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or
- g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or
- h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or
- i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

[0089] In one embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain binds to the same epitope as an antibody or antibody construct that comprises:

- a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225;
- b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147;
- c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region

comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309;

d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117;

e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123;

f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628;

g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576;

h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685;

i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or

j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

[0090] In one embodiment, the invention provides a T-cell receptor (TCR) comprising an isolated binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain binds to the same epitope as an antibody or antibody construct that comprises:

a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or

b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or

c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or

- d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or
- f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or
- g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or
- h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or
- i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

[0091] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain binds to the same epitope as an antibody or antibody construct that comprises a VH region selected from the group consisting of any VH region and/or a VL region as depicted in any of the sequences in Tables 27 (SEQ ID NOs: 550-697), 35 (SEQ ID NOs: 3083-3118), 43 (SEQ ID NOs: 3979-4010), 51 (SEQ ID NOs: 5023-5118), 57 (SEQ ID NOs: 9351-10066), or 67 (SEQ ID NOs: 16667-16718).

[0092] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain binds to the same epitope as an antibody or antibody construct that comprises a CDR-H1, CDR-H2, CDR-H3 from a VH region selected from the group consisting of any VH region as depicted in any of the sequences in Tables 24 (SEQ ID NOs: 322-537), 32 (SEQ ID NOs: 2984-3064), 40 (SEQ ID NOs: 3891-3962), 48 (SEQ ID NOs: 4759-4974), 56 (SEQ ID NOs: 7561-9350), or 66 (SEQ ID NOs: 16537-16666) and/or further comprises a CDR-L1, CDR-L2, CDR-L3 from a VL region selected from the group consisting of any VL region as depicted in any of the sequences in Tables 23 (SEQ ID NOs: 106-321), 31 (SEQ ID NOs: 2975-3055), 39 (SEQ ID NOs: 3883-3954), 47 (SEQ ID NOs: 4735-4950), 55 (SEQ ID NOs: 7203-8992), or 65 (SEQ ID NOs: 16511-16640).

[0093] In one embodiment, the invention provides an isolated antibody construct comprising a first binding domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises:

- a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or
- b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or
- c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or
- d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or
- f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or
- g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or
- h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or
- i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

and the second binding domain comprises:

k) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 547, CDR-H2 as depicted in SEQ ID NO: 548, and CDR-H3 as depicted in SEQ ID NO: 549, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 541, CDR-L2 as depicted in SEQ ID NO: 542 and CDR-L3 as depicted in SEQ ID NO: 543; or

l) a VH region as depicted in SEQ ID NO: 697, and a VL region as depicted in SEQ ID NO: 696.

[0094] In another embodiment, the invention provides an isolated antibody construct comprising a first binding domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain binds to the same epitope as an antibody or antibody construct that comprises:

a) [H6H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or

b) [N3H] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or

c) [Y8P] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or

d) [L7E] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or

e) [H6N] a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or

f) [H6H] a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or

g) [N3H] a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or

h) [Y8P] a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or

- i) [L7E] a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) [H6N] a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

and the second binding domain comprises:

- k) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 547, CDR-H2 as depicted in SEQ ID NO: 548, and CDR-H3 as depicted in SEQ ID NO: 549, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 541, CDR-L2 as depicted in SEQ ID NO: 542 and CDR-L3 as depicted in SEQ ID NO: 543; or
- l) a VH region as depicted in SEQ ID NO: 697, and a VL region as depicted in SEQ ID NO: 696.

[0095] In another embodiment, the invention provides an isolated antibody construct comprising a first binding domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH region selected from the group consisting of any VH region and/or a VL region as depicted in any of the sequences in Tables 27 (SEQ ID NOs: 550-697), 35 (SEQ ID NOs: 3083-3118), 43 (SEQ ID NOs: 3979-4010), 51 (SEQ ID NOs: 5023-5118), 57 (SEQ ID NOs: 9351-10066), or 67 (SEQ ID NOs: 16667-16718).

[0096] In another embodiment, the invention provides an isolated antibody construct comprising a first binding domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a CDR-H1, CDR-H2, CDR-H3 from a VH region selected from the group consisting of any VH region as depicted in any of the sequences in Tables 24 (SEQ ID NOs: 322-537), 32 (SEQ ID NOs: 2984-3064), 40 (SEQ ID NOs: 3891-3962), 48 (SEQ ID NOs: 4759-4974), 56 (SEQ ID NOs: 7561-9350), or 66 (SEQ ID NOs: 16537-16666) and/or further comprises a CDR-L1, CDR-L2, CDR-L3 from a VL region selected from the group consisting of any VL region as depicted in any of the sequences in Tables 23 (SEQ ID NOs: 106-321), 31 (SEQ ID NOs: 2975-3055), 39 (SEQ ID NOs: 3883-3954), 47 (SEQ ID NOs: 4735-4950), 55 (SEQ ID NOs: 7203-8992), or 65 (SEQ ID NOs: 16511-16640).

[0097] In another embodiment, the invention provides an isolated antibody construct comprising a first binding domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain binds to the same epitope as an antibody or antibody construct that comprises a VH region selected from the group consisting of any VH region and/or a VL region as depicted in any of the sequences in Tables 27 (SEQ ID NOs: 550-697), 35 (SEQ ID NOs: 3083-3118), 43 (SEQ ID NOs: 3979-1010), 51 (SEQ ID NOs: 5023-5118), 57 (SEQ ID NOs: 9351-10066), or 67 (SEQ ID NOs: 16667-16718).

[0098] In another embodiment, the invention provides an isolated antibody construct comprising a first binding domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain binds to the same epitope as an antibody or antibody construct that comprises a CDR-H1, CDR-H2, CDR-H3 from a VH region selected from the group consisting of any VH region as depicted in any of the sequences in Tables 24 (SEQ ID NOs: 322-537), 32 (SEQ ID NOs: 2984-3064), 40 (SEQ ID NOs: 3891-3962), 48 (SEQ ID NOs: 4759-4974), 56 (SEQ ID NOs: 7561-9350), or 66 (SEQ ID NOs: 16537-16666) and/or further comprises a CDR-L1, CDR-L2, CDR-L3 from a VL region selected from the group consisting of any VL region as depicted in any of the sequences in Tables 23 (SEQ ID NOs: 106-321), 31 (SEQ ID NOs: 2975-3055), 39 (SEQ ID NOs: 3883-3954), 47 (SEQ ID NOs: 4735-4950), 55 (SEQ ID NOs: 7203-8992), or 65 (SEQ ID NOs: 16511-16640).

[0099] In a further embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises consensus sequences of any of the VH and/or VL and/or CDRs and/or framework regions set forth in Tables 29 (SEQ ID NOs: 1832-2965), 37 (SEQ ID NOs: 3497-3874), 45 (SEQ ID NOs: 4361-4710), 53 (SEQ ID NOs: 5982-6844), 61 (SEQ ID NOs: 13276-16184), 62 (SEQ ID NOs: 13434-16257), 63 (SEQ ID NOs: 13507-16484), 71 (SEQ ID NOs: 16971-17195), 72 (SEQ ID NOs: 16980-17204), 73 (SEQ ID NOs: 16989-17222), 111, 112, 113, 114, 115, 116, or 117. Note that in the consensus sequence tables herein above (Tables 29, 37, 45, 53, 61, 62, 63, 71, 72, and 73), the "*" found in some of the germline sequences designates a stop codon within the consensus sequence. Tables 111-117 provide consensus sequences from the tables herein above, however, they are in a different format that provides numerical positions for each amino acid residue in the consensus sequence.

[00100] In a specific embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH that comprises the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, and Leu95.

[00101] In a specific embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, or at least fifteen of the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises at least one, at least two, at least three, at least four, at

least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, or at least eighteen of the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, and Leu95.

[00102] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH that comprises the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Ser66, Gly67, Trp90, Tyr92, and Gln95.

[00103] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, or at least fifteen of the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, or at least eighteen of the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Ser66, Gly67, Trp90, Tyr92, and Gln95.

[00104] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH that comprises the following amino acid residues: Ser30, Asn31, Trp33, Arg50, Arg52, Arg54, Ser55, Tyr56, Gly57, Thr59, Tyr103, Ser104, Gly105, Ser106, Tyr107, Tyr108, Asn109, Tyr110, Phe111, and Ser112; and a VL that comprises the following amino acid residues: Ser30, Ser31, Tyr32, Ala50, Ser67, Thr91, Tyr92, Ser93, Met94, and Phe96.

[00105] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, or at least nineteen of the following amino acid residues: Ser30, Asn31, Trp33, Arg50, Arg52, Arg54, Ser55, Tyr56, Gly57, Thr59, Tyr103, Ser104, Gly105, Ser106, Tyr107, Tyr108, Asn109, Tyr110, Phe111, and Ser112; and a VL that comprises at least one, at least two, at least three, at least four, at

least five, at least six, at least seven, at least eight, or at least nine of the following amino acid residues: Ser30, Ser31, Tyr32, Ala50, Ser67, Thr91, Tyr92, Ser93, Met94, and Phe96.

[00106] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Leu95, Asp96, and Trp97.

[00107] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Leu95, Asp96, and Trp97.

[00108] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Gln95, Gln96, and Gln97.

[00109] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Gln95, Gln96, and Gln97.

[00110] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Gln95, Arg96, and Gln97.

[00111] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Gln95, Arg96, and Gln97.

In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Leu95, Arg96, and His97.

[00112] In another embodiment, the invention provides an isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the

binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Leu95, Arg96, and His97.

[00113] In a further embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises consensus sequences of any of the VH and/or VL and/or CDRs and/or framework regions set forth in Tables 29 (SEQ ID NOs: 1832-2965), 37 (SEQ ID NOs: 3497-3874), 45 (SEQ ID NOs: 4361-4710), 53 (SEQ ID NOs: 5982-6844), 61 (SEQ ID NOs: 13276-16184), 62 (SEQ ID NOs: 13434-16257), 63 (SEQ ID NOs: 13507-16484), 71 (SEQ ID NOs: 16971-17195), 72 (SEQ ID NOs: 16980-17204), 73 (SEQ ID NOs: 16989-17222), 111, 112, 113, 114, 115, 116, or 117.

[00114] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH that comprises the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, and Leu95.

[00115] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, or at least fifteen of the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, or at least eighteen of the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, and Leu95.

[00116] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH that comprises the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that

comprises the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Ser66, Gly67, Trp90, Tyr92, and Gln95.

[00117] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, or at least fifteen of the following amino acid residues: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, and Gly105; and a VL that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, or at least eighteen of the following amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Ser66, Gly67, Trp90, Tyr92, and Gln95.

[00118] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH that comprises the following amino acid residues: Ser30, Asn31, Trp33, Arg50, Arg52, Arg54, Ser55, Tyr56, Gly57, Thr59, Tyr103, Ser104, Gly105, Ser106, Tyr107, Tyr108, Asn109, Tyr110, Phe111, and Ser112; and a VL that comprises the following amino acid residues: Ser30, Ser31, Tyr32, Ala50, Ser67, Thr91, Tyr92, Ser93, Met94, and Phe96.

[00119] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, or at least nineteen of the following amino acid residues: Ser30, Asn31, Trp33, Arg50, Arg52, Arg54, Ser55, Tyr56, Gly57, Thr59, Tyr103, Ser104, Gly105, Ser106, Tyr107, Tyr108, Asn109, Tyr110, Phe111, and Ser112; and a VL that comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, or at least nine of the following amino acid residues: Ser30, Ser31, Tyr32, Ala50, Ser67, Thr91, Tyr92, Ser93, Met94, and Phe96.

[00120] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain

comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Leu95, Asp96, and Trp97.

[00121] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Leu95, Asp96, and Trp97.

[00122] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Gln95, Gln96, and Gln97.

[00123] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Gln95, Gln96, and Gln97.

[00124] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Gln95, Arg96, and Gln97.

[00125] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Gln95, Arg96, and Gln97.

[00126] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain comprises a VH from any of the VH sequences provided herein, and a VL that comprises the following amino acid residues: Tyr92, Leu95, Arg96, and His97.

[00127] In another embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the first binding domain

comprises a VH from any of the VH sequences provided herein, and a VL that comprises at least one, at least two, or at least three of the following amino acid residues: Tyr92, Leu95, Arg96, and His97.

[00128] In another specific embodiment, the first domain of the antibody construct binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VH region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein CDR-H3 comprises a lysine at position 2, a valine at position 4, and/or a histidine at position 5.

[00129] In another specific embodiment, the first domain of the antibody construct binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VH region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein CDR-H2 comprises a glycine at position 5 and/or a tyrosine at position 11.

[00130] In another specific embodiment the first domain of the antibody construct binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VL region comprising a CDR-L1, a CDR-L2, and a CDR-L3, wherein CDR-L3 comprises a tryptophan at position 3 and/or a tyrosine at position 5.

[00131] Exemplary bispecific binding molecule full sequences are presented below:

H6H:

MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRIR
 SRSYGGTTDYAAPVKGRFTISRDDSKNTFLQMNLSKTEDAVYYCTTPSYSGSYNYFSVMDVWGQGTITVTVSSGG
 GSGGGGSGGGGSDIQMTQSPSSLSASVGDRTITCRISQSSSYLNWYQQKPGRAKLLFAASSLQGGVPSRFSGS
 GSGTDFTLTISSLQPEDFATYYCQQTYSMPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNK
 YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGN
 SYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQTVVTQEPSTVSPGGTVTLTCSSTGAVTSGNYPNWVQQ
 KPGQAPRGLIGGKFLAPGTPARFSGSLLGGKAALTSVGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKT
 HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR
 CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
 WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGG
 GSGGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
 NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
 HEALHNHYTQKSLSLSPGK
 (SEQ ID NO: 73)

N3H:

MDMRVPAQLLGLLLWLRGARCEVQLLESVGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGS

GGGTYAASVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYCATGKGVHLGFDYWGGQTLTVSSGGGGSGGGSG
GGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATL
TISRVEAGDEADYYCQVWDYSGQRQVFGCGTKLTVLSGGGGSEVQLVESGGGLVQP GGS LKLS CAASGFTFNKYAM
NWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYIS
YWAYWGQGT LTVSSGGGGSGGGSGGGGSQTVVTQEPLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPG
QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKHTCP
PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSG
GGGGSGGGSGGGSGGGSGGGSDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
LHNHYTQKSLSLSPGK

(SEQ ID NO: 47)

Y8P:

MDMRVPAQLLGLLLLWLRGARCEVQLLES GGGLVQP GGS LRLSCAASGFTFSSHAMSWVRQAPGKCLEWVSSISGS
GGGTYAASVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGGQTLTVSSGGGGSGGGGS
GGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTA
TLTISRVEAGDEADYYCQVWDYSPLRHVFGCGTKLTVLSGGGGSEVQLVESGGGLVQP GGS LKLS CAASGFTFNKYA
MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY
ISYWAYWGQGT LTVSSGGGGSGGGSGGGGSQTVVTQEPLTVSPGGTVTLTCSSTGAVTSGNYPNWVQKPG
GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKHTCP
PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGS
GGGGSGGGSGGGSGGGSGGGSDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

(SEQ ID NO: 101)

L7E:

MDMRVPAQLLGLLLLWLRGARCEVQLLES GGGLVQP GGS LRLSCAASGFTFSSHAMSWVRQAPGKCLEWVSTISGS
GGGTYAASVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGGQTLTVSSGGGGSGGGGS

GGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTA
 TLIISRVEAGDEADYYCQVWDYRTLWDVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSAASGFTFNKYA
 MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY
 ISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKP
 GQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKHTHC
 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
 SNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGS
 GGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
 WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMH
 EALHNHYTQKSLSLSPGK

(SEQ ID NO: 37)

H6N:

MDMRVPAQLLGLLLLWLRGARCEVQLLES GGGLVQP GGSLRLSCAASGFTFSSHAMSWVRQAPGKCLEWVSTISGS
 GGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGTTLTVSSGGGGSGGGGS
 GGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFGNTA
 TLIISRVEAGDEADYYCQVWDYRTLWDVFGCGTKLTVLSGGGGSEVQLVESGGGLVQP GGSLKLSAASGFTFNKYA
 MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSY
 ISYWAYWGQGTTLTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCSSTGAVTSGNYPNWWQQKP
 GQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKHTHC
 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVS
 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
 SNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGS
 GGGGSGGGGSGGGGSGGGGSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
 WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMH
 EALHNHYTQKSLSLSPGK

(SEQ ID NO: 39)

[00132] Additional exemplary bispecific binding molecule full sequences of the present invention are presented in Tables 88 (SEQ ID NOs: 17390-17398) and 94 (SEQ ID NOs: 18145-18147) herein.

[00133] In one embodiment, the invention provides an isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second binding domain that binds to human CD3 on the surface of a T cell, wherein the antibody construct comprises:

- a) SEQ ID NO: 73; or
- b) SEQ ID NO: 47; or
- c) SEQ ID NO: 101; or
- d) SEQ ID NO: 37; or
- e) SEQ ID NO: 39.

[00134] Affinity/Potency

[00135] The interaction between the binding domain and the epitope or the region comprising the epitope implies that a binding domain exhibits appreciable affinity for the epitope / the region comprising the epitope on a particular protein or antigen (here: the specific pMAGE-HLA and CD3, respectively, for both binding domains if present) and, unless otherwise specified, does not exhibit significant reactivity with proteins or antigens other than the pMAGE-HLA or CD3. In certain embodiments, only a pMAGE-HLA binding molecule is provided (i.e., the molecule does not also bind to another target such as CD3) and these molecules will exhibit appreciable affinity for the pMAGE-HLA target. This affinity can be measured by various techniques known to one skilled in the art, such as in a surface plasmon resonance assay, such as a Biacore assay, or in a cell based assay.

[00136] "Appreciable affinity" includes binding with an affinity of about 10^{-6} M (KD) or stronger. Preferably, binding is considered specific when the binding affinity is about 10^{-12} to 10^{-8} M, 10^{-12} to 10^{-9} M, 10^{-12} to 10^{-10} M, 10^{-11} to 10^{-8} M, preferably of about 10^{-11} to 10^{-9} M. Whether a binding domain specifically reacts with or binds to a target can be tested readily by, *inter alia*, comparing the reaction of said binding domain with a target protein or antigen with the reaction of said binding domain with proteins or antigens other than the pMAGE-HLA or CD3. Preferably, a binding domain of the invention does not essentially or substantially bind to proteins or antigens other than the pMAGE-HLA or CD3 (i.e., the first binding domain is not capable of binding to proteins other than the pMAGE-HLA and the second binding domain is not capable of binding to proteins other than CD3). In certain embodiments, it is an envisaged characteristic of the antibody constructs according to the present invention to have superior affinity characteristics in comparison to other HLE formats. Such a superior affinity, in consequence, suggests a prolonged half-life *in vivo*. In these embodiments, the longer half-life of the antibody constructs according to the present invention may reduce the duration and frequency of administration which typically contributes to improved patient compliance. This is of particular importance as the antibody constructs of the present invention are particularly beneficial for highly weakened or even multimorbid cancer patients.

[00137] It is notable that the pMAGE-HLA binding molecules of the present invention display surprising potency. This potency displayed by the binding molecules of the invention is a critical attribute for a therapeutic molecule, yet can be quite difficult to achieve without also resulting in off-target binding and associated side-effects and toxicities. This potency can be due to binding to the MAGEB2 peptide of SEQ ID NO: 1, and/or the MAGEA4 peptide of SEQ ID NO: 2, and/or the MAGEA8 peptide of SEQ ID NO: 3, in each case where the peptide is complexed with an HLA and present on the surface of a target cell. In one embodiment, the potency is measured in a cell based assay such as the TDCC assay as described herein, e.g., in the Examples.

[00138] Accordingly, in one embodiment the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <250 pM on endogenous pMAGE-HLA expressing cells. (e.g., cells with an HLA-A*02:01 complexed with a MAGEB2, MAGEA4, or MAGEA8 peptide). In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <200 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <150 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <100 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <50 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <25 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <10 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <5 pM on endogenous pMAGE-HLA expressing cells. In another embodiment, the pMAGE-HLA binding molecules of the present invention have an EC_{50} of <1 pM on endogenous pMAGE-HLA expressing cells.

[00139] Specificity

[00140] The term “does not significantly bind” means that an antibody construct or binding domain of the present invention does not bind to a protein or antigen other than the MAGEB2—HLA peptide complex (pMAGE-HLA) or CD3, when said protein or antigen is expressed on the surface of a cell. For example, an antibody construct or binding domain that exhibits binding to an HLA, e.g., HLA-A1*02:01, that is not presenting a MAGEB2 peptide (i.e., another peptide from the HLA peptidome) would not be a desirable antibody construct or binding molecule. The term “HLA peptidome” refers to a pool of peptides which specifically interact with a particular HLA class and can encompass thousands of different peptide sequences. HLA peptidomes include a diversity of peptides, derived from both normal and abnormal proteins expressed in the cells. In another example, an antibody construct or

binding domain that exhibits binding to an HLA, e.g., HLA-A1*02:01 without any complexed peptide also would not be a desirable antibody construct or binding molecule.

[00141] In the present invention, the pMAGE-HLA binding molecule possesses surprising levels of specificity and selectivity to its target, as evidenced by its lack of binding to target negative cells (e.g., HLA-A*02:01 negative and/or MAGE-B2 negative cells), including those cells that are expressing an HLA and peptides that are similar to the MAGEB2 peptide GVDGEEHSV (SEQ ID NO: 1), and/or the MAGEA4 peptide GVDGREHTV (SEQ ID NO: 2), and/or the MAGEA8 peptide GLYDGREHSV (SEQ ID NO: 3). See, for example, the similar peptides shown in Figure 1, where those similar peptides (e.g., KEA, MB, ADF, DPYSL4, CNPD2, MYOF, COX14, STXBP5, or SLK) complexed with HLA are not specifically bound by the pMAGE-HLA binding molecules of the present invention.

[00142] One skilled in the art would be led to expect quite the opposite. In a recent publication, the specificity of both bispecific T-cell receptors and bispecific antibodies that target peptide-HLA complexes was examined. (see Holland et al., J Clin Invest. 2020). Although favourable properties for the TCR-based molecules were reported, the antibodies that bind the peptide-HLA complex were reportedly much less specific, exhibiting greater levels of cross-reactivity which would not be desirable in a therapeutic molecule.

[00143] This specificity and selectivity is a highly desired, yet difficult to achieve, property for a therapeutic molecule as it limits, reduces, or eliminates off-target binding and any potential associated toxicities or side effects. The pMAGE-HLA binding molecules of the present invention unexpectedly achieve this desired specificity and selectivity.

[00144] In the present invention, it is also quite surprising, however, that the affinities of the various pMAGE-HLA binding molecules do not appear to be determinative for specificity and selectivity. For example, antibodies can possess very similar affinities towards the pMAGE-HLA target as expressed on cells, yet display quite different levels of specificity and selectivity against MAGEB2 negative cell lines. See, for example, Figure 11B.

[00145] Accordingly, in one embodiment, the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >50 nM on target negative cells (e.g., HLA-A*02:01 negative and/or MAGE-B2 negative cells). In another embodiment, the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >45 nM on target negative cells. In another embodiment, the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >40 nM on target negative cells. In another embodiment, the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >35 nM on target negative cells. In another embodiment, the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >30 nM on target negative cells. In another embodiment, the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >25 nM on target negative cells. In another embodiment the selectivity of the pMAGE-HLA binding molecule yields an EC₅₀ that is >20 nM on target negative cells. In another

embodiment the selectivity of the pMAGE-HLA binding molecule yields an EC_{50} that is >15 nM on target negative cells. In another embodiment the selectivity of the pMAGE-HLA binding molecule yields an EC_{50} that is >10 nM on target negative cells. This selectivity can be measured by one skilled in the art using the TDCC assay provided herein in the Examples.

[00146] Specific binding is believed to be effected by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of secondary modifications of said structures. The specific interaction of the antigen-interaction-side with its specific antigen may result in a simple binding of said side to the antigen. Moreover, the specific interaction of the antigen-interaction-side with its specific antigen may alternatively or additionally result in the initiation of a signal, *e.g.* due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

[00147] As discussed herein below regarding the structural analyses, the surprising specificity of the pMAGE-HLA binding molecules of the invention to a difficult target such as the pMAGE-HLA complex may be due to particular structural conformation of the molecule paratope that results in a “hole” that interacts with particular amino acids that protrude out of the pMAGE-HLA complex.

[00148] The first domain of the antibody construct of the invention binds to the pMAGE-HLA on the surface of a target cell. The “target cell” can be any cell expressing or displaying the MAGEB2 peptide on its surface; preferably the target cell is a cell that is part of the human or animal body, such as a specific MAGEB2 expressing cancer or tumor cell or a cell of a MAGEB2 positive neoplasm. It is understood that the term “on the surface”, in the context of the present invention, means that a domain of the antibody construct specifically binds to an epitope that comprises the MAGEB2 peptide (GVYDGEEHSV, SEQ ID NO: 1) complexed with the MHC (pMAGE-HLA) and presented by the MHC molecule on a cell surface. The first domain according to the invention may hence bind to the pMAGE-HLA when it is expressed naturally by MAGEB2 expressing cells or cell lines and/or by cells or cell lines transformed or (stably / transiently) transfected with MAGEB2, or even when the MHC is exogenously loaded with a peptide.

Competitive Binding

[00149] Whether or not an antibody or antibody construct competes for binding to an antigen (such as a pMAGE-HLA) on the surface of a target cell with another given antibody or antibody construct can be measured in a competition assay such as a competitive ELISA. Avidin-coupled microparticles (beads) can also be used. Similar to an avidin-coated ELISA plate, when reacted with a biotinylated protein, each of these beads can be used as a substrate on which an assay can be performed. Antigen is coated onto a bead and then precoated with the first antibody. The second antibody is added, and any additional binding is determined. Read-out occurs via flow cytometry. Preferably a cell-based competition assay is used, using either cells that naturally express MAGEB2 and

HLA, or cells that were stably or transiently transformed with MAGEB2 and/or HLA. The term “competes for binding”, in the present context, means that competition occurs between the two tested antibodies of at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80% or at least 90%, as determined by any one of the assays disclosed above, preferably the cell-based assay. The same analysis can of course be applied for other targets such as CD3.

[00150] Competitive antibody binding assays include assays determining the competitive binding of two antibodies/ antibody constructs to a cell surface bound antigen. Common methods aim to detect binding of two antibodies/ antibody constructs, A and B, to the same antigen on the surface of a cell may include steps of:

- a) blocking of the cell surface antigen by pre-incubation of cells with antibody/ antibody construct A followed by a sub-maximal addition of labeled antibody/ antibody construct B and detecting the binding of B compared with binding in the absence of A;
- b) titration (i.e. adding different amounts) of antibody/ antibody construct A in the presence of sub-maximal amounts of labeled antibody/ antibody construct B and detecting the effect on binding of B; or
- c) co-titration of A and B, wherein both antibodies/ antibody constructs are incubated together at maximal concentration and detecting whether the total binding equals or exceeds that of either A or B alone, i.e. a method which cannot be affected by the order of addition or relative amounts of the antibodies/ antibody constructs.

[00151] When two antibodies/ antibody constructs A and B compete for a cell surface bound antigen, the antibodies will very often compete with each other in blocking assays independently from the order of the addition of the antibodies. In other words, competition is detected if the assay is carried out in either direction. However, this is not always the case, and under certain circumstances the order of the addition of the antibodies or the direction of the assay may have an effect on the signal generated. This may be due to differences in affinities or avidities of the potentially competing antibodies/ antibody constructs. If the order of the addition has a significant effect on the signal generated, it is concluded that the two antibodies/antibody constructs do compete if competition is detected in at least one order.

Epitope Amino Acid Residues

[00152] The term “epitope” refers to a region on an antigen, or specific amino acid residues, to which a binding domain, such as an antibody or immunoglobulin, or a derivative, fragment or variant of an antibody or an immunoglobulin, specifically binds. An “epitope” is antigenic and thus the term epitope is sometimes also referred to herein as “antigenic structure” or “antigenic determinant”.

Thus, the binding domain is an “antigen interaction site”. Said binding/interaction is also understood to define a “specific recognition”.

[00153] “Epitopes” can be formed both by contiguous amino acids or non-contiguous amino acids juxtaposed by tertiary folding of a protein. A “linear epitope” is an epitope where a contiguous amino acid primary sequence comprises the recognized epitope. A linear epitope typically includes at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

[00154] A “conformational epitope”, in contrast to a linear epitope, is an epitope wherein the primary sequence of the amino acids comprising the epitope is not the sole defining component of the epitope recognized (e.g., an epitope wherein the primary sequence of amino acids is not necessarily recognized by the binding domain). Typically, a conformational epitope comprises an increased number of amino acids relative to a linear epitope, and comprises noncontiguous amino acid sequences. With regard to recognition of conformational epitopes, the binding domain paratope recognizes a three-dimensional structure of the antigen, preferably a peptide or protein or fragment thereof (in the context of the present invention, the antigenic structure for one of the binding domains is comprised within the target cell surface antigen protein). For example, when a protein molecule folds to form a three-dimensional structure, certain amino acids and/or the polypeptide backbone forming the conformational epitope become juxtaposed enabling the antibody to recognize the epitope. Methods of determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy.

[00155] In one embodiment of the present invention, the epitope comprises the MAGEB2 peptide GGYDGEHSV (SEQ ID NO: 1) complexed with an HLA molecule on a cell surface. In some embodiments, the antibody construct binds an epitope comprising only amino acid residues of the MAGEB2 peptide of SEQ ID NO: 1. In other embodiments, the antibody construct binds an epitope comprising the MAGEB2 peptide of SEQ ID NO: 1 and also comprising at least some amino acid residues of the HLA that is complexed with, i.e., presenting, the MAGEB2 peptide GGYDGEHSV (SEQ ID NO: 1).

[00156] Structural analysis of the interaction between the target polypeptide and binding domain of, for example, a BiTE® molecule contemplated herein provides amino acid residues of the target epitope involved with the binding interaction. Further, whether or not an antibody, antibody construct or binding domain binds to the same epitope of a pMAGE-HLA on the surface of a target cell as another given antibody, antibody construct or binding domain can be measured by different analyses as described herein. For example, in certain embodiments, the crystal structure of the target-binder interaction can provide these amino acid residues. In other embodiments, various other

analyses can be performed to ascertain amino acid residues involved in the binding interaction. For example, *in silico* modeling and analysis, Xscan, alanine scanning, arginine scanning, epitope mapping, and other techniques known to those skilled in the art.

[00157] In the context of the present invention where the MAGEB2 peptide or other MAGE peptide sequence is short, e.g., only ten amino acids for GGYDGEHVS (SEQ ID NO: 1), a more useful to determine the contribution of a specific residue of MAGEB2 or the MAGEB2 specific peptide to the recognition by an antibody construct or binding domain is a technique known as Xscan, which is known to those skilled in the art. X-scan is a peptide analysis technique where each amino acid residue of the peptide to be analyzed is mutated to all possible amino acids in turn. In certain instances, this approach can provide significantly enhanced sensitivity and specificity for detection of tolerated substitutions, or those substitutions that are not tolerated. A position is considered essential for binding in X-scan analysis if most amino acid substitutions are not allowed. In alternative embodiments of X-scan analysis, particular anchor residues within the peptide are not mutated.

[00158] These structural analyses presented herein in Examples 6-10 and 14 provide insight into why our pMAGE-HLA binding molecules have such surprising specificity. In certain determined molecule structures as depicted, it appears that the pMAGE-HLA complex has a small “groove” or a “cleft” on the surface caused by the protruding conformation of the 10-mer MAGEB2 peptide bound to the peptide-binding groove of the HLA, presenting a complementary and quite unexpected and remarkable surface for the pMAGE-HLA binders to specifically recognize.

[00159] The various MAGEB2 residues (1-10) all appear to contribute in varying ways to the target epitope of the pMAGE-HLA complex. Accordingly, in one embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide GGYDGEHVS (SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or ten of the amino acid residues Gly1, Val2, Tyr3, Asp4, Gly5, Glu6, Glu7, His8, Ser9, and/or Val10 of the MAGEB2 peptide is/are essential for the binding of a first domain. In this context, the term “is essential for the binding” means that the specified amino acid is necessary for the binding of the antibody construct binding domain to a MAGEB2 peptide to occur.

[00160] According to another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, at least twenty, at least twenty one, at least twenty two, at least twenty three, at least twenty four, at least twenty five, at least twenty six, at least twenty seven, at least

twenty eight, at least twenty nine, or at least thirty of the amino acid residues Arg65, Lys66, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Glu154, Gln155, Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Lys68, Ser71, Arg75, Gly79, Thr80, Arg82, Gly83, and/or Glu89 of the MHC is essential for the binding of the first domain. In this context, the term “is essential for the binding” means that the specified amino acid is necessary for the binding of the antibody construct binding domain to the MHC to occur.

[00161] In further embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, at least twenty, at least twenty one, at least twenty two, at least twenty three, or at least twenty four of the amino acid residues Glu55, Glu58, Tyr59, Asp61, Gly62, Glu63, Arg65, Lys66, Ala69, Ala158, Gly162, Thr163, Glu166, Trp167, Arg170 and also Gln54, Glu55, Gly56, Pro57, Glu58, Tyr59, Trp167, Arg170.

Paratope Amino Acid Residues

[00162] The region of the binding domain that binds to the epitope is called a “paratope.” Specific binding is believed to be accomplished by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of potential secondary modifications of said structures. As described above, structural analysis of the interaction between the target polypeptide and binding domain of, for example, a BiTE® molecule contemplated herein provides amino acid residues of the binding molecule paratope involved with the binding interaction with the target epitope. This structural analysis can be performed using the methods already described, e.g., crystal structure analysis or alanine scanning.

[00163] In one embodiment, the binding domain of an antibody construct binds to a human MAGEB2 peptide complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein the paratope comprises at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, at least twenty, at least twenty one, at least twenty two, at least twenty three, at least twenty four, at least twenty five, at least twenty six, at least twenty seven, at least twenty eight, at least twenty nine, at least thirty, at least thirty one, at least thirty two, at least thirty three, at least thirty four, or at least thirty five of the following amino acid residues:

Heavy Chain: Ser30, Ser31, His32, Tyr32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, or Gly105

Light Chain: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Phe66, Ser66, Gly67, Trp90, Tyr92, Arg93, Leu95, Gln95

[00164] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, or at least thirteen of the amino acid residue(s) Ser30, Ser31, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Val102, His103, Leu104, or Gly105 of the heavy chain is/are essential for the binding of the first domain to the MHC.

[00165] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve of the amino acid residue(s) Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Lys100, Gly101, Val102, His103, or Leu104 of the heavy chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00166] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, or at least sixteen of the amino acid residue(s) Trp33, Arg50, Arg52, Ser55, Tyr56, Gly57, Thr59, Tyr103, Gly105, Ser106, Tyr107, Tyr108, Asn109, Tyr110, Phe111, or Ser112 of the heavy chain is/are essential for the binding of the first domain to the MHC.

[00167] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or at least twenty of the amino acid residue(s) Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, Leu95 of the light chain is/are essential for the binding of the first domain MHC.

[00168] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a

target cell (pMAGE-HLA), wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, or at least ten of the amino acid residue(s) Ser30, Ser31, Tyr32, Ala50, Ser67, Thr91, Tyr92, Ser93, Met94, or Phe96 of the light chain is/are essential for the binding of the first domain MHC.

[00169] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide GVDGEEHSV (SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residue Trp90 of the light chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00170] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, or at least thirteen of the amino acid residue(s) Ser30, Ser31, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Val102, His103, Leu104, Gly105 of the heavy chain is/are essential for the binding of the first domain to the MHC.

[00171] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve of the amino acid residue(s) Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Lys100, Gly101, Val102, His103, or Leu104 of the heavy chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00172] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve of the amino acid residue(s) Ser30, Asn31, Arg54, Ser55, Tyr56, Ser104, Gly105, Ser106, or Tyr110 of the heavy chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00173] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, at least nineteen, or at least twenty of the amino acid residue(s) Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, Leu95 of the light chain is/are essential for the binding of the first domain MHC.

[00174] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residue Trp90 of the light chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00175] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at positions 92, 95, 96, or 97 of the light chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00176] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 92 of the light chain is Trp, Tyr, Phe, Leu, Arg, Met, Gln, or Glu.

[00177] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 92 of the light chain is Trp, Phe, Tyr, Leu, Glu, Gln, Arg, or Met.

[00178] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 92 of the light chain is Phe, Trp, Ile, Val, or Tyr.

[00179] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 92 of the light chain is Tyr, Trp, Phe, His, or Arg.

[00180] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 92 of the light chain is selected from any of those set forth as predicted alternatives in Figures 47-50 herein.

[00181] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 95 of the light chain is Trp, Tyr, Phe, Arg, Met, Lys, or Gln.

[00182] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 95 of the light chain is Trp, Phe, Met, Tyr, Gln, Arg, His, or Leu.

[00183] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 95 of the light chain is Trp, Arg, Tyr, Leu, Phe, Cys, or Met.

[00184] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 95 of the light chain is selected from any of those set forth as predicted alternatives in Figures 47-50 herein.

[00185] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 96 of the light chain is Met, Asn, His, or Asp.

[00186] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 96 of the light chain is Ile, Met, Leu, Thr, or His.

[00187] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 96 of the light chain is selected from any of those set forth as predicted alternatives in Figures 47-50 herein.

[00188] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 97 of the light chain is Tyr, Phe, Ile, Met, His, Asn, Ala, or Ser.

[00189] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 97 of the light chain is Val, His, or Lys.

[00190] In another embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 97 of the light chain is Phe, Tyr, Leu, Ile, Lys, or Val.

[00191] In a specific embodiment, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residues at position 97 of the light chain is selected from any of those set forth as predicted alternatives in Figures 47-50 herein.

[00192] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a

target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, or at least thirteen of the amino acid residue(s) Ser30, Ser31, Tyr32, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, His103, Leu104, or Gly105 of the heavy chain is/are essential for the binding of the first domain to the MHC.

[00193] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, or at least twelve of the amino acid residue(s) Ser30, Ser31, Tyr32, Ala33, Ser52, Gly53, Ser54, Lys100, Gly101, Val102, His103, or Leu104 of the heavy chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00194] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein at least one, at least two, at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, at least eleven, at least twelve, at least thirteen, at least fourteen, at least fifteen, at least sixteen, at least seventeen, at least eighteen, or at least nineteen of the amino acid residue(s) Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Ser66, Gly67, Trp90, Tyr92, or Gln95 of the light chain is/are essential for the binding of the first domain MHC.

[00195] In other embodiments, the first domain of the antibody construct of the invention binds to a human MAGEB2 peptide (e.g., SEQ ID NO: 1) complexed with an HLA on the surface of a target cell, wherein the amino acid residue at least one and/or at least two of the amino acid residues Trp90 or Gln95 of the light chain is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00196] In another specific embodiment, the first domain of the antibody construct binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VH region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein CDR-H3 comprises a lysine at position 2, a valine at position 4, and/or a histidine at position 5 that is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00197] In another specific embodiment, the first domain of the antibody construct binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VH region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein CDR-H2 comprises a glycine at position 5 and/or a tyrosine at position 11 that is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00198] In another specific embodiment the first domain of the antibody construct binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VL region comprising a CDR-L1, a CDR-L2, and a CDR-L3, wherein CDR-L3 comprises a tryptophan at position 3 and/or a tyrosine at position 5 that is/are essential for the binding of the first domain to the MAGEB2 peptide.

[00199] In this context, the term “is essential for the binding” means that the specified amino acid, or functional equivalents thereof, is necessary for the binding of the antibody construct binding domain to the target (e.g., the MAGEB2 peptide complexed with an HLA on the surface of a target cell) to occur.

CD3 Mechanism of cell killing

[00200] In embodiments where the antibody constructs comprise a second domain that binds to CD3, the mechanism for cell killing will be T cell mediated in most instances. T cells or T lymphocytes are a type of lymphocyte (itself a type of white blood cell) that play a central role in cell-mediated immunity. There are several subsets of T cells, each with a distinct function. T cells can be distinguished from other lymphocytes, such as B cells and NK cells, by the presence of a T cell receptor (TCR) on the cell surface. The TCR is responsible for recognizing antigens bound to major histocompatibility complex (MHC) molecules and is composed of two different protein chains. In 95% of the T cells, the TCR consists of an alpha (α) and beta (β) chain. When the TCR engages with antigenic peptide and MHC (peptide / MHC complex), the T lymphocyte is activated through a series of biochemical events mediated by associated enzymes, co-receptors, specialized adaptor molecules, and activated or released transcription factors.

[00201] In one embodiment, it is envisaged that the second domain of the antibody constructs of the invention binds to an extracellular epitope of the human and/or the Macaca CD3 ϵ chain.

[00202] The CD3 receptor complex is a protein complex and is composed of four chains. In mammals, the complex contains a CD3 γ (gamma) chain, a CD3 δ (delta) chain, and two CD3 ϵ (epsilon) chains. These chains associate with the T cell receptor (TCR) and the so-called ζ (zeta) chain to form the T cell receptor CD3 complex and to generate an activation signal in T lymphocytes. The CD3 γ (gamma), CD3 δ (delta), and CD3 ϵ (epsilon) chains are highly related cell-surface proteins of the immunoglobulin superfamily containing a single extracellular immunoglobulin domain. The intracellular tails of the CD3 molecules contain a single conserved motif known as an immunoreceptor tyrosine-based activation motif or ITAM for short, which is essential for the signaling capacity of the TCR. The CD3 epsilon molecule is a polypeptide which in humans is encoded by the CD3E gene which resides on chromosome 11. The most preferred epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain. It is envisaged that antibody constructs

according to the present invention typically and advantageously show less unspecific T cell activation, which is not desired in specific immunotherapy. This translates to a reduced risk of side effects.

[00203] The redirected lysis of target cells via the recruitment of T cells by a multispecific, at least bispecific, antibody construct involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis, and are not typically affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see, for example, WO 2007/042261. However, loss of MAGEB2 expression or even loss of MHC class I expression by tumor cells may be a possible escape mechanism.

CD3 Binding

[00204] The second domain of the antibody construct of the invention binds to CD3. More preferably, it binds to CD3 on the surface of a T cell. It is furthermore envisaged that the second domain binds to human CD3, preferably to human CD3 on the surface of a T cell. It is also envisaged that the second domain binds to CD3 epsilon. More preferably, it binds to human CD3 epsilon, e.g. to human CD3 epsilon on the surface of a T cell.

[00205] The CD3 binding domain of the antibody construct of the invention is/are preferably cross-species specific for members of the mammalian order of primates. Cross-species specific CD3 binding domains are, for example, described in WO 2008/119567. According to one embodiment, the CD3 binding domain, in addition to binding to human CD3, will also bind to CD3 of primates including (but not limited to) new world primates (such as *Callithrix jacchus*, *Saguinus Oedipus* or *Saimiri sciureus*), old world primates (such baboons and macaques), gibbons, and non-human homininae.

[00206] In one embodiment of the present invention, the second domain of the antibody construct binds to human CD3 epsilon (or human CD3 epsilon on the surface of a T cell) and to *Callithrix jacchus* or *Saimiri sciureus* CD3 epsilon. It is also envisaged that the second domain binds to an extracellular epitope of CD3 epsilon, preferably to an extracellular epitope of human CD3 epsilon. It is also envisaged that the second domain binds to an extracellular epitope of the human and the *Macaca* CD3 epsilon chain. One preferred epitope of CD3 epsilon is comprised within amino acid residues 1-27 of the human CD3 epsilon extracellular domain. Even more specifically, the epitope comprises at least the amino acid sequence Gln-Asp-Gly-Asn-Glu (SEQ ID NO: 18452). *Callithrix jacchus* is a new world primate belonging to the family of Callitrichidae, while *Saimiri sciureus* is a new world primate belonging to the family of Cebidae. Binders having such characteristics are described in detail in WO 2008/119567.

[00207] Antibodies or bispecific antibody constructs directed against (human) CD3 or specifically against CD3 epsilon are known in the art, and their CDRs, VH and VL sequences can serve as a basis for the second binding domain of the antibody construct of the invention. For example, Kung et al. reported in 1979 the development of OKT3 (Ortho Kung T3), the first mAb recognizing CD3 (specifically, the epsilon chain of CD3) on human T cells. OKT3 (muromonab) was the first monoclonal antibody of murine origin to become available for therapy in humans. Newer anti-CD3 monoclonal antibodies include orelizumab (TRX4), teplizumab (MGA031), foralumab and visilizumab, all targeting the epsilon chain of CD3. Bispecific antibody constructs directed against a (cancer) target and CD3 are also being developed and (pre-)clinically tested, and their CD3 binding domain (CDRs, VH, VL) may serve as a basis for the second binding domain of the antibody construct of the invention. Examples include, but are not limited to, Blinatumomab, Solitomab (MT110, AMG 110), Catumaxomab, Duvortuxizumab, Ertumaxomab, Mosunetuzumab, FBTA05 (Bi20, TPBs05), CEA-TCB (RG7802, RO6958688), AFM11, and MGD006 (S80880). Other examples of CD3 binding domains are disclosed e.g. in US 7,994,289 B2, US 7,728,114 B2, US 7,381,803 B1, US 6,706,265 B1.

[00208] It is envisaged for the antibody construct of the present invention that the second domain which binds to CD3 on the surface of a T cell comprises a VL region comprising a CDR-L1 (SEQ ID NO: 541), a CDR-L2 (SEQ ID NO: 542) and aCDR-L3 (SEQ ID NO: 543) and a VH region comprising CDR-H1 (SEQ ID NO: 547), CDR-H2 (SEQ ID NO: 548) and CDR-H3 (SEQ ID NO: 549).

[00209] It is envisaged for the antibody construct of the present invention that the second domain which binds to CD3 on the surface of a T cell comprises a VL (SEQ ID NO: 696) region and a VH region (SEQ ID NO: 697).

[00210] In some embodiments, the second domain of the antibody construct of the invention binds to human CD3 epsilon and/or to Macaca CD3 epsilon. In a preferred embodiment the second domain further binds to Callithrix jacchus, Saguinus Oedipus or Saimiri sciureus CD3 epsilon. Callithrix jacchus and Saguinus oedipus are both new world primate belonging to the family of Callitrichidae, while Saimiri sciureus is a new world primate belonging to the family of Cebidae.

[00211] In one embodiment, the antibody construct of the present invention the second domain which binds to an extracellular epitope of the human and/or the Macaca CD3 epsilon chain comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

- (a) CDR-L1 as depicted in SEQ ID NO: 27 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 28 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 29 of WO 2008/119567;
- (b) CDR-L1 as depicted in SEQ ID NO: 117 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 118 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 119 of WO 2008/119567; and
- (c) CDR-L1 as depicted in SEQ ID NO: 153 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 154 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 155 of WO 2008/119567.

[00212] In another embodiment of the antibody construct of the present invention, the second domain which binds to an extracellular epitope of the human and/or the Macaca CD3 epsilon chain comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:

- (a) CDR-H1 as depicted in SEQ ID NO: 12 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 13 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 14 of WO 2008/119567;
- (b) CDR-H1 as depicted in SEQ ID NO: 30 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 31 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 32 of WO 2008/119567;
- (c) CDR-H1 as depicted in SEQ ID NO: 48 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 49 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 50 of WO 2008/119567;
- (d) CDR-H1 as depicted in SEQ ID NO: 66 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 67 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 68 of WO 2008/119567;
- (e) CDR-H1 as depicted in SEQ ID NO: 84 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 85 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 86 of WO 2008/119567;
- (f) CDR-H1 as depicted in SEQ ID NO: 102 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 103 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 104 of WO 2008/119567;
- (g) CDR-H1 as depicted in SEQ ID NO: 120 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 121 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 122 of WO 2008/119567;
- (h) CDR-H1 as depicted in SEQ ID NO: 138 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 139 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 140 of WO 2008/119567;
- (i) CDR-H1 as depicted in SEQ ID NO: 156 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 157 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 158 of WO 2008/119567; and
- (j) CDR-H1 as depicted in SEQ ID NO: 174 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 175 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 176 of WO 2008/119567.

[00213] In another embodiment of the antibody construct of the invention the above described three groups of VL CDRs are combined with the above described ten groups of VH CDRs within the second binding domain to form (30) groups, each comprising CDR-L 1-3 and CDR-H 1-3.

[00214] It is preferred for the antibody construct of the present invention that the second domain which binds to CD3 comprises a VL region selected from the group consisting of those depicted in SEQ ID NOs: 17, 21, 35, 39, 53, 57, 71, 75, 89, 93, 107, 111, 125, 129, 143, 147, 161, 165, 179 or 183 of WO 2008/119567 or as depicted in SEQ ID NO: 696 according to the present invention.

[00215] It is also preferred that the second domain which binds to CD3 comprises a VH region selected from the group consisting of those depicted in SEQ ID NO: 15, 19, 33, 37, 51, 55, 69, 73, 87, 91, 105, 109, 123, 127, 141, 145, 159, 163, 177 or 181 of WO 2008/119567 or as depicted in SEQ ID NO: 697 according to the present invention.

[00216] More preferably, the antibody construct of the present invention is characterized by a second domain which binds to CD3 comprising a VL region and a VH region selected from the group consisting of:

- (a) a VL region as depicted in SEQ ID NO: 17 or 21 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 15 or 19 of WO 2008/119567;
- (b) a VL region as depicted in SEQ ID NO: 35 or 39 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 33 or 37 of WO 2008/119567;
- (c) a VL region as depicted in SEQ ID NO: 53 or 57 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 51 or 55 of WO 2008/119567;
- (d) a VL region as depicted in SEQ ID NO: 71 or 75 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 69 or 73 of WO 2008/119567;
- (e) a VL region as depicted in SEQ ID NO: 89 or 93 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 87 or 91 of WO 2008/119567;
- (f) a VL region as depicted in SEQ ID NO: 107 or 111 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 105 or 109 of WO 2008/119567;
- (g) a VL region as depicted in SEQ ID NO: 125 or 129 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 123 or 127 of WO 2008/119567;
- (h) a VL region as depicted in SEQ ID NO: 143 or 147 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 141 or 145 of WO 2008/119567;
- (i) a VL region as depicted in SEQ ID NO: 161 or 165 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 159 or 163 of WO 2008/119567; and
- (j) a VL region as depicted in SEQ ID NO: 179 or 183 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 177 or 181 of WO 2008/119567.

[00217] Also preferred in connection with the antibody construct of the present invention is a second domain which binds to CD3 comprising a VL region as depicted in SEQ ID NO: 696 and a VH region as depicted in SEQ ID NO: 697 of the present invention.

[00218] In other embodiments, the antibody construct of the present invention is characterized by a second domain which binds to CD3 comprising a VL region and a VH region selected from any of those presented in Tables 80 (SEQ ID NOs: 17230-17231), 85 (SEQ ID NOs: 17302-17305), 91 (SEQ ID NOs: 17507-17542), or 97 (SEQ ID NOs: 18184-18195) herein.

[00219] In yet other embodiments, the antibody construct of the present invention is characterized by a second domain which binds to CD3 comprising a VL region and a VH region which comprise CDRs selected from those presented in Tables 79 (SEQ ID NOs: 17224-17229), 84 (SEQ ID

NOs: 17290-17301), 89 (SEQ ID NOs: 17399-17488), 90 (SEQ ID NOs: 17417-17506), 95 (SEQ ID NOs: 18148-18177), or 96 (SEQ ID NOs: 18154-18183) herein.

[00220] In other embodiments, the antibody construct of the present invention is characterized by a second domain which binds to CD3 comprising a sequence selected from those presented in Tables 78 (SEQ ID NOs: 17223) or 83 (SEQ ID NOs: 17288-17289).

[00221] In yet other embodiments, the antibody construct of the present invention is characterized by a second domain which binds to CD3 comprising a sequence disclosed in U.S. Provisional Patent Application No. 63/110,545, entitled "Polypeptide Constructs Binding to CD3."

Antibody Constructs

[00222] In one embodiment, the present invention provides an antibody construct comprising a first domain which binds to a pMAGE-HLA complex on the surface of a target cell and a second domain which binds to CD3 on the surface of a T-cell.

[00223] The term "antibody construct" refers to a molecule in which the structure and/or function is/are based on the structure and/or function of an antibody, *e.g.*, of a full-length or whole immunoglobulin molecule. An antibody construct is capable of binding to its specific target or antigen and comprises the variable heavy chain (VH) and/or variable light chain (VL) domains of an antibody or fragment thereof. Furthermore, the domain which binds to its binding partner according to the present invention is understood herein as a binding domain of an antibody construct according to the invention. Typically, a binding domain according to the present invention comprises the minimum structural requirements of an antibody which allow for the target binding. This minimum requirement may *e.g.* be defined by the presence of at least the three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or the three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region), preferably of all six CDRs. An alternative approach to define the minimal structure requirements of an antibody is the definition of the epitope the antibody binds within the structure of a specific target, respectively, the protein domain of the target protein composing the epitope region (epitope cluster) or by reference to a specific antibody competing with the epitope of the defined antibody. Alternatively, the minimal structure requirements may be defined by the paratope sequences within the binding domain of the antibody. The antibodies on which the constructs according to the invention are based include for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies.

[00224] The term "variable" refers to the portions of the antibody or immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody (i.e., the "variable domain(s)"). The pairing of a variable heavy chain (VH) and a variable light chain (VL) together forms an antigen-binding site.

[00225] Variability is not evenly distributed throughout the variable domains of antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-domains are called “hypervariable regions” or “complementarity determining regions” (CDRs). The more conserved (i.e., non-hypervariable) portions of the variable domains are called the “framework” regions (FRM or FR) and provide a scaffold for the six CDRs in three dimensional space to form an antigen-binding surface. The variable domains of naturally occurring heavy and light chains each comprise four FRM regions (FR1, FR2, FR3, and FR4), largely adopting a β -sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β -sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding side (see Kabat et al., loc. cit.).

[00226] The terms “CDR”, and its plural “CDRs”, refer to the complementarity determining region of which three make up the binding character of a light chain variable region (CDR-L1, CDR-L2 and CDR-L3) and three make up the binding character of a heavy chain variable region (CDR-H1, CDR-H2 and CDR-H3). CDRs contain most of the residues responsible for specific interactions of the antibody with the antigen and hence contribute to the functional activity of an antibody molecule: they are the main determinants of antigen specificity.

[00227] The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called “hypervariable regions” within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat (an approach based on cross-species sequence variability), Chothia (an approach based on crystallographic studies of antigen-antibody complexes), and/or MacCallum (Kabat et al., loc. cit.; Chothia et al., J. Mol. Biol, 1987, 196: 901-917; and MacCallum et al., J. Mol. Biol, 1996, 262: 732). Still another standard for characterizing the antigen binding side is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, e.g., Protein Sequence and Structure Analysis of Antibody Variable Domains. In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg). To the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, the numbering in accordance with the Kabat system is preferred.

[00228] Typically, CDRs form a loop structure that can be classified as a canonical structure. The term “canonical structure” refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen

binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia et al., Nature, 1989, 342: 877; Martin and Thornton, J. Mol. Biol, 1996, 263: 800). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (i.e., outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues.

[00229] The term “canonical structure” may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat et al., loc. cit.). The Kabat numbering scheme (system) is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner and is the preferred scheme applied in the present invention as also mentioned elsewhere herein. Additional structural considerations can also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering can be described by the numbering system of Chothia et al. and/or revealed by other techniques, for example, crystallography and two- or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (e.g., based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia et al., loc. cit. and their implications for construing canonical aspects of antibody structure, are described in the literature. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, eds. Harlow et al., 1988.

[00230] In some embodiments, the CDR3 of the light chain and, particularly, the CDR3 of the heavy chain may constitute the most important determinants in antigen binding within the light and heavy chain variable regions. In some antibody constructs, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. *In vitro* selection schemes in which CDR3 alone is varied can be used to vary the binding properties of an antibody or determine which residues contribute to the binding of an antigen. Hence, CDR3 is often the greatest source of molecular diversity within the antibody-binding side. H3, for example, can be as short as two amino acid residues or greater than 26 amino acids.

[00231] The sequence of antibody genes after assembly and somatic mutation is highly varied, and these varied genes are estimated to encode 10¹⁰ different antibody molecules (Immunoglobulin Genes, 2nd ed., eds. Jonio et al., Academic Press, San Diego, CA, 1995). Accordingly, the immune system provides a repertoire of immunoglobulins. The term "repertoire" refers to at least one nucleotide sequence derived wholly or partially from at least one sequence encoding at least one immunoglobulin. The sequence(s) may be generated by rearrangement *in vivo* of the V, D, and J segments of heavy chains, and the V and J segments of light chains. Alternatively, the sequence(s) can be generated from a cell in response to which rearrangement occurs, e.g., *in vitro* stimulation. Alternatively, part or all of the sequence(s) may be obtained by DNA splicing, nucleotide synthesis, mutagenesis, and other methods, see, e.g., U.S. Patent 5,565,332. A repertoire may include only one sequence or may include a plurality of sequences, including ones in a genetically diverse collection.

[00232] Antibody constructs of the present invention comprise at least one binding domain. The term "binding domain" characterizes in connection with the present invention a domain which specifically binds to, interacts with, or recognizes a given target epitope or a given target region on the target molecule, e.g., pMAGE-HLA or CD3. The structure and function of the first binding domain (recognizing pMAGE-HLA), and also the structure and/or function of the second binding domain (recognizing CD3), is based on the structure and/or function of an antibody, e.g. of a full-length or whole immunoglobulin molecule, and is from the variable heavy chain (VH) and/or variable light chain (VL) domains of an antibody or fragment thereof. In certain embodiments, the first binding domain comprises the presence of three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). The second binding domain, if present, comprises at least three light chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VL region) and/or three heavy chain CDRs (i.e. CDR1, CDR2 and CDR3 of the VH region). In certain embodiments, the first and/or second binding domain is produced by or obtainable by phage-display or library screening methods rather than by grafting CDR sequences from a pre-existing (monoclonal) antibody into a scaffold.

[00233] The binding domain of an antibody construct according to the invention may, e.g., comprise the above referred groups of CDRs. Preferably, those CDRs are comprised in the framework of an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both. Fd fragments, for example, have two VH regions and often retain some antigen-binding function of the intact antigen-binding domain. Additional examples for the format of antibody fragments, antibody variants or binding domains include (1) a Fab fragment, a monovalent fragment having the VL, VH, CL and CH1 domains; (2) a F(ab')₂ fragment, a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; (3) an Fd fragment having the two VH and CH1 domains; (4) an Fv fragment having the VL and VH domains of a single arm

of an antibody, (5) a dAb fragment (Ward et al., (1989) Nature 341 :544-546), which has a VH domain; (6) an isolated complementarity determining region (CDR), and (7) a single chain Fv (scFv) , the latter being preferred (for example, derived from an scFv-library). Nonlimiting examples for embodiments of antibody constructs according to the invention are e.g. described in WO 00/006605, WO 2005/040220, WO 2008/119567, WO 2010/037838, WO 2013/026837, WO 2013/026833, US 2014/0308285, US 2014/0302037, WO 2014/144722, WO 2014/151910, and WO 2015/048272.

[00234] Also within the definition of “binding domain” or “domain which binds” are fragments of full-length antibodies, such as VH, VHH, VL, (s)dAb, Fv, light chain (VL-CL), Fd (VH-CH1), heavy chain, Fab, Fab', F(ab')₂ or “r IgG” (“half antibody” consisting of a heavy chain and a light chain). Antibody constructs according to the invention may also comprise modified fragments of antibodies, also called antibody variants or antibody derivatives. Examples include, but are not limited to, scFv, di-scFv or bi(s)-scFv, scFv-Fc, scFv-zipper, scFab, Fab₂, Fab₃, diabodies, single chain diabodies, tandem diabodies (Tandab's), tandem di-scFv, tandem tri-scFv, „minibodies“ exemplified by a structure which is as follows: (VH-VL-CH3)₂, (scFv-CH3)₂, ((scFv)₂-CH3 + CH3), ((scFv)₂-CH3) or (scFv-CH3-scFv)₂, multibodies such as triabodies or tetrabodies, and single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable region, which might be VHH, VH or VL, that specifically bind to an antigen or target independently of other variable regions or domains. Further possible formats of the antibody constructs according to the invention are cross bodies, maxi bodies, hetero Fc constructs, mono Fc constructs and scFc constructs. Examples for those formats will be described herein below.

[00235] According to the present invention, binding domains are in the form of one or more polypeptides. Such polypeptides may include proteinaceous parts and non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde). Proteins (including fragments thereof, preferably biologically active fragments, and peptides, usually having less than 30 amino acids) comprise two or more amino acids coupled to each other via a covalent peptide bond (resulting in a chain of amino acids).

[00236] The term "polypeptide" as used herein describes a group of molecules, which usually consist of more than 30 amino acids. Polypeptides may further form multimers such as dimers, trimers and higher oligomers, *i.e.*, consisting of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding higher order structures of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a heteromultimer is an antibody molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms “peptide”, “polypeptide” and “protein” also refer to naturally modified peptides / polypeptides / proteins wherein the modification is effected, *e.g.*, by post-translational modifications

like glycosylation, acetylation, phosphorylation and the like. A "peptide", "polypeptide" or "protein" when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art and described herein below.

[00237] The term "hinge" refers to the IgG hinge region. This region can be identified by analogy using the Kabat numbering, see e.g. Kabat positions 223-243. In line with the above, the minimal requirement for a "hinge" are the amino acid residues corresponding to the IgG1 sequence stretch of D231 to P243 according to the Kabat numbering.

[00238] In line with the present invention, the terms "CH2" and "CH3" refer to the immunoglobulin heavy chain constant regions 2 and 3. These regions can as well be identified by analogy using the Kabat numbering, see e.g. Kabat positions 244-360 for CH2 and Kabat positions 361-478 for CH3. It is understood that there is some variation between the immunoglobulins in terms of their IgG1 Fc region, IgG2 Fc region, IgG3 Fc region, IgG4 Fc region, IgM Fc region, IgA Fc region, IgD Fc region and IgE Fc region (see, e.g., Padlan, *Molecular Immunology*, 31(3), 169-217 (1993)).

[00239] The term "Fc region" refers to the last two heavy chain constant regions of IgA, IgD, and IgG, and the last three heavy chain constant regions of IgE and IgM. The Fc region can also include the flexible hinge N-terminal to these domains. For IgA and IgM, the Fc region may include the J chain. For IgG, the Fc region comprises immunoglobulin domains CH2 and CH3 and the hinge between the first two domains and CH2. Although the boundaries of the Fc region of an immunoglobulin may vary, an example for a human IgG heavy chain Fc portion comprising a functional hinge, CH2 and CH3 domain can be defined e.g. to comprise residues D231 (of the hinge domain) to P476 (of the C-terminus of the CH3 domain), or D231 to L476, respectively, for IgG4, wherein the numbering is according to Kabat.

[00240] The term "Fc portion" or "Fc monomer" means in connection with this invention a polypeptide comprising at least one domain having the function of a CH2 domain and at least one domain having the function of a CH3 domain of an immunoglobulin molecule. As apparent from the term "Fc monomer", the polypeptide comprising those CH domains is a "polypeptide monomer". An Fc monomer can be a polypeptide comprising at least a fragment of the constant region of an immunoglobulin excluding the first constant region immunoglobulin domain of the heavy chain (CH1), but maintaining at least a functional part of one CH2 domain and a functional part of one CH3 domain, wherein the CH2 domain is amino terminal to the CH3 domain.

[00241] In one embodiment of this definition, an Fc monomer can be a polypeptide constant region comprising a portion of the Ig-Fc hinge region, a CH2 region and a CH3 region, wherein the hinge region is amino terminal to the CH2 domain. It is envisaged that the hinge region of the present invention promotes dimerization. Such Fc polypeptide molecules can be obtained by papain digestion of an immunoglobulin region (of course resulting in a dimer of two Fc polypeptide), for example and

not limitation. In another aspect of this definition, an Fc monomer can be a polypeptide region comprising a portion of a CH2 region and a CH3 region. Such Fc polypeptide molecules can be obtained by pepsin digestion of an immunoglobulin molecule, for example and not limitation.

[00242] In one embodiment, the polypeptide sequence of an Fc monomer is substantially similar to an Fc polypeptide sequence of: an IgG1 Fc region, an IgG2 Fc region, an IgG3 Fc region, an IgG4 Fc region, an IgM Fc region, an IgA Fc region, an IgD Fc region and an IgE Fc region. (See, e.g., Padlan, *Molecular Immunology*, 31(3), 169-217 (1993)). Because there is some variation between immunoglobulins, and solely for clarity, Fc monomer refers to the last two heavy chain constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three heavy chain constant region immunoglobulin domains of IgE and IgM. As mentioned, the Fc monomer can also include the flexible hinge N-terminal to these domains. For IgA and IgM, the Fc monomer may include the J chain. For IgG, the Fc portion comprises immunoglobulin domains CH2 and CH3 and the hinge between the first two domains and CH2. Although the boundaries of the Fc portion may vary an example for a human IgG heavy chain Fc portion comprising a functional hinge, CH2 and CH3 domain can be defined e.g. to comprise residues D231 (of the hinge domain—corresponding to D234 in Table 3 below) to P476, respectively L476 (for IgG4) of the carboxyl-terminus of the CH3 domain, wherein the numbering is according to Kabat. The two Fc portion or Fc monomer, which are fused to each other via a peptide linker define the third domain of the antibody construct of the invention, which may also be defined as scFc domain.

[00243] In one embodiment of the invention it is envisaged that a scFc domain as disclosed herein, respectively the Fc monomers fused to each other are comprised only in the third domain of the antibody construct.

[00244] In some embodiments an IgG hinge region can be identified by analogy using the Kabat numbering as set forth in Table 3. In line with the above, it is envisaged that for a hinge domain/region of the present invention the minimal requirement comprises the amino acid residues corresponding to the IgG1 sequence stretch of D231 D234 to P243 according to the Kabat numbering. It is likewise envisaged that a hinge domain/region of the present invention comprises or consists of the IgG1 hinge sequence DKTHTCPPCP (SEQ ID NO: 4) (corresponding to the stretch D234 to P243 as shown in Table 3 below – variations of said sequence are also envisaged provided that the hinge region still promotes dimerization). In a preferred embodiment of the invention the glycosylation site at Kabat position 314 of the CH2 domains in the third domain of the antibody construct is removed by a N314X substitution, wherein X is any amino acid excluding Q. Said substitution is preferably a N314G substitution. In a more preferred embodiment, said CH2 domain additionally comprises the following substitutions (position according to Kabat) V321C and R309C (these substitutions introduce the intra domain cysteine disulfide bridge at Kabat positions 309 and 321).

[00245] Table 3: Kabat numbering of the amino acid residues of the hinge region

IMGT numbering for the hinge	IgG ₁ amino acid translation	Kabat numbering
1	(E)	226
2	P	227
3	K	228
4	S	232
5	C	233
6	D	234
7	K	235
8	T	236
9	H	237
10	T	238
11	C	239
12	P	240
13	P	241
14	C	242
15	P	243

[00246] In further embodiments of the present invention, the hinge domain/region comprises or consists of the IgG2 subtype hinge sequence ERKCCVECPCP (SEQ ID NO: 5), the IgG3 subtype hinge sequence ELKTPLDTHTCPRCP (SEQ ID NO: 6) or ELKTPLGDTHTCPRCP (SEQ ID NO: 7), and/or the IgG4 subtype hinge sequence ESKYGPPCPSCP (SEQ ID NO: 8). The IgG1 subtype hinge sequence may be the following one EPKSCDKTHTCPCP (SEQ ID NO: 9). These core hinge regions are thus also envisaged in the context of the present invention.

[00247] The location and sequence of the IgG CH2 and IgG CD3 domain can be identified by analogy using the Kabat numbering as set forth in Table 4:

Table 4: Kabat numbering of the amino acid residues of the IgG CH2 and CH3 region

IgG subtype	CH2 aa translation	CH2 Kabat numbering	CH3 aa translation	CH3 Kabat numbering
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IgG₁	APE... ...KAK	244... ...360	GQP... ...PGK	361... ...478
IgG₂	APP... ...KTK	244... ...360	GQP... ...PGK	361... ...478
IgG₃	APE... ...KTK	244... ...360	GQP... ...PGK	361... ...478
IgG₄	APE... ...KAK	244... ...360	GQP... ...LGK	361... ...478

[00248] In one embodiment of the invention the emphasized bold amino acid residues in the CH3 domain of the first or both Fc monomers are deleted.

[00249]

[00250] In a classical full-length antibody or immunoglobulin, each light (L) chain is linked to a heavy (H) chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. The heavy chain constant (CH) domain most proximal to VH is usually designated as CH1. The constant (“C”) domains are not directly involved in antigen binding, but exhibit various effector functions, such as antibody-dependent cell-mediated cytotoxicity (ADCC) and complement activation (complement dependent cytotoxicity, CDC). The Fc region of an antibody is the “tail” region of a classical antibody that interacts with cell surface receptors called Fc receptors and some proteins of the complement system. In IgG, IgA and IgD antibody isotypes, the Fc region is composed of two identical protein fragments, derived from the second and third constant domains (CH2 and CH3) of the antibody's two heavy chains. IgM and IgE Fc regions contain three heavy chain constant domains (CH2, CH3 and CH4) in each polypeptide chain. The Fc regions also contains part of the so-called “hinge” region held together by one or more disulfides and noncovalent interactions. The Fc region of a naturally occurring IgG bears a highly conserved N-glycosylation site. Glycosylation of the Fc fragment is essential for Fc receptor-mediated activity.

[00251] In molecules comprising an Fc region, antibody-dependent cellular cytotoxicity (“ADCC”), another mechanism of cell killing mediated by the Fc region is contemplated. ADCC is a mechanism of cell-mediated immune defense whereby an effector cell of the immune system actively lyses a target cell, whose membrane-surface antigens have been bound by specific antibodies. ADCC requires an immune effector cell which classically is known to be a natural killer (NK) cell that typically interacts with IgG antibodies. However, ADCC can also be mediated by macrophages, neutrophils and eosinophils. ADCC involves activation of effector cells expressing Fc receptors by antibodies expressing an Fc portion. For example, the most common Fc receptor on the surface of an NK cell is called CD16 or FcγRIII. Once the Fc receptor binds to the Fc region of IgG, the NK cell releases cytotoxic factors that cause the death of the target cell. Likewise, the Fc receptor (FcεRI) of an eosinophil will recognize IgE. In CDC, in contrast, the molecule “C1q” of the complement system binds to the antibody Fc region,

and this binding triggers the complement cascade which leads to the formation of the membrane attack complex (MAC) at the surface of the target cell, as a result of the classical pathway complement activation. In therapeutic antibodies or antibody constructs, both ADCC and CDC can be modulated by Fc isotype engineering, Fc genetic mutations, or Fc glycosylation profile modifications.

[00252] In some embodiments of the invention the CH2 domain of one or preferably each (both) polypeptide monomers of the third domain comprises an intra domain cysteine disulfide bridge. As known in the art the term "cysteine disulfide bridge" refers to a functional group with the general structure R-S-S-R. The linkage is also called an SS-bond or a disulfide bridge or a cysteine clamp and is derived by the coupling of two thiol groups of cysteine residues. In certain embodiments, the cysteines forming the cysteine disulfide bridge in the mature antibody construct are introduced into the amino acid sequence of the CH2 domain corresponding to 309 and 321 (Kabat numbering). In other embodiments, the cysteine clamps are introduced in other domains of the antibody constructs. See also, e.g. US 2016/0193295.

[00253] In one embodiment of the invention a glycosylation site in Kabat position 314 of the CH2 domain is removed. It is preferred that this removal of the glycosylation site is achieved by a N314X substitution, wherein X is any amino acid excluding Q. Said substitution is preferably a N314G. In a more preferred embodiment, said CH2 domain additionally comprises the following substitutions (position according to Kabat) V321C and R309C (these substitutions introduce the intra domain cysteine disulfide bridge at Kabat positions 309 and 321).

[00254] The definition of "antibody" according to the invention comprises full-length antibodies, also including camelid antibodies and other immunoglobulins generated by biotechnological or protein engineering methods or processes. These full-length antibodies may be for example monoclonal, recombinant, chimeric, deimmunized, humanized and human antibodies, as well as antibodies from other species such as mouse, hamster, rabbit, rat, goat, or non-human primates.

[00255] Given that the antibody constructs according to some embodiments of the invention comprise one domain binding to a pMAGE-HLA and, alternatively, another domain binding to CD3, they do not occur naturally and they are markedly different in their function from naturally occurring products. An antibody construct of the invention is hence an artificial molecule comprising at least two distinct binding domains with different specificities.

[00256] As used herein, the terms "single-chain Fv," "single-chain antibodies" or "scFv" refer to single polypeptide chain antibody fragments that comprise the variable regions from both the heavy and light chains, but lack the constant regions. Generally, a single-chain antibody further comprises a polypeptide linker between the VH and VL domains which enables it to form the desired structure which would allow for antigen binding. Single chain antibodies are discussed in detail by Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds. Springer-Verlag,

New York, pp. 269-315 (1994). Various methods of generating single chain antibodies are known, including those described in U.S. Pat. Nos. 4,694,778 and 5,260,203; International Patent Application Publication No. WO 88/01649; Bird (1988) Science 242:423-442; Huston *et al.* (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883; Ward *et al.* (1989) Nature 334:54454; Skerra *et al.* (1988) Science 242:1038-1041. In specific embodiments, single-chain antibodies can also be bispecific, multispecific, human, and/or humanized and/or synthetic.

[00257] In certain embodiments either the first, the second or the first and the second domain may comprise a single domain antibody, respectively the variable domain or at least the CDRs of a single domain antibody. Single domain antibodies comprise merely one (monomeric) antibody variable domain which is able to bind selectively to a specific antigen, independently of other V regions or domains. The first single domain antibodies were engineered from heavy chain antibodies found in camelids, and these are called VHH fragments. Cartilaginous fishes also have heavy chain antibodies (IgNAR) from which single domain antibodies called VNAR fragments can be obtained. An alternative approach is to split the dimeric variable domains from common immunoglobulins e.g. from humans or rodents into monomers, hence obtaining VH or VL as a single domain Ab. Although most research into single domain antibodies is currently based on heavy chain variable domains, nanobodies derived from light chains have also been shown to bind specifically to target epitopes. Examples of single domain antibodies are called sdAb, nanobodies or single variable domain antibodies.

[00258] A (single domain mAb)₂ is hence a monoclonal antibody construct composed of (at least) two single domain monoclonal antibodies, which are individually selected from the group comprising VH, VL, VHH and VNAR. The linker is preferably in the form of a peptide linker. Similarly, an “scFv-single domain mAb” is a monoclonal antibody construct composed of at least one single domain antibody as described above and one scFv molecule as described above. Again, the linker is preferably in the form of a peptide linker.

[00259] Furthermore, the definition of the term “antibody construct” includes monovalent, bivalent and polyvalent / multivalent constructs and, thus, bispecific constructs, specifically binding to only two antigenic structures, as well as polyspecific / multispecific constructs, which specifically bind more than two antigenic structures, e.g. three, four or more, through distinct binding domains. Moreover, the definition of the term “antibody construct” includes molecules consisting of only one polypeptide chain as well as molecules consisting of more than one polypeptide chain, which chains can be either identical (homodimers, homotrimers or homo oligomers) or different (heterodimer, heterotrimer or heterooligomer). Examples for the above identified antibodies and variants or derivatives thereof are described *inter alia* in Harlow and Lane, Antibodies a laboratory manual, CSHL Press (1988) and Using Antibodies: a laboratory manual, CSHL Press (1999), Kontermann and Dübel,

Antibody Engineering, Springer, 2nd ed. 2010 and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009.

[00260] The term “bispecific” as used herein refers to an antibody construct which is “at least bispecific”, *i.e.*, it comprises at least a first binding domain and a second binding domain, wherein the first binding domain binds to one antigen or target (e.g., peptide GGYDGEHVS, SEQ ID NO: 1 of MAGEB2 in the context of an HLA), and the second binding domain binds to another antigen or target (e.g., CD3). Accordingly, antibody constructs according to the invention comprise specificities for at least two different antigens or targets. For example, the first domain does preferably not bind to an extracellular epitope of CD3ε of one or more of the species as described herein. The term “target cell surface antigen” refers to an antigenic structure expressed by a cell and which is present at the cell surface such that it is accessible for an antibody construct as described herein. It may be a protein, preferably the extracellular portion of a protein, or a carbohydrate structure, preferably a carbohydrate structure of a protein, such as a glycoprotein. It is preferably a tumor antigen, and in more specific embodiments, a peptide tumor antigen presented on a tumor cell surface by an HLA. The term “bispecific antibody construct” of the invention also encompasses multispecific antibody constructs such as trispecific antibody constructs, the latter ones including three binding domains, or constructs having more than three (e.g. four, five...) specificities.

[00261] In a specific embodiment, the first and the second domain of the antibody construct of the invention is a “bispecific single chain antibody construct”, including but not limited to, a bispecific “single chain Fv” (scFv). Although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker – as described hereinbefore – that enables them to be made as a single protein chain in which the VL and VH regions pair to form a monovalent molecule; see e.g., Huston et al. (1988) Proc. Natl. Acad. Sci USA 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are whole or full-length antibodies. A single-chain variable fragment (scFv) is hence a fusion protein of the variable region of the heavy chain (VH) and of the light chain (VL) of immunoglobulins, usually connected with a short linker peptide of about ten to about 25 amino acids, preferably about 15 to 20 amino acids. The linker is usually rich in glycine for flexibility, as well as serine or threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa. This protein retains the specificity of the original immunoglobulin, despite removal of the constant regions and introduction of the linker.

[00262] Bispecific single chain antibody constructs are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl,

Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56. Techniques described for the production of single chain antibodies (see, inter alia, US Patent 4,946,778, Kontermann and Dübel (2010), loc. cit. and Little (2009), loc. cit.) can be adapted to produce single chain antibody constructs specifically recognizing (an) elected target(s).

[00263] Bivalent (also called divalent) or bispecific single-chain variable fragments (bi-scFvs or di-scFvs having the format (scFv)₂ can be engineered by linking two scFv molecules (e.g. with linkers as described hereinbefore). If these two scFv molecules have the same binding specificity, the resulting (scFv)₂ molecule will preferably be called bivalent (i.e. it has two valences for the same target epitope). If the two scFv molecules have different binding specificities, the resulting (scFv)₂ molecule will preferably be called bispecific. The linking can be done by producing a single peptide chain with two VH regions and two VL regions, yielding tandem scFvs (see e.g. Kufer P. et al., (2004) Trends in Biotechnology 22(5):238-244). Another possibility is the creation of scFv molecules with linker peptides that are too short for the two variable regions to fold together (e.g. about five amino acids), forcing the scFvs to dimerize. This type is known as diabodies (see e.g. Hollinger, Philipp et al., (July 1993) Proceedings of the National Academy of Sciences of the United States of America 90 (14): 6444-8).

[00264] Bispecific antibody constructs can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai & Lachmann, Clin. Exp. Immunol. 79:315-321 (1990). Bispecific antibody constructs can be produced by other methods that would be apparent to one skilled in the art, including, e.g., use of any of the binding domain sequences provided herein.

[00265] Bispecific antibody derived molecules such as BiTE[®] antibody constructs are recombinant protein constructs made from two flexibly linked antibody derived binding domains. One binding domain of BiTE[®] antibody constructs is specific for a selected tumor-associated surface antigen on target cells; the second binding domain is specific for CD3, a subunit of the T cell receptor complex on T cells. By their particular design, BiTE[®] antibody constructs are uniquely suited to transiently connect T cells with target cells and, at the same time, potentially activate the inherent cytolytic potential of T cells against target cells. An important further development of the first generation of BiTE[®] antibody constructs (see WO 99/54440 and WO 2005/040220) developed into the clinic as AMG 103 and AMG 110 was the provision of bispecific antibody constructs binding to a context independent epitope at the N-terminus of the CD3ε chain (WO 2008/119567). BiTE[®] antibody constructs binding to this elected epitope do not only show cross-species specificity for the human and the Macaca, or *Callithrix jacchus*, *Saguinus oedipus* or *Saimiri sciureus* CD3ε chain, but also, due to recognizing this specific epitope (instead of previously described epitopes of CD3 binders in bispecific T cell engaging molecules), do not demonstrate unspecific activation of T cells to the same degree as observed for the previous generation of T cell engaging antibodies. This reduction in T cell activation

was connected with less or reduced T cell redistribution in patients, the latter being identified as a risk for side effects, e.g. in pasotuximab.

[00266] Antibody constructs as described in WO 2008/119567 are characterized by rapid clearance from the body; thus, while they are able to reach most parts of the body rapidly, their *in vivo* applications may be limited by their brief persistence *in vivo*. On the other hand, their concentration in the body can be adapted and fine-tuned at short notice. Prolonged administration by continuous intravenous infusion is used to achieve therapeutic effects because of the short *in vivo* half-life of this small, single chain molecule. However, now bispecific antibody constructs are available which have more favorable pharmacokinetic properties, including a longer half-life. An increased half-life is generally useful in *in vivo* applications of immunoglobulins, especially antibodies and most especially antibody fragments or constructs of small size, e.g. in the interest of patient compliance.

[00267] In some embodiments, the antibody constructs of the present invention are “*in vitro* generated antibody constructs”. This term refers to an antibody construct according to the above definition where all or part of the variable region (e.g., at least one CDR) is generated in a non-immune cell selection, e.g., an *in vitro* phage display, protein chip or any other method in which candidate sequences can be tested for their ability to bind to an antigen. In other embodiments, the antibody construct sequences are generated by genomic rearrangement in an immune cell in an animal. This term thus preferably excludes sequences generated solely by genomic rearrangement in an immune cell in an animal. It is envisaged that the first and/or second domain of the antibody construct is produced by or obtainable by phage display or library screening methods rather than by grafting CDR sequences from a pre-existing (monoclonal) antibody into a scaffold. However, the use of CDR sequences from a monoclonal antibody generated as taught in the present disclosure is not precluded and would be readily apparent to one skilled in the art.

[00268] A “recombinant antibody” is an antibody made through the use of recombinant DNA technology or genetic engineering.

[00269] The term “monoclonal antibody” (mAb) or “monoclonal antibody construct” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post-translation modifications (e.g., isomerizations, amidations) that may be present in minor amounts, and refers to an overall polypeptide structure that is similar to naturally occurring antibodies as understood by one of skill in the art (e.g., an IgG with the structure of two heavy chains and two light chains). Monoclonal antibodies are highly specific, being directed against a single antigenic site or epitope on the antigen, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different antigenic sites or epitopes. In addition to their specificity, the monoclonal antibodies are advantageous in that they are

synthesized by clonal cell culture and are uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method.

[00270] For the preparation of monoclonal antibodies, any technique providing antibodies produced by continuous cell line cultures can be used. For example, monoclonal antibodies to be used may be made by the hybridoma method first described by Koehler *et al.*, Nature, 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567). Examples for further techniques to produce human monoclonal antibodies include the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96).

[00271] Hybridomas can then be screened using standard methods, such as enzyme-linked immunosorbent assay (ELISA) and surface plasmon resonance analysis, e.g. Biacore™ to identify one or more hybridomas that produce an antibody that specifically binds with a specified antigen. Any form of the relevant antigen may be used as the immunogen, e.g., recombinant antigen, naturally occurring forms, any variants or fragments thereof, as well as an antigenic peptide thereof. Surface plasmon resonance as employed in the Biacore system can be used to increase the efficiency of phage antibodies which bind to an epitope of a target cell surface antigen (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13).

[00272] Another exemplary method of making monoclonal antibodies includes screening protein expression libraries, e.g., phage display or ribosome display libraries. Phage display is described, for example, in Ladner *et al.*, U.S. Patent No. 5,223,409; Smith (1985) Science 228:1315-1317, Clackson *et al.*, Nature, 352: 624-628 (1991) and Marks *et al.*, J. Mol. Biol., 222: 581-597 (1991).

[00273] In addition to the use of display libraries, the relevant antigen can be used to immunize a non-human animal, e.g., a rodent (such as a mouse, hamster, rabbit or rat). In one embodiment, the non-human animal includes at least a part of a human immunoglobulin gene. For example, it is possible to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig (immunoglobulin) loci. Using the hybridoma technology, antigen-specific monoclonal antibodies derived from the genes with the desired specificity may be produced and selected. See, e.g., XENOMOUSE™, Green *et al.* (1994) Nature Genetics 7:13-21, US 2003-0070185, WO 96/34096, and WO 96/33735.

[00274] A monoclonal antibody can also be obtained from a non-human animal, and then modified, e.g., humanized, deimmunized, rendered chimeric etc., using recombinant DNA techniques known in the art. Examples of modified antibody constructs include humanized variants of non-human antibodies, "affinity matured" antibodies (see, e.g. Hawkins *et al.* J. Mol. Biol. 254, 889-896 (1992) and

Lowman *et al.*, Biochemistry 30, 10832- 10837 (1991)) and antibody mutants with altered effector function(s) (see, *e.g.*, US Patent 5,648,260, Kontermann and Dübel (2010), *loc. cit.* and Little (2009), *loc. cit.*).

[00275] In immunology, affinity maturation is the process by which B cells produce antibodies with increased affinity for antigen during the course of an immune response. With repeated exposures to the same antigen, a host will produce antibodies of successively greater affinities. Like the natural prototype, the *in vitro* affinity maturation is based on the principles of mutation and selection. The *in vitro* affinity maturation has successfully been used to optimize antibodies, antibody constructs, and antibody fragments. Random mutations inside the CDRs are introduced using radiation, chemical mutagens or error-prone PCR. In addition, the genetic diversity can be increased by chain shuffling. Two or three rounds of mutation and selection using display methods like phage display usually results in antibody fragments with affinities in the low nanomolar range.

[00276] A preferred type of an amino acid substitutional variation of the antibody constructs involves substituting one or more hypervariable region residues of a parent antibody (*e. g.* a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sides (*e. g.* 6-7 sides) are mutated to generate all possible amino acid substitutions at each side. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (*e. g.* binding affinity) as herein disclosed. In order to identify candidate hypervariable region sides for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the binding domain and, *e.g.*, the pMAGE-HLA. Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

[00277] The antibody constructs of the present invention specifically include “chimeric” antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to

another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Patent No. 4,816,567; Morrison *et al.*, Proc. Natl. Acad. Sci. USA, 81: 6851-6855 (1984)). Chimeric antibodies of interest herein include "primitized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (e.g., Old World Monkey, Ape etc.) and human constant region sequences. A variety of approaches for making chimeric antibodies have been described. See *e.g.*, Morrison *et al.*, Proc. Natl. Acad. Sci. U.S.A. 81:6851, 1985; Takeda *et al.*, Nature 314:452, 1985, Cabilly *et al.*, U.S. Patent No. 4,816,567; Boss *et al.*, U.S. Patent No. 4,816,397; Tanaguchi *et al.*, EP 0171496; EP 0173494; and GB 2177096.

[00278] An antibody, antibody construct, antibody fragment or antibody variant may also be modified by specific deletion of human T cell epitopes (a method called "deimmunization") by the methods disclosed for example in WO 98/52976 or WO 00/34317. Briefly, the heavy and light chain variable domains of an antibody can be analyzed for peptides that bind to MHC class II; these peptides represent potential T cell epitopes (as defined in WO 98/52976 and WO 00/34317). For detection of potential T cell epitopes, a computer modeling approach termed "peptide threading" can be applied, and in addition a database of human MHC class II binding peptides can be searched for motifs present in the VH and VL sequences, as described in WO 98/52976 and WO 00/34317. These motifs bind to any of the 18 major MHC class II DR allotypes, and thus constitute potential T cell epitopes. Potential T cell epitopes detected can be eliminated by substituting small numbers of amino acid residues in the variable domains, or preferably, by single amino acid substitutions. Typically, conservative substitutions are made. Often, but not exclusively, an amino acid common to a position in human germline antibody sequences may be used. Human germline sequences are disclosed *e.g.* in Tomlinson, *et al.* (1992) J. Mol. Biol. 227:776-798; Cook, G.P. *et al.* (1995) Immunol. Today Vol. 16 (5): 237-242; and Tomlinson *et al.* (1995) EMBO J. 14: 14:4628-4638. The V BASE directory provides a comprehensive directory of human immunoglobulin variable region sequences (compiled by Tomlinson, LA. *et al.* MRC Centre for Protein Engineering, Cambridge, UK). These sequences can be used as a source of human sequence, *e.g.*, for framework regions and CDRs. Consensus human framework regions can also be used, for example as described in US Patent No. 6,300,064.

[00279] "Humanized" antibodies, antibody constructs, variants or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) are antibodies or immunoglobulins of mostly human sequences, which contain (a) minimal sequence(s) derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region (also CDR) of the recipient are replaced by residues from a hypervariable region of a non-human (*e.g.*, rodent) species (donor antibody) such as mouse, rat, hamster or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework region (FR) residues of the human immunoglobulin are replaced by

corresponding non-human residues. Furthermore, "humanized antibodies" as used herein may also comprise residues which are found neither in the recipient antibody nor the donor antibody. These modifications are made to further refine and optimize antibody performance. The humanized antibody may also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see Jones *et al.*, Nature, 321: 522-525 (1986); Reichmann *et al.*, Nature, 332: 323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2: 593-596 (1992).

[00280] Humanized antibodies or fragments thereof can be generated by replacing sequences of the Fv variable domain that are not directly involved in antigen binding with equivalent sequences from human Fv variable domains. Exemplary methods for generating humanized antibodies or fragments thereof are provided by Morrison (1985) Science 229:1202-1207; by Oi *et al.* (1986) BioTechniques 4:214; and by US 5,585,089; US 5,693,761; US 5,693,762; US 5,859,205; and US 6,407,213. Those methods include isolating, manipulating, and expressing the nucleic acid sequences that encode all or part of immunoglobulin Fv variable domains from at least one of a heavy or light chain. Such nucleic acids may be obtained from a hybridoma producing an antibody against a predetermined target, as described above, as well as from other sources. The recombinant DNA encoding the humanized antibody molecule can then be cloned into an appropriate expression vector.

[00281] Humanized antibodies may also be produced using transgenic animals such as mice that express human heavy and light chain genes, but are incapable of expressing the endogenous mouse immunoglobulin heavy and light chain genes. Winter describes an exemplary CDR grafting method that may be used to prepare the humanized antibodies described herein (U.S. Patent No. 5,225,539). All of the CDRs of a particular human antibody may be replaced with at least a portion of a non-human CDR, or only some of the CDRs may be replaced with non-human CDRs. It is only necessary to replace the number of CDRs required for binding of the humanized antibody to a predetermined antigen.

[00282] A humanized antibody can be optimized by the introduction of conservative substitutions, consensus sequence substitutions, germline substitutions and/or back mutations. Such altered immunoglobulin molecules can be made by any of several techniques known in the art, (*e.g.*, Teng *et al.*, Proc. Natl. Acad. Sci. U.S.A., 80: 7308-7312, 1983; Kozbor *et al.*, Immunology Today, 4: 7279, 1983; Olsson *et al.*, Meth. Enzymol., 92: 3-16, 1982, and EP 239 400).

[00283] The term "human antibody", "human antibody construct" and "human binding domain" includes antibodies, antibody constructs and binding domains having antibody regions such as variable and constant regions or domains which correspond substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat *et al.* (1991) (*loc. cit.*). The human antibodies, antibody constructs or binding domains of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*,

mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs, and in particular, in CDR3. The human antibodies, antibody constructs or binding domains can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. The definition of human antibodies, antibody constructs and binding domains as used herein also contemplates fully human antibodies, which include only non-artificially and/or genetically altered human sequences of antibodies as those can be derived by using technologies or systems such as the Xenomouse.

Preferably, a “fully human antibody” does not include amino acid residues not encoded by human germline immunoglobulin sequences.

[00284] Preferably the binding domain which binds to pMAGE-HLA and/or the binding domain which binds to CD3ε is/are human binding domains. Antibodies and antibody constructs comprising at least one human binding domain avoid some of the problems associated with antibodies or antibody constructs that possess non-human such as rodent (*e.g.* murine, rat, hamster or rabbit) variable and/or constant regions. The presence of such rodent derived proteins can lead to the rapid clearance of the antibodies or antibody constructs or can lead to the generation of an immune response against the antibody or antibody construct by a patient. In order to avoid the use of rodent derived antibodies or antibody constructs, human or fully human antibodies / antibody constructs can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

[00285] The ability to clone and reconstruct megabase-sized human loci in yeast artificial chromosomes YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful models of human disease. Furthermore, the use of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

[00286] An important practical application of such a strategy is the “humanization” of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated offers the opportunity to study the mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs) – an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies or antibody constructs are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies / antibody constructs. The use

of fully human antibodies or antibody constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which require repeated compound administrations.

[00287] One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be readily produced and selected. This general strategy was demonstrated in connection with the generation of the first XenoMouse mouse strains (see Green et al. *Nature Genetics* 7:13-21 (1994)). The XenoMouse strains were engineered with YACs containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions may recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was recently extended to the introduction of greater than approximately 80% of the human antibody repertoire through introduction of megabase sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez *et al.* *Nature Genetics* 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620.

[00288] The production of the XenoMouse® animals is further discussed and delineated in U.S. patent applications Ser. No. 07/466,008, Ser. No. 07/610,515, Ser. No. 07/919,297, Ser. No. 07/922,649, Ser. No. 08/031,801, Ser. No. 08/112,848, Ser. No. 08/234,145, Ser. No. 08/376,279, Ser. No. 08/430,938, Ser. No. 08/464,584, Ser. No. 08/464,582, Ser. No. 08/463,191, Ser. No. 08/462,837, Ser. No. 08/486,853, Ser. No. 08/486,857, Ser. No. 08/486,859, Ser. No. 08/462,513, Ser. No. 08/724,752, and Ser. No. 08/759,620; and U.S. Pat. Nos. 6,162,963; 6,150,584; 6,114,598; 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez *et al.* *Nature Genetics* 15:146-

156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998), EP 0 463 151 B1, WO 94/02602, WO 96/34096, WO 98/24893, WO 00/76310, and WO 03/47336.

[00289] In an alternative approach, others, including GenPharm International, Inc., have utilized a “minilocus” approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more VH genes, one or more DH genes, one or more JH genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani *et al.* and U.S. Pat. Nos. 5,545,806; 5,625,825; 5,625,126; 5,633,425; 5,661,016; 5,770,429; 5,789,650; 5,814,318; 5,877,397; 5,874,299; and 6,255,458 each to Lonberg and Kay, U.S. Pat. Nos. 5,591,669 and 6,023,010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205; 5,721,367; and 5,789,215 to Berns *et al.*, and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, Ser. No. 07/575,962, Ser. No. 07/810,279, Ser. No. 07/853,408, Ser. No. 07/904,068, Ser. No. 07/990,860, Ser. No. 08/053,131, Ser. No. 08/096,762, Ser. No. 08/155,301, Ser. No. 08/161,739, Ser. No. 08/165,699, Ser. No. 08/209,741. See also EP 0 546 073 B1, WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175. See further Taylor *et al.* (1992), Chen *et al.* (1993), Tuaillon *et al.* (1993), Choi *et al.* (1993), Lonberg *et al.* (1994), Taylor *et al.* (1994), and Tuaillon *et al.* (1995), Fishwild *et al.* (1996).

[00290] Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961. Xenex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996; 5,698,767; and 5,958,765.

[00291] Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. It is however expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or multi-dose utilizations of the antibody. Thus, it would be desirable to provide antibody constructs comprising a human binding domain against a pMAGE-HLA and a human binding domain against CD3ε in order to vitiate concerns and/or effects of HAMA or HACA response.

[00292] In some embodiments, the antibody constructs of the invention are “isolated” or “substantially pure” antibody constructs. “Isolated” or “substantially pure”, when used to describe the antibody constructs disclosed herein, means an antibody construct that has been identified, separated

and/or recovered from a component of its production environment. Preferably, the antibody construct is free or substantially free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. It is understood that the isolated protein may constitute a wide range of percent concentration, e.g., from 5% to 99.9% by weight of the total protein content, depending on the circumstances. The polypeptide may be made at a significantly higher concentration through the use of an inducible promoter or high expression promoter, such that it is made at increased concentration levels. The definition includes the production of an antibody construct in a wide variety of organisms and/or host cells that are known in the art. In preferred embodiments, the antibody construct will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain.

Ordinarily, however, an isolated antibody construct will be prepared by at least one purification step.

[00293] Peptides are short chains of amino acid monomers linked by covalent peptide (amide) bonds. Hence, peptides fall under the broad chemical classes of biological oligomers and polymers. Amino acids that are part of a peptide or polypeptide chain are termed “residues” and can be consecutively numbered. All peptides except cyclic peptides have an N-terminal residue at one end and a C-terminal residue at the other end of the peptide. An oligopeptide consists of only a few amino acids (usually between two and twenty). A polypeptide is a longer, continuous, and unbranched peptide chain. Peptides are distinguished from proteins on the basis of size, and as an arbitrary benchmark can be understood to contain approximately 50 or fewer amino acids. Proteins consist of one or more polypeptides, usually arranged in a biologically functional way. While aspects of the lab techniques applied to peptides versus polypeptides and proteins differ (e.g., the specifics of electrophoresis, chromatography, etc.), the size boundaries that distinguish peptides from polypeptides and proteins are not absolute. Therefore, in the context of the present invention, the terms “peptide”, “polypeptide” and “protein” may be used interchangeably, and the term “polypeptide” is often preferred.

[00294] Polypeptides may further form multimers such as dimers, trimers and higher oligomers, which consist of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding structures of higher order of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a heteromultimer is an antibody or immunoglobulin molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide

chains. The terms “peptide”, “polypeptide” and “protein” also refer to naturally modified peptides / polypeptides / proteins wherein the modification is accomplished *e.g.* by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A “peptide”, “polypeptide” or “protein” when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art and described herein below.

[00295] An antigen binding protein is said to “specifically bind” or “immunospecifically bind” to its antigen when the antigen binding protein binds its antigen with a dissociation constant (KD) is $\leq 10^{-7}$ M as measured via a surface plasma resonance technique (*e.g.*, BIAcore, GE-Healthcare Uppsala, Sweden) or Kinetic Exclusion Assay (KinExA, Sapidyne, Boise, Idaho). In accordance with this invention an antigen binding protein specifically binds or immunospecifically binds to pMAGE-HLA (*e.g.*, GGYDGEHHSV (SEQ ID NO: 1) complexed with HLA-A*02:01) and CD3ε.

[00296] Because of the sequence similarity between homologous proteins in different species, an antibody construct or a binding domain that specifically binds to its target (such as a human target) may, however, cross-react with homologous target molecules from different species (such as, from non-human primates). The term “specific / immunospecific binding” can hence include the binding of an antibody construct or binding domain to epitopes or structurally related epitopes in more than one species.

[00297] Moreover, because of sequence similarity between, for example, different MAGE peptides, an antibody construct or binding domain may cross-react with the various peptides. See Figure 1 for a sequence comparison. For example, in some embodiments the antibody construct or binding domain may specifically bind to a pMAGE-HLA, where the peptide is GGYDGEHHSV, SEQ ID NO: 1, GGYDGREHTV, SEQ ID NO: 2, and/or GGYDGREHSV, SEQ ID NO: 3. In other embodiments, the antibody construct or binding domain may specifically bind only to GGYDGEHHSV, SEQ ID NO: 1 in the context of a pMAGE-HLA.

Linkers

[00298] The at least two binding domains and the variable domains (VH / VL) of the antibody construct of the present invention may or may not comprise peptide linkers (spacer peptides). The term “peptide linker” comprises in accordance with the present invention an amino acid sequence by which the amino acid sequences of one (variable and/or binding) domain and another (variable and/or binding) domain of the antibody construct of the invention are linked with each other. The peptide linkers can also be used to fuse the third domain to the other domains of the antibody construct of the invention. An essential technical feature of such peptide linker is that it does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344. The peptide linkers can also be used to attach other

domains or modules or regions (such as half-life extending domains) to the antibody construct of the invention.

[00299] Examples of useful peptide linkers are provided herein, in addition to those known in the art. Nonlimiting examples of linkers include:

[00300]	G4S linker	GGGGG (SEQ ID NO: 10)
[00301]	(G4S)2 linker	GGGGSGGGGS (SEQ ID NO: 11)
[00302]	(G4S)3 linker	GGGGSGGGSGGGGS (SEQ ID NO: 12)
[00303]	(G4S)4 linker	GGGGSGGGSGGGSGGGGS (SEQ ID NO: 13)
[00304]	(G4S)5 linker	GGGGSGGGSGGGSGGGSGGGGS (SEQ ID NO: 14)
[00305]	(G4S)6 linker	GGGGSGGGSGGGSGGGSGGGSGGGGS (SEQ ID NO: 15)
[00306]	(G4S)7 linker	GGGGSGGGSGGGSGGGSGGGSGGGSGGGGS (SEQ ID NO: 16)
[00307]	(G4S)8 linker	GGGGSGGGSGGGSGGGSGGGSGGGSGGGSGGGGS (SEQ ID NO: 17)
[00308]	Peptide linker	PGGGGS (SEQ ID NO: 18)
[00309]	Peptide linker	PGGDGS (SEQ ID NO: 19)
[00310]	Peptide linker	SGGGGS (SEQ ID NO: 20)
[00311]	Peptide linker	GGGG (SEQ ID NO: 21)

[00312] In the present context, a “short” linker has between 2 and 50 amino acids, preferably between 3 and 35, between 4 and 30, between 5 and 25, between 6 and 20 or between 6 and 17 amino acids. The linker between two variable regions of one binding domain may have a different length (e.g. may be longer) than the linker between the two binding domains. For example, the linker between two variable regions of one binding domain may have a length between 7 and 15 amino acids, preferably between 9 and 13, and the linker between the two binding domains may have a length between 3 and 10 amino acids, preferably between 4 and 8. It is further envisaged that the peptide linkers are glycine/serine linkers, such as those depicted in SEQ ID NOs: 10-17. In some embodiments, the majority of the amino acids in glycine/serine linkers are selected from glycine and serine.

[00313] In the event that a linker is used to fuse the first domain to the second domain, or the first or second domain to the third domain, this linker is preferably of a length and sequence sufficient to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. For peptide linkers which connect the at least two binding domains (or two variable domains) in the antibody construct of the invention, those peptide linkers are preferred which comprise only a few number of amino acid residues, e.g. 12 amino acid residues or less. Thus, peptide linkers of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s), wherein Gly-rich linkers are preferred.

[00314] A “single amino acid” linker in the context of said “peptide linker” is Gly. Accordingly, said peptide linker may consist of the single amino acid Gly. Another embodiment of a peptide linker

is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e., Gly4Ser (SEQ ID NO: 10), or polymers thereof, i.e. (Gly4Ser)_x, where x is an integer of 1 or greater (e.g. 2 or 3) (SEQ ID NO: 18448). The characteristics of said peptide linkers are known in the art and are described e.g. in Dall'Acqua et al. (Biochem. (1998) 37, 9266-9273), Cheadle et al. (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which do not promote any secondary structures are preferred. The linkage of said domains to each other can be provided, e.g., by genetic engineering. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (e.g. WO 99/54440 or Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001).

[00315] The peptide linker, by whom the polypeptide monomers ("Fc portion" or "Fc monomer") of the third domain are fused to each other, in one embodiment comprises at least 25 amino acid residues (25, 26, 27, 28, 29, 30 etc.). In another embodiment, this peptide linker comprises at least 30 amino acid residues (30, 31, 32, 33, 34, 35 etc.). In a further embodiment the linker comprises up to 40 amino acid residues, up to 35 amino acid residues, or exactly 30 amino acid residues. A specific embodiment of such peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly4Ser (SEQ ID NO: 10), or polymers thereof, i.e. (Gly4Ser)_x, where x is an integer of 5 or greater (e.g. 6, 7 or 8) (SEQ ID NO: 18449). Preferably the integer is 6 or 7, more preferably the integer is 6.

Exemplary Molecule Formats

[00316] As described herein above, the invention provides an embodiment wherein the antibody construct is in a format selected from the group consisting of (scFv)₂, scFv-single domain mAb, diabodies and oligomers of any of the aforementioned formats. The term "is in a format" does not

exclude that the construct can be further modified, e.g. by attachment or fusion to other moieties, as described herein.

[00317] The antibody construct of the invention may hence comprise in an N- to C-terminal order:

[00318] (a) the first domain;

[00319] (b) a peptide linker;

[00320] (c) the second domain;

[00321] (d) a peptide linker;

[00322] (e) the first polypeptide monomer of the third domain (comprising a hinge, a CH2 and a CH3 domain);

[00323] (f) a peptide linker ; and

[00324] (g) the second polypeptide monomer of the third domain (comprising a hinge, a CH2 and a CH3 domain).

[00325] According to one embodiment of the antibody construct of the present invention, the first and/or the second domain are in the format of an scFv. In an scFv, the VH region and the VL region are arranged in the order VH-VL or VL-VH (from N- to C-terminus). It is envisaged that the VH and the VL regions of the first and/or the second binding domain are connected via a linker, preferably a peptide linker. According to one embodiment of the first and/or the second domain, the VH-region is positioned N-terminally of the linker, and the VL-region is positioned C-terminally of the linker. In other words, in one embodiment of the first and/or the second domain, the scFv comprises from the N-terminus to the C-terminus: VH-linker-VL. It is furthermore envisaged that the first domain and the second domain of the antibody construct are connected via a linker, preferably a peptide linker. The antibody construct may e.g. comprise the domains in the order (from N-terminus to C-terminus) first domain – linker – second domain. The inverse order (second domain – linker – first domain) is also possible.

[00326] According to one embodiment of the invention, the antibody construct of the invention is a “single chain antibody construct”. It is also envisaged that either the first or the second or both binding domains may be in the format of a “single chain Fv” (scFv). Although the two domains of the Fv fragment, VL and VH, are coded for by separate genes, they can be joined, using recombinant methods, by an artificial linker – as described hereinbefore – that enables them to be made as a single protein chain in which the VL and VH regions pair to form a monovalent molecule; see e.g., Huston et al. (1988) Proc. Natl. Acad. Sci USA 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are full-length antibodies or IgGs. A single-chain variable fragment (scFv) is hence a fusion protein of the variable region of the heavy chain (VH) and of the light chain (VL)

of immunoglobulins, usually connected with a short linker peptide. The linker is usually rich in glycine for flexibility, as well as serine or also threonine for solubility, and can either connect the N-terminus of the VH with the C-terminus of the VL, or vice versa. This protein retains the specificity of the original immunoglobulin, despite removal of the constant regions and introduction of the linker.

[00327] In certain embodiments of the antibody construct of the present invention the first and second domain form an antibody construct in a format selected from the group consisting of (scFv)₂, scFv-single domain mAb, diabody and oligomers of any of these formats.

[00328] In certain embodiments, a bispecific binding molecule may not be desired, and instead a more standard antibody format (e.g., an IgG monoclonal antibody) may be the molecule desired. Accordingly, in one embodiment the invention provides an antibody comprising a VH and VL. In another embodiment, the invention provides an antibody comprising a VH-CDR1, VH-CDR2, VH-CDR3 and a VL-CDR1, VL-CDR2, VL-CDR3.

[00329] In one embodiment of the invention either the first, the second or the first and the second domain may comprise a single domain antibody, the variable domain, or at least the CDRs of a single domain antibody.

[00330] Antibody constructs denominated “single domain antibodies” comprise one (monomeric) antibody variable region which is able to bind selectively to a specific antigen, independently of other variable regions. The first single domain antibodies were engineered from heavy chain antibodies found in camelids, and these are called VHH fragments. Cartilaginous fishes also have heavy chain antibodies (IgNAR) from which single domain antibodies called VNAR fragments can be obtained. An alternative approach is to split the dimeric variable regions from common immunoglobulins into monomers, hence obtaining VH or VL as a single domain Ab. Although most research into single domain antibodies is currently based on heavy chain variable regions, nanobodies derived from light chains were also shown to bind specifically to target epitopes. Examples of single domain antibodies are called sdAb, nanobodies or single variable domain antibodies.

[00331] A (single domain mAb)₂ is hence a monoclonal antibody construct composed of (at least) two single domain monoclonal antibody constructs, which are individually selected from the group comprising VH, VL, VHH and VNAR. The linker is preferably in the form of a peptide linker. Similarly, an “scFv-single domain mAb” is a monoclonal antibody construct composed of at least one single domain antibody as described above and one scFv molecule as described above. Again, the linker is preferably in the form of a peptide linker.

[00332] It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target molecules the pMAGE-HLA and CD3, a further function. In this format, the antibody construct may be a trifunctional or multifunctional antibody construct by targeting target cells through the pMAGE-HLA binding, mediating cytotoxic T cell activity through CD3 binding and

providing a further function such as means or domains to enhance or extend serum half-life, a fully functional or modified Fc constant domain mediating ADCC through recruitment of effector cells, a label (fluorescent etc.), a therapeutic agent such as a toxin or radionuclide, etc.

[00333] According to another embodiment, the antibody construct of the invention comprises (in addition to the first and second domain) a third domain which comprises two polypeptide monomers, each comprising a hinge, a CH2 and a CH3 domain, wherein said two polypeptide monomers are fused to each other via a peptide linker. It is envisaged that said third domain comprises in an N-terminal to C-terminal order: hinge-CH2-CH3-linker-hinge-CH2-CH3. Amino acid sequences that can be used for said third domain are depicted in SEQ ID NOs: 22-29. Each of said polypeptide monomers can have an amino acid sequence that is selected from the group consisting of SEQ ID NOs: 22-29, or that is at least 90% identical to those sequences. In another embodiment, the first and second domains of the antibody construct of the invention are fused to the third domain via a peptide linker.

Half-Life Extension

[00334] Examples for means or domains to extend serum half-life of the antibody constructs of the invention include peptides, proteins or domains of proteins, which are fused or otherwise attached to the antibody constructs. The group of peptides, proteins or protein domains includes peptides binding to other proteins with preferred pharmacokinetic profile in the human body such as serum albumin (see WO 2009/127691). An alternative concept of such half-life extending peptides includes peptides binding to the neonatal Fc receptor (FcRn, see WO 2007/098420), which can also be used in the antibody constructs of the present invention. The concept of attaching larger domains of proteins or complete proteins includes the fusion of human serum albumin, variants or mutants of human serum albumin (see WO 2011/051489, WO 2012/059486, WO 2012/150319, WO 2013/135896, WO 2014/072481, WO 2013/075066) or domains thereof, as well as the fusion of an immunoglobulin constant region (Fc domain) and variants thereof. Such variants of Fc domains are called Fc-based domains and may e.g. be optimized / modified in order to allow the desired pairing of dimers or multimers, to abolish Fc receptor binding (e.g. to avoid ADCC or CDC) or for other reasons. A further concept known in the art to extend the half-life of substances or molecules in the human body is the pegylation of those molecules (such as the antibody constructs of the present invention).

[00335] In one embodiment, the antibody constructs according to the invention are linked (e.g. via peptide bond) with a fusion partner (such as a protein, polypeptide or peptide), e.g. for the purpose of extending the construct's serum half-life. These fusion partners can be selected from human serum albumin ("HSA" or "HALB") as well as sequence variants thereof, peptides binding to HSA, peptides binding to FcRn ("FcRn BP"), or constructs comprising an (antibody derived) Fc region. In

general, the fusion partners may be linked to the N-terminus or to the C-terminus of the antibody constructs according to the invention, either directly (e.g. via peptide bond) or through a peptide linker such as (GGGGS)_n (wherein “n” is an integer of 2 or greater, e.g. 2 or 3 or 4) (SEQ ID NO: 18450). Suitable peptide linkers are provided herein.

Amino Acid Sequence Modifications

[00336] Amino acid sequence modifications of the antibody constructs described herein are also contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody construct. Amino acid sequence variants of the antibody constructs are prepared by peptide synthesis or by introducing appropriate nucleotide changes into the nucleic acid molecule encoding the antibody constructs. All below described amino acid sequence modifications should result in an antibody construct which retains the desired biological activity of the unmodified parental molecule (such as binding to a pMAGE-HLA and to CD3, inducing cytotoxicity against MAGEB2 positive target cells).

[00337] The term “amino acid” or “amino acid residue” typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H); isoleucine (Ile or I); leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); proline (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. There are basically four different classes of amino acids determined by different side chains:

- (1) non-polar and neutral (uncharged): Ala, Gly, Ile, Leu, Met, Phe, Pro, Val
- (2) polar and neutral (uncharged): Asn, Cys (being only slightly polar), Gln, Ser, Thr, Trp (being only slightly polar), Tyr
- (3) acidic and polar (negatively charged): Asp and Glu
- (4) basic and polar (positively charged): Arg, His, Lys

[00338] Hydrophobic amino acids can be divided according to whether they have aliphatic or aromatic side chains. Phe and Trp (being very hydrophobic), Tyr and His (being less hydrophobic) are classified as aromatic amino acids. Strictly speaking, aliphatic means that the side chain contains only hydrogen and carbon atoms. By this strict definition, the amino acids with aliphatic side chains are alanine, isoleucine, leucine (also norleucine), proline and valine. Alanine’s side chain, being very short, means that it is not particularly hydrophobic, and proline has an unusual geometry that gives it special roles in proteins. It is often convenient to consider methionine in the same category as isoleucine, leucine and valine, although it also contains a sulphur atom. The unifying theme is that these amino

acids contain largely non-reactive and flexible side chains. The amino acids alanine, cysteine, glycine, proline, serine and threonine are often grouped together for the reason that they are all small in size. Gly and Pro may influence chain orientation.

[00339] Amino acid modifications include, for example, deletions of residues from, insertions of residues into, and/or substitutions of residues within the amino acid sequences of the antibody constructs. Any combination of deletion, insertion, and/or substitution is made to arrive at a final antibody construct, provided that the final construct possesses the desired characteristics, e.g. the biological activity of the unmodified parental molecule (such as binding to a pMAGE-HLA and to CD3, inducing cytotoxicity against MAGEB2 positive target cells). The amino acid changes may also alter post-translational processes of the antibody constructs, such as changing the number or position of glycosylation sites.

[00340] For example, 1, 2, 3, 4, 5, or 6 amino acids may be inserted, deleted and/or substituted in each of the CDRs (of course, dependent on their respective length), while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be inserted, deleted and/or substituted in each of the FRs. Amino acid sequence insertions also include N-terminal and/or C-terminal additions of amino acids ranging in length from e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 residues to polypeptides containing more than 10, e.g. one hundred or more residues, as well as intra-sequence insertions of single or multiple amino acid residues. An insertional variant of the antibody construct of the invention includes the fusion of a polypeptide which increases or extends the serum half-life of the antibody construct to the N-terminus or to the C-terminus of the antibody construct. It is also conceivable that such insertion occurs within the antibody construct, e.g. between the first and the second domain.

[00341] The sites of greatest interest for amino acid modifications, in particular for amino acid substitutions, include the hypervariable regions, in particular the individual CDRs of the heavy and/or light chain, but FR alterations in the heavy and/or light chain are also contemplated. The substitutions can be conservative substitutions as described herein. Preferably, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids may be substituted in a CDR, while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be substituted in the framework regions (FRs), depending on the length of the CDR or FR, respectively. For example, if a CDR sequence encompasses 6 amino acids, it is envisaged that one, two or three of these amino acids are substituted. Similarly, if a CDR sequence encompasses 15 amino acids it is envisaged that one, two, three, four, five or six of these amino acids are substituted.

[00342] As described herein, a useful method for the identification of certain residues or regions within the antibody constructs that are preferred locations for mutagenesis is called "alanine scanning mutagenesis," which is a mature technology, and is further described e.g. in Cunningham B.C. and Wells J.A. (Science. 1989 Jun 2;244(4908):1081-5) and Morrison KL & Weiss GA. (Cur Opin Chem

Biol. 2001 Jun;5(3):302-7). Here, a residue or group of residues within the antibody construct is/are identified (e.g. charged residues such as Arg, His, Lys, Asp, and Glu) and replaced by a neutral or non-polar amino acid (most preferably alanine or polyalanine), e.g., via peptide synthesis or site-directed mutagenesis, to affect the interaction of the respective amino acid(s) with the epitope of the target protein. Alanine scanning is a technique used to determine the contribution of a specific residue to the stability or function of given protein. Alanine is used because of its non-bulky, chemically inert, methyl functional group that nevertheless mimics the secondary structure preferences that many of the other amino acids possess. Sometimes bulky amino acids such as valine or leucine can be used in cases where conservation of the size of mutated residues is needed. This technique can also be useful to determine whether the side chain of a specific residue plays a significant role in bioactivity. Alanine scanning is usually accomplished by site-directed mutagenesis or randomly by creating a PCR library. Furthermore, computational methods to estimate thermodynamic parameters based on a theoretical alanine substitutions have been developed. The data can be tested by IR, NMR Spectroscopy, mathematical methods, bioassays, etc.

[00343] Those amino acid locations demonstrating functional sensitivity to the substitutions (as determined e.g. by alanine scanning) can then be refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site or region for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se needs not to be predetermined. For example, to analyze or optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at a target codon or region, and the expressed antibody construct variants are screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in the DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done e.g. using assays of antigen (e.g. pMAGE-HLA or CD3) binding activity and/or of cytotoxic activity.

[00344] Generally, if amino acids are substituted in one or more or all of the CDRs of the heavy and/or light chain, it is envisaged that the then-obtained "substituted" sequence is at least 60% or 65%, more preferably 70% or 75%, even more preferably 80% or 85%, and particularly preferably 90% or 95% identical / homologous to the "original" or "parental" CDR sequence. This means that the degree of identity / homology between the original and the substituted sequence depends on the length of the CDR. For example, a CDR having 5 amino acids in total and comprising one amino acid substitution is 80% identical to the "original" or "parental" CDR sequence, while a CDR having 10 amino acids in total and comprising one amino acid substitution is 90% identical to the "original" or "parental" CDR sequence. Accordingly, the substituted CDRs of the antibody construct of the invention may have different degrees of identity to their original sequences, e.g., CDRL1 may have 80%, while

CDRL3 may have 90% of homology. The same considerations apply to the framework regions and to the entire VH and VL regions.

[00345] A “variant CDR” is a CDR with a specific sequence homology, similarity, or identity to the parent CDR of the invention, and shares biological function with the parent CDR, including, but not limited to, at least 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the specificity and/or activity of the parent CDR. Generally, the amino acid homology, similarity, or identity between individual variant CDRs is at least 60% to the parent sequences depicted herein, and more typically with increasing homologies, similarities or identities of at least 65% or 70%, preferably at least 75% or 80%, more preferably at least 85%, 90%, 91%, 92%, 93%, 94%, and most preferably 95%, 96%, 97%, 98%, 99%, and almost 100%. The same applies to “variant VH” and “variant VL”. According to one embodiment, the sequence variations within a “variant VH” and/or a “variant VL” do not extend to the CDRs. The present invention is hence directed to an antibody construct as defined herein, comprising VH and VL sequences having a certain sequence homology (see above) to the specific sequences as defined herein (the “parental” VH and VL), wherein the CDR sequences are 100% identical to the specific CDR sequences as defined herein (the “parental” CDRs).

[00346] Preferred substitutions (or replacements) are conservative substitutions. However, any substitution (including non-conservative substitutions or one or more from the “exemplary substitutions” listed in Table 5, below) is envisaged, as long as the antibody construct retains its capacity to bind to a pMAGE-HLA via the first domain and to CD3 or CD3 epsilon via the second domain, and/or provided its CDRs, FRs, VH and/or VL sequences have a degree of identity to the original or parental sequence of at least 60% or 65%, more preferably at least 70% or 75%, even more preferably at least 80% or 85%, and particularly preferably at least 90% or 95%.

[00347] A conservative replacement (also called a conservative mutation or a conservative substitution) is an amino acid replacement that changes a given amino acid to a different amino acid with similar biochemical properties (e.g. charge, hydrophobicity, size). Conservative replacements in proteins often have a smaller effect on protein function than non-conservative replacements. Conservative substitutions are shown in Table 5. Exemplary conservative substitutions are shown as “exemplary substitutions”. If such substitutions result in a change in biological activity, then more substantial changes, as further described herein in reference to amino acid classes, may be introduced and the products screened for a desired characteristic.

Table 5: Amino acid substitutions (aa = amino acid)

Original aa	Conservative substitutions	Exemplary Substitutions
Ala (A)	Small aa	Gly, Ser, Thr

Arg (R)	Polar aa, in particular Lys	Lys, Gln, Asn
Asn (N)	Polar aa, in particular Asp	Asp, Gln, His, Lys, Arg
Asp (D)	Glu or other polar aa, in particular Asn	Glu, Asn
Cys (C)	Small aa	Ser, Ala
Gln (Q)	Polar aa, in particular Glu	Glu, Asn
Glu (E)	Asp or other polar aa, in particular Gln	Asp, Gln
Gly (G)	Small aa, such as Ala	Ala
His (H)		Asn, Gln, Arg, Lys, Tyr
Ile (I)	Hydrophobic, in particular aliphatic aa	Ala, Val, Met, Leu, Phe
Leu (L)	Hydrophobic, in particular aliphatic aa	Norleucine, Ile, Ala, Val, Met
Lys (K)	Polar aa, in particular Arg	Arg, Gln, Asn
Met (M)	Hydrophobic, in particular aliphatic aa	Leu, Ala, Ile, Val, Phe
Phe (F)	Aromatic or hydrophobic aa, in particular Tyr	Tyr, Trp, Leu, Val, Ile, Ala
Pro (P)	Small aa	Ala
Ser (S)	Polar or small aa, in particular Thr	Thr
Thr (T)	Polar aa, in particular Ser	Ser
Trp (W)	Aromatic aa	Tyr, Phe
Tyr (Y)	Aromatic aa, in particular Phe	Phe, Trp, Thr, Ser
Val (V)	Hydrophobic, in particular aliphatic aa	Leu, Ile, Ala, Met, Phe

[00348] Substantial modifications in the biological properties of the antibody construct of the present invention are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Non-conservative substitutions will usually entail exchanging a member of one of the above defined amino acid classes (such as polar, neutral, acidic, basic, aliphatic, aromatic, small...) for another class. Any cysteine residue not involved in maintaining the proper conformation of the antibody construct may be substituted, generally with serine, to improve the oxidative stability of the antibody construct.

[00349] In addition to the above described substitutions, other substitutions within the CDRs that contribute to binding can be made. For example, the consensus sequences set forth in Tables 29 (SEQ ID NOs: 1832-2965), 37 (SEQ ID NOs: 3497-3874), 45 (SEQ ID NOs: 4361-4710), 53 (SEQ ID NOs:

5982-6844), 61 (SEQ ID NOs: 13276-16184), 62 (SEQ ID NOs: 13434-16257), 63 (SEQ ID NOs: 13507-16484), 71 (SEQ ID NOs: 16971-17195), 72 (SEQ ID NOs: 16980-17204), 73 (SEQ ID NOs: 16989-17222), 111, 112, 113, 114, 115, 116, or 117 herein provide such substitutions. In certain embodiments, deletions as guided by the provided consensus sequences may also be made. With the guidance provided herein by the consensus sequences set forth in Tables 29 (SEQ ID NOs: 1832-2965), 37 (SEQ ID NOs: 3497-3874), 45 (SEQ ID NOs: 4361-4710), 53 (SEQ ID NOs: 5982-6844), 61 (SEQ ID NOs: 13276-16184), 62 (SEQ ID NOs: 13434-16257), 63 (SEQ ID NOs: 13507-16484), 71 (SEQ ID NOs: 16971-17195), 72 (SEQ ID NOs: 16980-17204), 73 (SEQ ID NOs: 16989-17222), 111, 112, 113, 114, 115, 116, or 117 various amino acid substitutions, and functional equivalents thereof, or deletions, can be readily made by one of ordinary skill in the art.

[00350] Sequence identity, homology and/or similarity of amino acid sequences is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch (*J Mol Biol.* 1970 Mar;48(3):443-53), the search for similarity method of Pearson and Lipman (*Proc Natl Acad Sci USA.* 1988 Apr;85(8):2444-8), computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux et al. (*Nucleic Acids Res.* 1984 Jan 11;12(1 Pt 1):387-95), preferably using the default settings, or by inspection. It is envisaged that percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30. See also "Current Methods in Sequence Comparison and Analysis," *Macromolecule Sequencing and Synthesis, Selected Methods and Applications*, pp 127-149 (1988), Alan R. Liss, Inc.

[00351] An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng and Doolittle (*J Mol Evol.* 1987;25(4):351-60); the method is similar to that described by Higgins and Sharp (*Comput Appl Biosci.* 1989 Apr;5(2):151-3). Useful PILEUP parameters include a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

[00352] Another example of a useful algorithm is the BLAST algorithm, described in: Altschul et al. (*J Mol Biol.* 1990 Oct 5;215(3):403-10.); Altschul et al., (*Nucleic Acids Res.* 1997 Sep 1;25(17):3389-402); and Karlin and Altschul (*Proc Natl Acad Sci U S A.* 1993 Jun 15;90(12):5873-7). A particularly useful BLAST program is the WU-Blast-2 program which was obtained from Altschul et al., (*Methods Enzymol.* 1996; 266:460-80). WU-Blast-2 uses several search parameters, most of which are set to the

default values. The adjustable parameters are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

[00353] An additional useful algorithm is gapped BLAST as reported by Altschul et al. (Nucleic Acids Res. 1997 Sep 1;25(17):3389-402). Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9; the two-hit method to trigger ungapped extensions, charges gap lengths of k a cost of 10+k; Xu set to 16, and Xg set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

[00354] In line herewith, the term “percent (%) nucleic acid sequence identity / homology / similarity” with respect to the nucleic acid sequence encoding the antibody constructs identified herein is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the coding sequence of the antibody construct. One method to align two sequences and thereby determine their homology uses the BLASTN module of WU-Blast2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Generally, the nucleic acid sequence homology, similarity, or identity between the nucleotide sequences encoding individual variant CDRs and the nucleotide sequences depicted herein are at least 60%, and more typically with increasing homologies, similarities or identities of at least 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, and almost 100%. Again, the same applies to nucleic acid sequence encoding the “variant VH” and/or “variant VL”.

[00355] In one embodiment, the percentage of identity to human germline of the antibody constructs according to the invention, or of the first and second domain (binding domains) of these antibody constructs, is $\geq 70\%$ or $\geq 75\%$, more preferably $\geq 80\%$ or $\geq 85\%$, even more preferably $\geq 90\%$, and most preferably $\geq 91\%$, $\geq 92\%$, $\geq 93\%$, $\geq 94\%$, $\geq 95\%$ or even $\geq 96\%$. Identity to human antibody germline gene products is thought to be an important feature to reduce the risk of therapeutic proteins to elicit an immune response against the drug in the patient during treatment. Hwang W.Y. and Foote J. (Methods. 2005 May;36(1):3-10) demonstrate that the reduction of non-human portions of drug antibody constructs leads to a decrease of risk of inducing anti-drug antibodies in the patients during treatment. By comparing an exhaustive number of clinically evaluated antibody drugs and the respective immunogenicity data, the trend is shown that humanization of the variable regions of antibodies / antibody constructs makes the protein less immunogenic (average 5.1 % of patients) than antibodies / antibody constructs carrying unaltered non-human variable regions (average 23.59 % of

patients). A higher degree of identity to human sequences is hence desirable for protein therapeutics based on variable regions and in the form of antibody constructs. For the purpose of determining the germline identity, the V-regions of VL can be aligned with the amino acid sequences of human germline V segments and J segments (<http://www2.mrc-lmb.cam.ac.uk/vbase/>) using Vector NTI software and the amino acid sequence calculated by dividing the identical amino acid residues by the total number of amino acid residues of the VL in percent. The same can be done for the VH segments (<http://www2.mrc-lmb.cam.ac.uk/vbase/>) with the exception that the VH CDR3 may be excluded due to its high diversity and a lack of existing human germline VH CDR3 alignment partners. Recombinant techniques can then be used to increase sequence identity to human antibody germline genes.

Nucleotides Encoding the Antibody Constructs

[00356] The invention further provides a polynucleotide / nucleic acid molecule encoding an antibody construct of the invention. Nucleic acid molecules are biopolymers composed of nucleotides. A polynucleotide is a biopolymer composed of 13 or more nucleotide monomers covalently bonded in a chain. DNA (such as cDNA) and RNA (such as mRNA) are examples of polynucleotides / nucleic acid molecules with distinct biological function. Nucleotides are organic molecules that serve as the monomers or subunits of nucleic acid molecules like DNA or RNA. The nucleic acid molecule or polynucleotide of the present invention can be double stranded or single stranded, linear or circular. It is envisaged that the nucleic acid molecule or polynucleotide is comprised in a vector. It is furthermore envisaged that such vector is comprised in a host cell. Said host cell is, e.g. after transformation or transfection with the vector or the polynucleotide / nucleic acid molecule of the invention, capable of expressing the antibody construct. For this purpose, the polynucleotide or nucleic acid molecule is operatively linked with control sequences.

[00357] The genetic code is the set of rules by which information encoded within genetic material (nucleic acids) is translated into proteins. Biological decoding in living cells is accomplished by the ribosome which links amino acids in an order specified by mRNA, using tRNA molecules to carry amino acids and to read the mRNA three nucleotides at a time. The code defines how sequences of these nucleotide triplets, called codons, specify which amino acid will be added next during protein synthesis. With some exceptions, a three-nucleotide codon in a nucleic acid sequence specifies a single amino acid. Because the vast majority of genes are encoded with exactly the same code, this particular code is often referred to as the canonical or standard genetic code.

[00358] Degeneracy of codons is the redundancy of the genetic code, exhibited as the multiplicity of three-base pair codon combinations that specify an amino acid. Degeneracy results because there are more codons than encodable amino acids. The codons encoding one amino acid may differ in any of their three positions; however, more often than not, this difference is in the

second or third position. For instance, codons GAA and GAG both specify glutamic acid and exhibit redundancy; but, neither specifies any other amino acid and thus demonstrate no ambiguity. The genetic codes of different organisms can be biased towards using one of the several codons that encode the same amino acid over the others – that is, a greater frequency of one will be found than expected by chance. For example, leucine is specified by six distinct codons, some of which are rarely used. Codon usage tables detailing genomic codon usage frequencies for most organisms are available. Recombinant gene technologies commonly take advantage of this effect by implementing a technique termed codon optimization, in which those codons are used to design a polynucleotide which are preferred by the respective host cell (such as a cell of human hamster origin, an *Escherichia coli* cell, or a *Saccharomyces cerevisiae* cell), e.g. in order to increase protein expression. It is hence envisaged that the polynucleotides / nucleic acid molecules of the present disclosure are codon optimized. Nevertheless, the polynucleotide / nucleic acid molecule encoding an antibody construct of the invention may be designed using any codon that encodes the desired amino acid.

[00359] According to one embodiment, the polynucleotide / nucleic acid molecule of the present invention encoding the antibody construct of the invention is in the form of one single molecule or in the form of two or more separate molecules. If the antibody construct of the present invention is a single chain antibody construct, the polynucleotide / nucleic acid molecule encoding such construct will most likely also be in the form of one single molecule. However, it is also envisaged that different components of the antibody construct (such as the different domains, e.g. the domain which binds to the pMAGE-HLA, the domain which binds to CD3, and/or further domains such as antibody constant domains) are located on separate polypeptide chains, in which case the polynucleotide / nucleic acid molecule is most likely in the form of two or more separate molecules.

[00360] The same applies for the vector comprising a polynucleotide / nucleic acid molecule of the present invention. If the antibody construct of the present invention is a single chain antibody construct, one vector may comprise the polynucleotide which encodes the antibody construct in one single location (as one single open reading frame, ORF). One vector may also comprise two or more polynucleotides / nucleic acid molecules at separate locations (with individual ORFs), each one of them encoding a different component of the antibody construct of the invention. It is envisaged that the vector comprising the polynucleotide / nucleic acid molecule of the present invention is in the form of one single vector or two or more separate vectors. In one embodiment, and for the purpose of expressing the antibody construct in a host cell, the host cell of the invention should comprise the polynucleotide / nucleic acid molecule encoding the antibody construct or the vector comprising such polynucleotide / nucleic acid molecule in their entirety, meaning that all components of the antibody construct – whether encoded as one single molecule or in separate molecules / locations – will

assemble after translation and form together the biologically active antibody construct of the invention.

[00361] The invention also provides a vector comprising a polynucleotide / nucleic acid molecule of the invention. A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell, usually for the purpose of replication and/or expression. The term “vector” encompasses – but is not restricted to – plasmids, viruses, cosmids, and artificial chromosomes. Some vectors are designed specifically for cloning (cloning vectors), others for protein expression (expression vectors). So-called transcription vectors are mainly used to amplify their insert. The manipulation of DNA is normally conducted on E. coli vectors, which contain elements necessary for their maintenance in E. coli. However, vectors may also have elements that allow them to be maintained in another organism such as yeast, plant or mammalian cells, and these vectors are called shuttle vectors. Insertion of a vector into the target or host cell is usually called transformation for bacterial cells and transfection for eukaryotic cells, while insertion of a viral vector is often called transduction.

[00362] In general, engineered vectors comprise an origin of replication, a multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the “backbone” of the vector. While the genetic code determines the polypeptide sequence for a given coding region, other genomic regions can influence when and where these polypeptides are produced. Modern vectors may therefore encompass additional features besides the transgene insert and a backbone: promoter, genetic marker, antibiotic resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences.

[00363] The term “control sequences” refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, a Kozak sequence and enhancers.

[00364] A nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, “operably linked” means that the nucleotide sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in

reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[00365] “Transfection” is the process of deliberately introducing nucleic acid molecules or polynucleotides (including vectors) into target cells. The term is mostly used for non-viral methods in eukaryotic cells. Transduction is often used to describe virus-mediated transfer of nucleic acid molecules or polynucleotides. Transfection of animal cells typically involves opening transient pores or “holes” in the cell membrane, to allow the uptake of material. Transfection can be carried out using biological particles (such as viral transfection, also called viral transduction), chemical-based methods (such as using calcium phosphate, lipofection, Fugene, cationic polymers, nanoparticles) or physical treatment (such as electroporation, microinjection, gene gun, cell squeezing, magnetofection, hydrostatic pressure, impalefection, sonication, optical transfection, heat shock).

[00366] The term “transformation” is used to describe non-viral transfer of nucleic acid molecules or polynucleotides (including vectors) into bacteria, and also into non-animal eukaryotic cells, including plant cells. Transformation is hence the genetic alteration of a bacterial or non-animal eukaryotic cell resulting from the direct uptake through the cell membrane(s) from its surroundings and subsequent incorporation of exogenous genetic material (nucleic acid molecules). Transformation can be effected by artificial means. For transformation to happen, cells or bacteria must be in a state of competence, which might occur as a time-limited response to environmental conditions such as starvation and cell density, and can also be artificially induced.

[00367] Moreover, the invention provides a host cell transformed or transfected with the polynucleotide / nucleic acid molecule of the invention or with the vector of the invention.

[00368] As used herein, the terms “host cell” or “recipient cell” are intended to include any individual cell or cell culture that can be or has been recipient of vectors, exogenous nucleic acid molecules and/or polynucleotides encoding the antibody construct of the present invention; and/or recipients of the antibody construct itself. The introduction of the respective material into the cell is carried out by way of transformation, transfection and the like (vide supra). The term “host cell” is also intended to include progeny or potential progeny of a single cell. Because certain modifications may occur in succeeding generations due to either natural, accidental, or deliberate mutation or due to environmental influences, such progeny may not, in fact, be completely identical (in morphology or in genomic or total DNA complement) to the parent cell, but is still included within the scope of the term as used herein. Suitable host cells include prokaryotic or eukaryotic cells, and also include – but are

not limited to – bacteria (such as *E. coli*), yeast cells, fungi cells, plant cells, and animal cells such as insect cells and mammalian cells, e.g., hamster, murine, rat, macaque or human.

[00369] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the antibody construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, *Kluyveromyces* hosts such as *K. lactis*, *K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickerhamii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilae* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402 226); *Pichia pastoris* (EP 183 070); *Candida*; *Trichoderma reesei* (EP 244 234); *Neurospora crassa*; *Schwanniomyces* such as *Schwanniomyces occidentalis*; and filamentous fungi such as *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

[00370] Suitable host cells for the expression of a glycosylated antibody construct are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

[00371] Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, *Arabidopsis* and tobacco can also be used as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See e.g. Hiatt et al., *Nature* (1989) 342: 76-78, Owen et al. (1992) *Bio/Technology* 10: 790-794, Artsaenko et al. (1995) *The Plant J* 8: 745-750, and Fecker et al. (1996) *Plant Mol Biol* 32: 979-986.

[00372] However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (cell culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (such as COS-7, ATCC CRL 1651); human embryonic kidney line (such as 293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen Virol.* 36 : 59 (1977)); baby hamster kidney cells (such as BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (such as CHO, Urlaub et al., *Proc. Natl. Acad. Sci. USA* 77: 4216 (1980)); mouse sertoli cells (such as TM4, Mather, *Biol. Reprod.* 23: 243-251 (1980)); monkey kidney cells (such as CV1 ATCC CCL 70); African green monkey kidney cells (such as VERO-76, ATCC CRL1587); human cervical carcinoma cells (such as HELA, ATCC CCL 2); canine kidney cells (such as MDCK, ATCC CCL 34); buffalo rat liver cells (such as BRL 3A, ATCC CRL 1442); human lung cells (such as W138, ATCC CCL 75);

human liver cells (such as Hep G2, 1413 8065); mouse mammary tumor (such as MMT 060562, ATCC CCL-51); TRI cells (Mather et al., Annals N. Y Acad. Sci. (1982) 383: 44-68); MRC 5 cells; FS4 cells; and a human hepatoma line (such as Hep G2).

[00373] Production of Antibody Constructs

[00374] In a further embodiment, the invention provides a process for producing an antibody construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and recovering the produced antibody construct from the culture.

[00375] As used herein, the term “culturing” refers to the *in vitro* maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium. Cells are grown and maintained in a cell growth medium at an appropriate temperature and gas mixture. Culture conditions vary widely for each cell type. Typical growth conditions are a temperature of about 37°C, a CO₂ concentration of about 5% and a humidity of about 95%. Recipes for growth media can vary e.g. in pH, concentration of the carbon source (such as glucose), nature and concentration of growth factors, and the presence of other nutrients (such as amino acids or vitamins). The growth factors used to supplement media are often derived from the serum of animal blood, such as fetal bovine serum (FBS), bovine calf serum (FCS), equine serum, and porcine serum. Cells can be grown either in suspension or as adherent cultures. There are also cell lines that have been modified to be able to survive in suspension cultures so they can be grown to a higher density than adherent conditions would allow.

[00376] The term “expression” includes any step involved in the production of an antibody construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, folding, post-translational modification, targeting to specific subcellular or extracellular locations, and secretion. The term “recovering” refers to a series of processes intended to isolate the antibody construct from the cell culture. The “recovering” or “purification” process may separate the protein and non-protein parts of the cell culture, and finally separate the desired antibody construct from all other polypeptides and proteins. Separation steps usually exploit differences in protein size, physico-chemical properties, binding affinity and biological activity. Preparative purifications aim to produce a relatively large quantity of purified proteins for subsequent use, while analytical purification produces a relatively small amount of a protein for a variety of research or analytical purposes.

[00377] When using recombinant techniques, the antibody construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed

fragments, are removed, for example, by centrifugation or ultrafiltration. The antibody construct of the invention may e.g. be produced in bacteria such as *E. coli*. After expression, the construct is isolated from the bacterial cell paste in a soluble fraction and can be purified e.g. via affinity chromatography and/or size exclusion. Final purification can be carried out in a manner similar to the process for purifying an antibody construct expressed in mammalian cells and secreted into the medium. Carter et al. (Biotechnology (NY) 1992 Feb;10(2):163-7) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*.

[00378] Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an ultrafiltration unit.

[00379] The antibody construct of the invention prepared from the host cells can be recovered or purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography. Other techniques for protein purification such as fractionation on an ion-exchange column, mixed mode ion exchange, HIC, ethanol precipitation, size exclusion chromatography, reverse phase HPLC, chromatography on silica, chromatography on heparin sepharose, chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), immunoaffinity (such as Protein A/G/L) chromatography, chromato-focusing, SDS-PAGE, ultracentrifugation, and ammonium sulfate precipitation are also available depending on the antibody construct to be recovered.

[00380] A protease inhibitor may be included in any of the foregoing steps to inhibit proteolysis, and antibiotics may be included to prevent the growth of contaminants.

Molecule Properties

[00381] A molecule may exhibit various different properties that are desired in a therapeutic pharmaceutical, e.g., stability during various storage states, *in vivo* stability, purity, and other properties that can be assayed.

[00382] Accordingly, in a further embodiment, the bispecific antibody constructs of the present invention exhibit high monomer yields under standard research scale conditions, e.g., in a standard two-step purification process. Preferably the monomer yield of the antibody constructs according to the invention is ≥ 0.25 mg/L supernatant, more preferably ≥ 0.5 mg/L, even more preferably ≥ 1 mg/L, and most preferably ≥ 3 mg/L supernatant.

[00383] Likewise, the yield of the dimeric antibody construct isoforms and hence the monomer percentage (i.e., monomer: (monomer+dimer)) of the antibody constructs can be determined. The productivity of monomeric and dimeric antibody constructs and the calculated monomer percentage can e.g. be obtained in the SEC purification step of culture supernatant from standardized research-

scale production in roller bottles. In one embodiment, the monomer percentage of the antibody constructs is $\geq 80\%$, more preferably $\geq 85\%$, even more preferably $\geq 90\%$, and most preferably $\geq 95\%$.

[00384] In one embodiment, the antibody constructs have a preferred plasma stability (ratio of EC50 with plasma to EC50 w/o plasma) of ≤ 5 or ≤ 4 , more preferably ≤ 3.5 or ≤ 3 , even more preferably ≤ 2.5 or ≤ 2 , and most preferably ≤ 1.5 or ≤ 1 . The plasma stability of an antibody construct can be tested by incubation of the construct in human plasma at 37°C for 24 hours followed by EC50 determination in a 51chromium release cytotoxicity assay. The effector cells in the cytotoxicity assay can be stimulated enriched human CD8 positive T cells. Target cells can e.g. be cells transfected with human MAGEB2. The effector to target cell (E:T) ratio can be chosen as 10:1 or 5:1. The human plasma pool used for this purpose is derived from the blood of healthy donors collected by EDTA coated syringes. Cellular components are removed by centrifugation and the upper plasma phase is collected and subsequently pooled. As control, antibody constructs are diluted immediately prior to the cytotoxicity assay in RPMI-1640 medium. The plasma stability is calculated as ratio of EC50 (after plasma incubation) to EC50 (control).

[00385] It is furthermore preferred that the monomer to dimer conversion of antibody constructs of the invention is low. The conversion can be measured under different conditions and analyzed by high performance size exclusion chromatography. For example, incubation of the monomeric isoforms of the antibody constructs can be carried out for 7 days at 37°C and concentrations of e.g. 100 µg/ml or 250 µg/ml in an incubator. Under these conditions, it is preferred that the antibody constructs of the invention show a dimer percentage that is $\leq 5\%$, more preferably $\leq 4\%$, even more preferably $\leq 3\%$, even more preferably $\leq 2.5\%$, even more preferably $\leq 2\%$, even more preferably $\leq 1.5\%$, and most preferably $\leq 1\%$ or $\leq 0.5\%$ or even 0%.

[00386] It is also preferred that the bispecific antibody constructs of the present invention present with very low dimer conversion after a number of freeze/thaw cycles. For example, the antibody construct monomer is adjusted to a concentration of 250 µg/ml e.g. in generic formulation buffer and subjected to three freeze/thaw cycles (freezing at -80°C for 30 min followed by thawing for 30 min at room temperature), followed by high performance SEC to determine the percentage of initially monomeric antibody construct, which had been converted into dimeric antibody construct. Preferably the dimer percentages of the bispecific antibody constructs are $\leq 5\%$, more preferably $\leq 4\%$, even more preferably $\leq 3\%$, even more preferably $\leq 2.5\%$, even more preferably $\leq 2\%$, even more preferably $\leq 1.5\%$, and most preferably $\leq 1\%$ or even $\leq 0.5\%$, for example after three freeze/thaw cycles.

[00387] The bispecific antibody constructs of the present invention preferably show a favorable thermostability with aggregation temperatures $\geq 45^\circ\text{C}$ or $\geq 50^\circ\text{C}$, more preferably $\geq 52^\circ\text{C}$ or $\geq 54^\circ\text{C}$, even more preferably $\geq 56^\circ\text{C}$ or $\geq 57^\circ\text{C}$, and most preferably $\geq 58^\circ\text{C}$ or $\geq 59^\circ\text{C}$. The thermostability parameter can be determined in terms of antibody aggregation temperature as follows: Antibody

solution at a concentration 250 µg/ml is transferred into a single use cuvette and placed in a Dynamic Light Scattering (DLS) device. The sample is heated from 40°C to 70°C at a heating rate of 0.5°C/min with constant acquisition of the measured radius. Increase of radius indicating melting of the protein and aggregation is used to calculate the aggregation temperature of the antibody.

[00388] Alternatively, temperature melting curves can be determined by Differential Scanning Calorimetry (DSC) to determine intrinsic biophysical protein stabilities of the antibody constructs. These experiments are performed using a MicroCal LLC (Northampton, MA, U.S.A) VP-DSC device. The energy uptake of a sample containing an antibody construct is recorded from 20°C to 90°C compared to a sample containing only the formulation buffer. The antibody constructs are adjusted to a final concentration of 250 µg/ml e.g. in SEC running buffer. For recording of the respective melting curve, the overall sample temperature is increased stepwise. At each temperature T energy uptake of the sample and the formulation buffer reference is recorded. The difference in energy uptake C_p (kcal/mole/°C) of the sample minus the reference is plotted against the respective temperature. The melting temperature is defined as the temperature at the first maximum of energy uptake.

[00389] The pMAGE-HLA xCD3 bispecific antibody constructs of the invention are also envisaged to have a turbidity (as measured by OD340 after concentration of purified monomeric antibody construct to 2.5 mg/ml and overnight incubation) of ≤ 0.2 , preferably of ≤ 0.15 , more preferably of ≤ 0.12 , even more preferably of ≤ 0.1 , and most preferably of ≤ 0.08 .

[00390] In a further embodiment the antibody construct according to the invention is stable at physiologic or slightly lower pH, i.e. about pH 7.4 to 6.0. The more tolerant the antibody construct behaves at unphysiologic pH such as about pH 6.0, the higher is the recovery of the antibody construct eluted from an ion exchange column relative to the total amount of loaded protein. Recovery of the antibody construct from an ion (e.g., cation) exchange column at about pH 6.0 is preferably $\geq 30\%$, more preferably $\geq 40\%$, more preferably $\geq 50\%$, even more preferably $\geq 60\%$, even more preferably $\geq 70\%$, even more preferably $\geq 80\%$, even more preferably $\geq 90\%$, even more preferably $\geq 95\%$, and most preferably $\geq 99\%$.

[00391] In a further embodiment, the antibody construct according to the invention is stable at acidic pH. The more tolerant the antibody construct behaves at unphysiologic pH such as pH 5.5 (a pH which is required to run e.g. a cation exchange chromatography), the higher is the recovery of the antibody construct eluted from an ion exchange column relative to the total amount of loaded protein. Recovery of the antibody construct from an ion (e.g., cation) exchange column at pH 5.5 is preferably $\geq 30\%$, more preferably $\geq 40\%$, more preferably $\geq 50\%$, even more preferably $\geq 60\%$, even more

preferably $\geq 70\%$, even more preferably $\geq 80\%$, and most preferably $\geq 95\%$. The percentage represents the area under the curve (= AUC) of the main peak.

[00392] Changes in the potency of a target x CD3 antibody construct as a function of preincubation of the construct on the target cells in the absence of T cells can be measured. If an antibody construct is internalized, it is expected to undergo lysosomal degradation. The effective concentration is hence expected to decrease over time, and thus the apparent potency should decrease as well. The effect has been observed with some targets, for which this is a known phenomenon. Antibody constructs of the invention are envisaged to not be internalized or to not undergo significant internalization by the target cell. The rate of internalization can be assayed e.g. as described in the following: T cells are counted and diluted to a concentration of 1×10^5 / ml in assay media. Target positive target cells are counted and plated e.g. at 2500 cells per well (cpw). The antibody construct is diluted serially 1:2, e.g. at a starting concentration of 100 nM. The antibody construct is added to the culture assay plates to allow for 0 hours, 1 hour or 2 hours of incubation prior to addition of the T cells. Then the T cells are plated at 25000 cpw (E:T = 10:1), and the assay is incubated for 48 hours at 37°C. Target cell survival is analyzed e.g. with the Steady-Glo® system (25 μ l/well). Preferably, the internalization rate (e.g. measured as a decrease in cytotoxicity) is $\leq 20\%$ after a 2-hour (pre-)incubation of the antibody construct with the target cell, more preferably $\leq 15\%$, even more preferably $\leq 10\%$, and most preferably $\leq 5\%$.

[00393] It is furthermore envisaged for an antibody construct of the invention that shed or soluble target does not significantly impair its efficacy or biologic activity. This can be measured e.g. in a cytotoxicity assay where soluble target is added at increasing concentrations to the assay, e.g. at 0 nM – 0.3 nM – 0.7 nM – 1 nM – 3 nM – 7 nM – 12 nM. An exemplary E:T value is 10:1. The EC50 value of the tested antibody construct should not be significantly increased in the presence of soluble target.

[00394] It is furthermore envisaged that the antibody constructs of the present invention exhibit therapeutic efficacy, which manifests as anti-tumor activity or tumor growth inhibition. This can, e.g., be assessed in a study as disclosed in Example 10. In one embodiment, the tumor growth inhibition of the antibody construct of the invention T/C [%] is ≤ 70 , ≤ 60 , ≤ 50 , ≤ 40 , ≤ 30 , ≤ 20 , ≤ 10 , ≤ 5 , ≤ 4 , ≤ 3 , or ≤ 2 . Modification or adjustment of certain parameters of these studies (such as the number of injected tumor cells, the site of injection, the number of transplanted human T cells, the amount of antibody constructs to be administered, and the timelines) is also envisaged, while still arriving at a meaningful and reproducible result.

Covalent Modifications of Constructs

[00395] Covalent modifications of the antibody constructs are also included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antibody construct are introduced into the molecule by reacting specific amino acid residues of the antibody construct with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

[00396] Cysteiny l residues most commonly are reacted with α -haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteiny l residues also are derivatized by reaction with bromotrifluoroacetone, α -bromo- β -(5-imidazolyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

[00397] Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1 M sodium cacodylate at pH 6.0. Lysiny l and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysiny l residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimide; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[00398] Arginy l residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[00399] The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidazole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives,

respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

[00400] Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides ($\text{R}'\text{—N}=\text{C}=\text{N}\text{—R}'$), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginy and glutaminy residues by reaction with ammonium ions.

[00401] Derivatization with bifunctional agents is useful for crosslinking the antibody constructs of the present invention to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimide yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates as described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

[00402] Glutaminy and asparaginy residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[00403] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[00404] Another type of covalent modification of the antibody constructs included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of particular glycosylation amino acid residues, discussed

below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed herein.

[00405] Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[00406] Addition of glycosylation sites to the antibody construct is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the amino acid sequence of an antibody construct is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[00407] Another means of increasing the number of carbohydrate moieties on the antibody construct is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330, and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306.

[00408] Removal of carbohydrate moieties present on the starting antibody construct may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent

compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259:52 and by Edge et al., 1981, Anal. Biochem. 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol. 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin et al., 1982, J. Biol. Chem. 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

[00409] Other modifications of the antibody construct are also contemplated herein. For example, another type of covalent modification of the antibody construct comprises linking the antibody construct to various non-proteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody construct, e.g. in order to facilitate the addition of polymers such as PEG.

[00410] In some embodiments, the covalent modification of the antibody constructs of the invention comprises the addition of one or more labels. The labelling group may be coupled to the antibody construct via spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and can be used in performing the present invention. The term "label" or "labelling group" refers to any detectable label. In general, labels fall into a variety of classes, depending on the assay in which they are to be detected – the following examples include, but are not limited to:

- a) isotopic labels, which may be radioactive or heavy isotopes, such as radioisotopes or radionuclides (e.g., ^3H , ^{14}C , ^{15}N , ^{35}S , ^{89}Zr , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I)
- b) magnetic labels (e.g., magnetic particles)
- c) redox active moieties
- d) optical dyes (including, but not limited to, chromophores, phosphors and fluorophores) such as fluorescent groups (e.g., FITC, rhodamine, lanthanide phosphors), chemiluminescent groups, and fluorophores which can be either "small molecule" fluors or proteinaceous fluors
- e) enzymatic groups (e.g. horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase)
- f) biotinylated groups

- g) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sides for secondary antibodies, metal binding domains, epitope tags, etc.)

[00411] Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., 1988, Science 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe et al., 1994, FEBS Letters 344:191. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow et al., 1994, Semin. Immunol. 6:267-78.

[00412] The antibody construct of the invention may also comprise additional domains, which are *e.g.* helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of the molecule. Domains helpful for the isolation of an antibody construct may be selected from peptide motives or secondarily introduced moieties, which can be captured in an isolation method, *e.g.* an isolation column. Non-limiting embodiments of such additional domains comprise peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants thereof (*e.g.* StrepII-tag) and His-tag. All herein disclosed antibody constructs may comprise a His-tag domain, which is generally known as a repeat of consecutive His residues in the amino acid sequence of a molecule, preferably of five, and more preferably of six His residues (hexa-histidine) (SEQ ID NO: 18451). The His-tag may be located *e.g.* at the N- or C-terminus of the antibody construct, preferably it is located at the C-terminus. Most preferably, a hexa-histidine tag (HHHHHH) (SEQ ID NO: 30) is linked via peptide bond to the C-terminus of the antibody construct according to the invention. Additionally, a conjugate system of PLGA-PEG-PLGA may be combined with a poly-histidine tag for sustained release application and improved pharmacokinetic profile.

[00413] By “fluorescent label” is meant any molecule that may be detected via its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red,

IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland.

[00414] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie et al., 1994, Science 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, Biotechniques 24:462-471; Heim et al., 1996, Curr. Biol. 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki et al., 1993, J. Immunol. 150:5408-5417), β galactosidase (Nolan et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5,292,658; 5,418,155; 5,683,888; 5,741,668; 5,777,079; 5,804,387; 5,874,304; 5,876,995; 5,925,558).

Pharmaceutical Formulations

[00415] Moreover, the invention provides a pharmaceutical composition or formulation comprising an antibody construct of the invention or an antibody construct produced according to the process of the invention.

[00416] As used herein, the term “pharmaceutical composition” relates to a composition which is suitable for administration to a patient, preferably a human patient. The particularly preferred pharmaceutical composition of this invention comprises one or a plurality of the antibody construct(s) of the invention, preferably in a therapeutically effective amount. Preferably, the pharmaceutical composition further comprises suitable formulations of one or more (pharmaceutically effective) carriers, stabilizers, excipients, diluents, solubilizers, surfactants, emulsifiers, preservatives and/or adjuvants. Acceptable constituents of the composition are preferably nontoxic to recipients at

the dosages and concentrations employed. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

[00417] The compositions may comprise a pharmaceutically acceptable carrier. In general, as used herein, “pharmaceutically acceptable carrier” means any and all aqueous and non-aqueous solutions, sterile solutions, solvents, buffers, e.g. phosphate buffered saline (PBS) solutions, water, suspensions, emulsions, such as oil/water emulsions, various types of wetting agents, liposomes, dispersion media and coatings, which are compatible with pharmaceutical administration, in particular with parenteral administration. The use of such media and agents in pharmaceutical compositions is well known in the art, and the compositions comprising such carriers can be formulated by well-known conventional methods.

[00418] Certain embodiments provide pharmaceutical compositions comprising the antibody construct of the invention and further one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and/or to stabilize such formulations and processes against degradation and spoilage e.g. due to stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter. Excipients should in general be used in their lowest effective concentrations.

[00419] In certain embodiments, the pharmaceutical composition may contain formulation materials for the purpose of modifying, maintaining or preserving certain characteristics of the composition such as the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration (see, Remington’s Pharmaceutical Sciences, 18th Edition, 1990, Mack Publishing Company). In such embodiments, suitable formulation materials may include, but are not limited to, e.g., amino acids, antimicrobials such as antibacterial and antifungal agents, antioxidants, buffers, buffer systems and buffering agents which are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8 or 9, non-aqueous solvents, vegetable oils, and injectable organic esters, aqueous carriers including water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media, biodegradable polymers such as polyesters, bulking agents, chelating agents, isotonic and absorption delaying agents, complexing agents, fillers, carbohydrates, (low molecular weight) proteins, polypeptides or proteinaceous carriers, preferably of human origin, coloring and flavouring agents, sulfur containing reducing agents, diluting agents, emulsifying agents, hydrophilic polymers, salt-forming counter-ions, preservatives, metal complexes, solvents and co-solvents, sugars and sugar

alcohols, suspending agents, surfactants or wetting agents, stability enhancing agents, tonicity enhancing agents, parenteral delivery vehicles, or intravenous delivery vehicles.

[00420] Different constituents of the pharmaceutical composition can have different effects, for example, and amino acid can act as a buffer, a stabilizer and/or an antioxidant; mannitol can act as a bulking agent and/or a tonicity enhancing agent; sodium chloride can act as delivery vehicle and/or tonicity enhancing agent; etc.

[00421] In the context of the present invention, a pharmaceutical composition may comprise: (a) an antibody construct as described herein, (b) at least one buffer agent, (c) at least one saccharide, and (d) at least one surfactant; wherein the pH of the pharmaceutical composition is in the range of 3.5 to 6.

[00422] In the composition described above, the first domain preferably has an isoelectric point (pI) in the range of 4 to 9.5; the second domain has a pI in the range of 8 to 10, preferably 8.5 to 9.0; and the antibody construct optionally comprises a third domain comprising two polypeptide monomers, each comprising a hinge, a CH2 domain and a CH3 domain, wherein said two polypeptide monomers are fused to each other via a peptide linker;

[00423] In the composition described above, it is further envisaged that the at least one buffer agent is present at a concentration range of 5 to 200 mM, more preferably at a concentration range of 10 to 50 mM. It is also envisaged that the at least one saccharide is selected from the group consisting of monosaccharide, disaccharide, cyclic polysaccharide, sugar alcohol, linear branched dextran or linear non-branched dextran. It is also envisaged that the disacchade is selected from the group consisting of sucrose, trehalose and mannitol, sorbitol, and combinations thereof. It is further envisaged that the sugar alcohol is sorbitol. It is also envisaged that the at least one saccharide is present at a concentration in the range of 1 to 15% (m/V), preferably in a concentration range of 9 to 12% (m/V). It is further envisaged that the antibody construct is present in a concentration range of 0.1 to 8 mg/ml, preferably of 0.2-2.5 mg/ml, more preferably of 0.25-1.0 mg/ml.

[00424] According to one embodiment of the composition described above, the at least one surfactant is selected from the group consisting of polysorbate 20, polysorbate 40, polysorbate 60, polysorbate 80, poloxamer 188, pluronic F68, triton X-100, polyoxyethylen, PEG 3350, PEG 4000 and combinations thereof. It is further envisaged that the at least one surfactant is present at a concentration in the range of 0.004 to 0.5 % (m/V), preferably in the range of 0.001 to 0.01% (m/V). It is envisaged that the pH of the composition is in the range of 4.0 to 5.0, preferably 4.2. It is also envisaged that the pharmaceutical composition has an osmolarity in the range of 150 to 500 mOsm. It is further envisaged that the pharmaceutical composition further comprises an excipient selected from the group consisting of one or more polyol(s) and one or more amino acid(s). It is envisaged in the

context of the present invention that said one or more excipient is present in the concentration range of 0.1 to 15 % (w/V).

- [00425]** The present invention also provides a pharmaceutical composition comprising
- (a) the antibody construct as described herein, preferably in a concentration range of 0.1 to 8 mg/ml, preferably of 0.2-2.5 mg/ml, more preferably of 0.25-1.0 mg/ml;
 - (b) 10 mM glutamate or acetate;
 - (c) 9% (m/V) sucrose or 6% (m/V) sucrose and 6% (m/V) hydroxypropyl- β -cyclodextrin;
 - (d) 0.01% (m/V) polysorbate 80;

wherein the pH of the liquid pharmaceutical composition is 4.2.

[00426] It is envisaged that the composition of the invention might comprise, in addition to the antibody construct of the invention defined herein, further biologically active agents, depending on the intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions, drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art. It is also envisaged that the antibody construct of the present invention is applied in a co-therapy, i.e., in combination with another anti-cancer medicament.

[00427] In this context, it is envisaged that the pharmaceutical composition of the invention (which comprises an antibody construct comprising a first domain which binds to the pMAGE-HLA on the surface of a target cell and a second domain which binds to CD3 on the surface of a T cell, as described in more detail herein above) furthermore comprises an agent, preferably an antibody or antibody construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). The present invention also refers to a combination of an antibody construct according to the invention (which comprises an antibody construct comprising a first domain which binds to the pMAGE-HLA on the surface of a target cell and a second domain which binds to CD3 on the surface of a T cell, as described in more detail herein above) and an agent, preferably an antibody or antibody construct, which binds to a protein of the immune checkpoint pathway (such as PD-1 or CTLA-4) or to a co-stimulatory immune checkpoint receptor (such as 4-1BB). Due to the nature of the at least two ingredients of the combination, namely their pharmaceutical activity, the combination can also be referred to as a therapeutic combination. In some embodiments, the combination can be in the form of a pharmaceutical composition or of a kit. According to one embodiment, the pharmaceutical composition or the combination comprises an

antibody construct of the invention and an antibody or antibody construct which binds to PD-1. Anti-PD-1 binding proteins useful for this purpose are e.g. described in detail in PCT/US2019/013205.

[00428] In certain embodiments, the optimal pharmaceutical composition is determined depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, Remington's Pharmaceutical Sciences, *supra*. In certain embodiments, such compositions may influence the physical state, stability, rate of *in vivo* release and rate of *in vivo* clearance of the antibody construct of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection or physiological saline solution, possibly supplemented with other materials common in compositions for parenteral administration. In certain embodiments, the compositions comprising the antibody construct of the invention may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (Remington's Pharmaceutical Sciences, *supra*) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the antibody construct of the invention may be formulated as a lyophilizate using appropriate excipients.

[00429] When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired antibody construct of the invention in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the antibody construct of the invention is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent that may provide controlled or sustained release of the product which can be delivered via depot injection, or that may promote sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antibody construct.

[00430] Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving the antibody construct of the invention in sustained or controlled delivery formulations. Techniques for formulating a variety of sustained- or controlled-delivery means are known to those skilled in the art. The antibody construct may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, in colloidal drug delivery systems, or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

[00431] Pharmaceutical compositions used for *in vivo* administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral

administration can be stored in lyophilized form or in a solution. Parenteral compositions are generally placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[00432] Another aspect of the invention includes self-buffering formulations comprising the antibody construct of the invention, which can be used as pharmaceutical compositions, as described in international patent application WO 2006/138181. A variety of publications are available on protein stabilization and formulation materials and methods useful in this regard, such as Arawaka T. et al., *Pharm Res.* 1991 Mar;8(3):285-91; Kendrick et al., "Physical stabilization of proteins in aqueous solution" in: *Rational Design of Stable Protein Formulations: Theory and Practice*, Carpenter and Manning, eds. *Pharmaceutical Biotechnology*. 13: 61-84 (2002), and Randolph and Jones, *Pharm Biotechnol.* 2002;13:159-75, see particularly the parts pertinent to excipients and processes for self-buffering protein formulations, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

[00433] Salts may be used in accordance with certain embodiments of the invention, e.g. in order to adjust the ionic strength and/or the isotonicity of a composition or formulation and/or to improve the solubility and/or physical stability of an antibody construct or other ingredient of a composition in accordance with the invention. Ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, in particular, the denatured peptide linkages (–CONH) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

[00434] Ionic species differ significantly in their effects on proteins. A number of categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic". Destabilizing solutes are referred to as "chaotropic". Kosmotropes are commonly used at high concentrations to precipitate proteins from solution ("salting-out"). Chaotropes are commonly used to denature and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

[00435] Free amino acids can be used in formulations or compositions comprising the antibody construct of the invention in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as for other standard uses. Certain amino acids can be used for

stabilizing proteins in a formulation, others are useful during lyophilization to ensure correct cake structure and properties of the active ingredient. Some amino acids may be useful to inhibit protein aggregation in both liquid and lyophilized formulations, and others are useful as antioxidants.

[00436] Polyols are kosmotropic and are useful as stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols are also useful for adjusting the tonicity of formulations and for protecting against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Polyols can also serve as cryoprotectants in the context of the present invention.

[00437] Certain embodiments of the formulation or composition comprising the antibody construct of the invention can comprise surfactants. Proteins may be susceptible to adsorption on surfaces and to denaturation and resulting aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These deleterious interactions generally scale inversely with protein concentration and are typically exacerbated by physical agitation, such as that generated during the shipping and handling of a product. Surfactants are routinely used to prevent, minimize, or reduce surface adsorption. Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein specific, since one specific surfactant will typically stabilize some proteins and destabilize others.

[00438] Certain embodiments of the formulation or composition comprising the antibody construct of the invention can comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can also be used to prevent oxidative degradation of proteins. It is envisaged that antioxidants for use in therapeutic protein formulations in accordance with the present invention can be water-soluble and maintain their activity throughout the shelf life of the product (the composition comprising the antibody construct). Antioxidants can also damage proteins and should hence – among other things – be selected in a way to eliminate or sufficiently reduce the possibility of antioxidants damaging the antibody construct or other proteins in the formulation.

[00439] Formulations in accordance with the invention may include metal ions that are protein co-factors and that are necessary to form protein coordination complexes, such as zinc necessary to form certain insulin suspensions. Metal ions also can inhibit some processes that degrade proteins. However, metal ions also catalyze physical and chemical processes that degrade proteins. Magnesium ions (10-120 mM) can be used to inhibit isomerization of aspartic acid to isoaspartic acid. Ca²⁺ ions (up to 100 mM) can increase the stability of human deoxyribonuclease. Mg²⁺, Mn²⁺, and Zn²⁺, however,

can destabilize rhDNase. Similarly, Ca^{+2} and Sr^{+2} can stabilize Factor VIII, it can be destabilized by Mg^{+2} , Mn^{+2} and Zn^{+2} , Cu^{+2} and Fe^{+2} , and its aggregation can be increased by Al^{+3} ions.

[00440] Certain embodiments of the formulation or composition comprising the antibody construct of the invention can comprise one or more preservatives. Preservatives are necessary for example when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that include preservatives can be challenging. Preservatives very often have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

[00441] As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time during which a preservative is in contact with the antibody construct, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life. An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components. Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration.

[00442] The antibody construct of the invention will generally be designed for specific routes and methods of administration, for specific dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. The materials of the composition are preferably formulated in concentrations that are acceptable for the site of administration. Formulations and compositions thus may be designed in accordance with the invention for delivery by any suitable route of administration. In the context of the present

invention, the routes of administration include, but are not limited to topical routes, enteral routes and parenteral routes.

[00443] The pharmaceutical compositions and the antibody construct of this invention are particularly useful for parenteral administration, e.g., subcutaneous or intravenous delivery, for example by injection such as bolus injection, or by infusion such as continuous infusion.

Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163.

[00444] In particular, the present invention provides for an uninterrupted administration of the suitable composition. As a non-limiting example, uninterrupted or substantially uninterrupted, i.e. continuous administration may be realized by a small pump system worn by the patient for metering the influx of therapeutic agent into the body of the patient. The pharmaceutical composition comprising the antibody construct of the invention can be administered by using said pump systems. Such pump systems are generally known in the art, and commonly rely on periodic exchange of cartridges containing the therapeutic agent to be infused. When exchanging the cartridge in such a pump system, a temporary interruption of the otherwise uninterrupted flow of therapeutic agent into the body of the patient may ensue. In such a case, the phase of administration prior to cartridge replacement and the phase of administration following cartridge replacement would still be considered within the meaning of the pharmaceutical means and methods of the invention together make up one “uninterrupted administration” of such therapeutic agent.

[00445] The continuous or uninterrupted administration of the antibody constructs of the invention may be intravenous or subcutaneous by way of a fluid delivery device or small pump system including a fluid driving mechanism for driving fluid out of a reservoir and an actuating mechanism for actuating the driving mechanism. Pump systems for subcutaneous administration may include a needle or a cannula for penetrating the skin of a patient and delivering the suitable composition into the patient's body. Said pump systems may be directly fixed or attached to the skin of the patient independently of a vein, artery or blood vessel, thereby allowing a direct contact between the pump system and the skin of the patient. The pump system can be attached to the skin of the patient for 24 hours up to several days. The pump system may be of small size with a reservoir for small volumes. As a non-limiting example, the volume of the reservoir for the suitable pharmaceutical composition to be administered can be between 0.1 and 50 ml.

[00446] The continuous administration may also be transdermal by way of a patch worn on the skin and replaced at intervals. One of skill in the art is aware of patch systems for drug delivery suitable for this purpose. It is of note that transdermal administration is especially amenable to

uninterrupted administration, as exchange of a first exhausted patch can advantageously be accomplished simultaneously with the placement of a new, second patch, for example on the surface of the skin immediately adjacent to the first exhausted patch and immediately prior to removal of the first exhausted patch. Issues of flow interruption or power cell failure do not arise.

[00447] If the pharmaceutical composition has been lyophilized, the lyophilized material is first reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline, phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization. The pharmaceutical compositions and the antibody construct of this invention are particularly useful for parenteral administration, e.g., intravenous delivery, for example by injection or infusion.

Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163.

[00448] In an embodiment, a pharmaceutical composition comprising a binding domain or antibody construct, e.g. a bispecific antibody, described herein specifically targeting pMAGE-HLA derived from MAGEB2 and/or a modified T cell, e.g. a CAR-T cell, expressing a binding domain or antibody construct, e.g. a bispecific antibody, may be administered to a subject in need thereof in order to increase a cellular immune response. The immune response may include, for example, cellular immune responses mediated by cytotoxic T cells capable of killing cancer cells, regulatory T cells, and helper T cell responses. Humoral immune responses, mediated primarily by helper T cells capable of activating B cells thus leading to antibody production, may also be induced. A variety of techniques may be used for analyzing the type of immune responses induced by the compositions, which are described in the literature for example, in Current Protocols in Immunology, Edited by: John E. Coligan, Ada M. Kruisbeek, David H. Margulies, Ethan M. Shevach, Warren Strober (2001) John Wiley & Sons, NY, N.Y, the content of which is herein incorporated by reference in its entirety.

[00449] Human Leukocyte Antigen (HLA) System

[00450] The human leukocyte antigen system (HLA) is the human version of the gene complex which encodes the major histocompatibility complex (MHC). Those of ordinary skill in the art will recognize that the terms "major histocompatibility complex (MHC)", "MHC molecules", "MHC proteins" and "human leukocyte antigen (HLA) system", "HLA molecules", "HLA proteins" are used interchangeably herein.

[00451] HLA proteins are classified into two types, referred to as HLA class I (corresponding to MHC class I) and HLA class II (corresponding to MHC class II), and includes the three main HLA class I molecules (A, B & C) and also the three main HLA class II molecules (DP, DQ, & DR).

[00452] The structures of the proteins of the two HLA classes are very similar; however, they have very different functions. Class I HLA proteins are present on the surface of almost all cells of the body, including most tumor cells. Class I HLA proteins have bound, or “loaded”, peptide antigens that usually originate from endogenous proteins or from pathogens present inside cells. These proteins are processed by the cell into peptides which bind the Class I HLA, and are then presented on the cell surface to immune cells, such as cytotoxic T-lymphocytes (CTLs). This can also be referred to as the peptide—HLA complex, or more specifically, the MAGEB2 peptide—HLA complex, or pMAGE-HLA, or peptide-MHC, or simply pMHC.

[00453] HLA class II proteins are present on antigen presenting cells (APCs), including but not limited to dendritic cells, B cells, and macrophages. They typically present peptides, which are derived from external antigen sources, i.e. outside of the cells, that have been internalized and processed into peptides. The HLA class II with peptide bound to it is then presented to immune cells such as helper T cells. Most of the peptides bound by the HLA class I proteins originate from cytoplasmic proteins produced in the healthy host cells of an organism itself, and do not normally stimulate an immune reaction.

[00454] Of particular relevance to the present invention, HLA class I alleles A, B, and C present peptides (e.g., the MAGEB2 peptide of SEQ ID NO: 1) derived from proteins expressed within the cell, such as the MAGEB2 protein. See, Janeway CA Jr, Travers P, Walport M, et al. Immunobiology: The Immune System in Health and Disease. 5th edition. New York: Garland Science; 2001. The major histocompatibility complex and its functions. See also, Tissue Antigens. 2013 Apr; 81(4): 194–203, and Human Immunology, Volume 68, Issue 5, May 2007, Pages 392-417.

[00455] Class I HLA molecules consist of a heavy chain and a light chain and are capable of binding a peptide of about 7 to 13 amino acids, if this peptide has suitable binding motifs, and presenting it to cytotoxic T-lymphocytes. The peptides bound by class I HLA molecules originate from an endogenous protein antigen. The heavy chain of the HLA molecules of class I can be an HLA-A, HLA-B or HLA-C monomer, and the light chain is β -2-microglobulin. Class I HLA occurs as an α chain composed of three domains— α 1, α 2, and α 3. This chain is often referred to as the class I heavy chain, and is referred to herein as the class I alpha-chain. The α 1 rests upon a unit of the non-HLA molecule β 2 microglobulin (encoded on human chromosome 15). The α 3 domain is transmembrane, anchoring the HLA class I molecule to the cell membrane. The peptide being presented is held by the floor of the peptide-binding groove, in the central region of the α 1/ α 2 heterodimer (a molecule composed of two nonidentical subunits). Class I HLA-A, HLA-B or HLA-C are highly polymorphic.

[00456] There is a known geographic distribution of the different HLA alleles. For example, one HLA allele of particular interest, HLA-A*02:01, is widely expressed throughout North America, Europe and Australia. Peptides presented by, for example, the HLA-A*02:01 can be referred to as being "HLA-A*02:01 restricted". Other HLA-A alleles of particular interest include HLA-A*02:02, HLA-A*02:05, HLA-A*02:06, and HLA-A*02:07.

[00457] In one embodiment, the invention provides a binding domain that binds to a MAGEB2 peptide (SEQ ID NO: 1) complexed with a class I HLA, wherein the HLA is an HLA-A. In a further embodiment, the invention provides a binding domain that binds to a MAGEB2 peptide (SEQ ID NO: 1) complexed with a class I HLA, wherein the HLA is an HLA-A*02. In a specific embodiment, the invention provides a binding domain that binds to a MAGEB2 peptide (SEQ ID NO: 1) complexed with a class I HLA, wherein the HLA is an HLA-A*02:01. In a specific embodiment, the invention provides a binding domain that binds to a MAGEB2 peptide (SEQ ID NO: 1) complexed with a class I HLA, wherein the HLA is an HLA-A*02:05. In a specific embodiment, the invention provides a binding domain that binds to a MAGEB2 peptide (SEQ ID NO: 1) complexed with a class I HLA, wherein the HLA is an HLA-A*02:06. In a specific embodiment, the invention provides a binding domain that binds to a MAGEB2 peptide (SEQ ID NO: 1) complexed with a class I HLA, wherein the HLA is an HLA-A*02:07.

[00458] Other HLA-A alleles of interest are HLA-A*01:01, HLA-A*24:02, HLA-A*11:01, HLA-A*03:01, HLA-A*02:03, HLA-A*02:04, HLA-A*29:02, HLA-A*31:01, HLA-A*68:02, HLA-A*68:01, HLA-A*26:01, HLA-A*74:01, and HLA-A*32:01, and accordingly it is envisaged that the binding domains of the invention bind to one of these aforementioned HLA-A alleles complexed with the MAGEB2 peptide (SEQ ID NO: 1).

[00459] Widely expressed HLA-B alleles of interest are HLA-B*35:01, HLA-B*07:02 and HLA-B*35:02. Other HLA-B alleles of interest are HLA-B*35:01, HLA-B*44:02, HLA-B*44:03, HLA-B*51:01, HLA-B*54:01, HLA-B*57:01.

[00460] HLA-C alleles of interest are HLA-C*01:02, HLA-C*03:02, HLA-C*03:04, HLA-C*04:01, HLA-C*05:01, HLA-C*06:02, HLA-C*07:02, HLA-C*08:01, HLA-C*08:02, HLA-C*12:02, HLA-C*14:02, HLA-C*14:03, HLA-C*15:02, and HLA-C*16:01.

Cytotoxicity assays

[00461] The Examples herein provide exemplary cytotoxicity assays and results for the various binding constructs of the invention. However, cytotoxicity mediated by the constructs of the invention can be measured in various other ways. Effector cells can be e.g. stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). The target cells should express MAGEB2, e.g. human MAGEB2, and present pMAGE-HLA on their surface, or have the desired MAGEB2 peptide exogenously loaded onto the MHC. Target cells can be an HLA (e.g., HLA-

A*02:01) positive cell line which is stably or transiently transfected with MAGEB2, e.g. human MAGEB2, or alternatively an HLA positive cell line that endogenously expresses sufficient levels of MAGEB2, or an HLA positive cell line that is exogenously loaded with the MAGEB2 peptide. Usually EC50 values are expected to be lower with target cell lines expressing higher levels of the MAGEB2 peptide—HLA complex on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of bispecific antibody constructs can be measured in a 51Cr-release assay (incubation time of about 18 hours), a luciferase readout, in a FACS-based cytotoxicity assay (incubation time of about 48 hours), or other assay techniques known to one skilled in the art. Modifications of the assay incubation time (cytotoxic reaction) are also possible. Other methods of measuring cytotoxicity are well-known to the skilled person and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

[00462] As discussed herein above with regard to affinity and potency, the cytotoxic activity mediated by pMAGE-HLAxCD3 bispecific antibody constructs of the present invention can be measured in a cell-based cytotoxicity assay, such as the TDCC assay described herein in the Examples. This activity is represented by the EC50 value, which corresponds to the half maximal effective concentration (concentration of the antibody construct which induces a cytotoxic response halfway between the baseline and maximum). Preferably, the EC50 value of the MAGEB2xCD3 bispecific antibody constructs is ≤ 5000 pM or ≤ 4000 pM, more preferably ≤ 3000 pM or ≤ 2000 pM, even more preferably ≤ 1000 pM or ≤ 500 pM, even more preferably ≤ 400 pM or ≤ 300 pM, even more preferably ≤ 200 pM, even more preferably ≤ 100 pM, even more preferably ≤ 50 pM, even more preferably

≤20 pM or ≤10 pM, and most preferably ≤5 pM or lower.

[00463] The above given EC50 values can be measured in different assays. The skilled person is aware that an EC50 value can be expected to be lower when stimulated / enriched CD8+ T cells are used as effector cells, compared with unstimulated PBMC. It can furthermore be expected that the EC50 values are lower when the target cells express a high number of pMAGE-HLA compared with a low target expression. For example, when stimulated / enriched human CD8+ T cells are used as effector cells (and either MAGEB2 transfected cells, MAGEB2 peptide loaded cells, or MAGEB2 positive human cell lines are used as target cells), the EC50 value of the pMAGE-HLAxCD3 bispecific antibody construct is preferably ≤5000 pM or ≤4000 pM, more preferably ≤3000 pM or ≤2000 pM, even more preferably ≤1000 pM or ≤500 pM, even more preferably ≤400 pM or ≤300 pM, even more preferably ≤200 pM, even more preferably ≤100 pM, even more preferably ≤50 pM, even more preferably ≤20 pM or ≤10 pM, and most preferably ≤5 pM or lower. When human PBMCs are used as effector cells, the EC50 value of the pMAGE-HLAxCD3 bispecific antibody construct is preferably ≤5000 pM or ≤4000 pM, more preferably ≤3000 pM or ≤2000 pM, even more preferably ≤1000 pM or ≤500 pM, even more preferably ≤400 pM or ≤300 pM, even more preferably ≤200 pM, even more preferably ≤100 pM, even more preferably ≤50 pM, even more preferably ≤20 pM or ≤10 pM, and most preferably ≤5 pM or lower.

[00464] Preferably, the pMAGE-HLAxCD3 bispecific antibody constructs of the present invention do not induce and/or mediate lysis or do not essentially induce and/or mediate lysis of MAGEB2 negative cells at particular desired concentrations of molecule. The term “do not induce lysis”, “do not essentially induce lysis”, “do not mediate lysis” or “do not essentially mediate lysis” means that an antibody construct of the present invention does not induce or mediate lysis of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1% or less of MAGEB2 negative cells, whereby lysis of a MAGEB2 positive human cell line that has on its surface the pMAGE-HLA (e.g., the MAGEB2 peptide of SEQ ID NO:1 complexed with an HLA-A*02:01) is set to be 100%. This usually applies for concentrations of the antibody construct of up to 500 nM. The skilled person can readily measure cell lysis using known techniques and the guidance provided herein.

Activity Assays for Patients

[00465] The biological activity of the pharmaceutical composition defined herein can be determined for instance by cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth et al. (Cancer Immunol. Immunother. 20 (2005), 1-12). “Efficacy” or “*in vivo* efficacy” as used herein refers to the response to therapy by the pharmaceutical composition of formulation of the invention, using e.g. standardized NCI response criteria. The success or *in vivo*

efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, i.e. the ability of the composition to cause its desired effect, i.e. depletion of pathologic cells, e.g. tumor cells. The *in vivo* efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to, white blood cell counts, differentials, fluorescence activated cell sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography, positron-emission tomography scanning, lymph node biopsies/histologies and other established standard methods may be used.

[00466] Pharmacokinetics

[00467] Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that affect the ability of a particular drug to treat a given condition, can be established.

Pharmacokinetic parameters of the drug influencing the ability of a drug for treating a certain disease entity include, but are not limited to: half-life, volume of distribution, hepatic first-pass metabolism and the degree of blood serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

[00468] "Half-life" is the time required for a quantity to reduce to half its initial value. The medical sciences refer to the half-life of substances or drugs in the human body. In a medical context, half-life may refer to the time it takes for a substance / drug to lose one-half of its activity, e.g. pharmacologic, physiologic, or radiological activity. The half-life may also describe the time that it takes for the concentration of a drug or substance (e.g., an antibody construct of the invention) in blood plasma / serum to reach one-half of its steady-state value ("serum half-life"). Typically, the elimination or removal of an administered substance / drug refers to the body's cleansing through biological processes such as metabolism, excretion, also involving the function of kidneys and liver. The "first-pass metabolism" is a phenomenon of drug metabolism whereby the concentration of a drug is reduced before it reaches the circulation. It is the fraction of drug lost during the process of absorption. Accordingly, by "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver. "Volume of distribution" (VD) means the degree to which a drug is distributed in body tissue rather than the blood plasma, a higher VD indicating a greater amount of tissue distribution. The retention of a drug can occur throughout the various compartments of the body, such as intracellular and extracellular spaces, tissues and organs, etc. "Degree of blood serum binding" means the propensity of a drug to interact

with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

[00469] Pharmacokinetic parameters also include bioavailability, lag time (T lag), Tmax, absorption rates, and/or Cmax for a given amount of drug administered. "Bioavailability" refers to the fraction of an administered dose of a drug / substance that reaches the systemic circulation (the blood compartment). When a medication is administered intravenously, its bioavailability is considered to be 100%. However, when a medication is administered via other routes (such as orally), its bioavailability generally decreases. "Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma. Cmax is the maximum plasma concentration that a drug achieves after its administration (and before the administration of a second dose). Tmax is the time at which Cmax is reached. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is influenced by all parameters. Pharmacokinetic parameters of antibody constructs exhibiting cross-species specificity may be determined in preclinical animal testing in non-chimpanzee primates as outlined above and set forth e.g. in Schlereth et al. (supra).

Treatment Methods

[00470] One embodiment provides the antibody construct of the invention (or the antibody construct produced according to the process of the invention) for use in the prevention, treatment or amelioration of a disease, preferably a neoplasm. Another embodiment provides the use of the antibody construct of the invention (or of the antibody construct produced according to the process of the invention) in the manufacture of a medicament for the prevention, treatment or amelioration of a disease, preferably a neoplasm. It is also envisaged to provide a method for the prevention, treatment or amelioration of a disease, preferably a neoplasm, comprising the step of administering to a subject in need thereof the antibody construct of the present invention (or the antibody construct produced according to the process of the present invention).

[00471] The terms "subject in need", "patient" or those "in need of treatment" include those already with the disease, as well as those in which the disease is to be prevented. The terms also include human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

[00472] The antibody constructs of the invention and the formulations / pharmaceutical compositions described herein are useful in the treatment, amelioration and/or prevention of the medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Treatment includes the application or administration of the antibody constructs / pharmaceutical composition to the body, to

an isolated tissue, or to a cell from a patient or a subject in need who has a disease/disorder as described herein, a symptom of such disease/disorder, or a predisposition toward such disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disease, the symptom of the disease, or the predisposition toward the disease.

[00473] The term “amelioration” as used herein refers to any improvement of the disease state of a patient, by the administration of an antibody construct according to the invention to such patient or subject in need thereof. Such an improvement may be seen as a slowing or stopping of the progression of the disease of the patient, and/or as a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease.

[00474] The term “prevention” as used herein means the avoidance of the occurrence or of the re-occurrence of a disease as specified herein, by the administration of an antibody construct according to the invention to a subject in need thereof.

[00475] The term “disease” refers to any condition that would benefit from treatment with the antibody construct or the pharmaceutical composition described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the mammal to the disease in question. The disease is preferably a neoplasm, cancer or tumor. The disease, neoplasm, cancer or tumor is preferably MAGEB2 positive, i.e. it is characterized by expression or overexpression of MAGEB2.

[00476] A “neoplasm” is an abnormal growth of tissue, usually but not always forming a mass. When also forming a mass, it is commonly referred to as a “tumor”. In brain tumors, the uncontrolled division of cells means that the mass of a neoplasm increases in size, and in a confined space such as the intracranial cavity this quickly becomes problematic because the mass invades the space of the brain pushing it aside, leading to compression of the brain tissue and increased intracranial pressure and destruction of brain parenchyma. Neoplasms or tumors can be benign, potentially malignant (pre-cancerous), or malignant (cancerous). Malignant neoplasms / tumors are commonly called cancer. They usually invade and destroy the surrounding tissue and may form metastases, i.e., they spread to other parts, tissues or organs of the body. A “primary tumor” is a tumor growing at the anatomical site where tumor progression began and proceeded to yield a cancerous mass. For example, a brain tumor occurs when abnormal cells form within the brain. Most cancers develop at their primary site but then go on to metastasize or spread to other parts (e.g. tissues and organs) of the body. These further tumors are “secondary tumors”. Most cancers continue to be called after their primary site, even after they have spread to other parts of the body.

[00477] Lymphomas and leukemias are lymphoid neoplasms. For the purposes of the present invention, they are also encompassed by the terms “tumor” or “cancer”. For the purposes of the

present invention, the terms “neoplasm”, “tumor” and “cancer” may be used interchangeably, and they comprise both primary tumors / cancers and secondary tumors / cancers (or “metastases”), as well as mass-forming neoplasms (tumors) and lymphoid neoplasms (such as lymphomas and leukemias), and also MRD.

[00478] The term “minimal residual disease” (MRD) refers to the evidence for the presence of small numbers of residual cancer cells that remain in the patient after cancer treatment, e.g. when the patient is in remission (no symptoms or signs of disease). A very small number of remaining cancer cells usually cannot be detected by routine means because the standard tests used to assess or detect cancer are not sensitive enough to detect MRD. Nowadays, very sensitive molecular biology tests for MRD are available, such as flow cytometry, PCR and next-generation sequencing. These tests can measure minimal levels of cancer cells in tissue samples, sometimes as low as one cancer cell in a million normal cells. In the context of the present invention, the terms “prevention”, “treatment” or “amelioration” of a cancer are envisaged to also encompass “prevention, treatment or amelioration of MRD”, whether the MRD was detected or not.

[00479] In one embodiment, the neoplasm, cancer or tumor is selected from the group including, but not limited to, gastrointestinal cancer, ovarian cancer and lung cancer. According to one embodiment of the invention, the gastrointestinal cancer is selected from the group consisting of gastric or stomach cancer, esophageal cancer, gastroesophageal cancer, pancreatic cancer, and colorectal cancer. According to another embodiment of the invention, the ovarian cancer is mucinous ovarian cancer. According to a further embodiment of the invention, the lung cancer is non-small cell lung cancer.

[00480] In a specific embodiment of the invention, the neoplasm, cancer or tumor is selected from the group including, but not limited to, (or consisting of) non-small cell lung carcinoma (NSCLC), hepatocellular carcinoma (HCC), head and neck carcinoma (HNSCC), colon adenocarcinoma (COAD), rectal adenocarcinoma (READ), and stomach adenocarcinoma (STAD). The non-small cell lung carcinoma can be a squamous cell carcinoma (LUSC) or an adenocarcinoma (LUAD).

[00481] The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. in dose escalating studies. As set forth above, the antibody construct of the invention exhibiting cross-species specificity as described herein can also be advantageously used in preclinical testing in non-chimpanzee primates. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical art, dosages for any one patient depend upon many factors, including the patient's size, body surface area,

age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

[00482] An “effective dose” is an amount of a therapeutic agent sufficient to achieve or at least partially achieve a desired effect. A “therapeutically effective dose” is an amount sufficient to cure or at least partially arrest the disease and its complications, signs and symptoms in a patient suffering from the disease. Amounts or doses effective for this use will depend on the disease to be treated (the indication), the delivered antibody construct, the therapeutic context and objectives, the severity of the disease, prior therapy, the patient's clinical history and response to the therapeutic agent, the route of administration, the size (body weight, body surface) and/or condition (the age and general health) of the patient, and the general state of the patient's own immune system. The proper dose can be adjusted according to the judgment of the attending physician, in order to obtain the optimal therapeutic effect.

[00483] A therapeutically effective amount of an antibody construct of the invention preferably results in a decrease in severity of disease symptoms, an increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease. In the treatment of MAGEB2-expressing tumors, a therapeutically effective amount of the antibody construct of the invention preferably inhibits tumor cell growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may also be evaluated in an animal model predictive of efficacy in human tumors.

[00484] In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, an antibody construct produced according to the process of the invention, a polynucleotide of the invention, a vector of the invention, and/or a host cell of the invention. In the context of the present invention, the term “kit” means two or more components – one of which corresponding to the antibody construct, the pharmaceutical composition, the polynucleotide, the vector or the host cell of the invention – packaged together in a container, recipient or otherwise. A kit can hence be described as a set of products and/or utensils that are sufficient to achieve a certain goal, which can be marketed as a single unit.

[00485] The kit may comprise one or more recipients (such as vials, ampoules, containers, syringes, bottles, bags) of any appropriate shape, size and material (preferably waterproof, e.g. plastic or glass) containing the antibody construct or the pharmaceutical composition of the present invention in an appropriate dosage for administration (see above). The kit may additionally contain directions for use (e.g. in the form of a leaflet or instruction manual), means for administering the antibody construct or the pharmaceutical composition of the present invention such as a syringe, pump, infuser

or the like, means for reconstituting the antibody construct of the invention and/or means for diluting the antibody construct of the invention.

[00486] The invention also provides kits for a single-dose administration unit. The kit of the invention may also contain a first recipient comprising a dried / lyophilized antibody construct or pharmaceutical composition and a second recipient comprising an aqueous formulation. In certain embodiments of this invention, kits containing single-chambered and multi-chambered pre-filled syringes are provided.

[00487] As used herein, the singular forms “a”, “an”, and “the” include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a reagent” includes one or more of such different reagents and reference to “the method” includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

[00488] Unless otherwise indicated, the term “at least” preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

[00489] The term “and/or” wherever used herein includes the meaning of “and”, “or” and “all or any other combination of the elements connected by said term”.

[00490] The term “about” or “approximately” as used herein means within $\pm 20\%$, preferably within $\pm 15\%$, more preferably within $\pm 10\%$, and most preferably within $\pm 5\%$ of a given value or range. It also includes the concrete value, e.g., “about 50” includes the value “50”.

[00491] Throughout this specification and the claims, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term “comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having”.

[00492] When used herein “consisting of” excludes any element, step, or ingredient not specified in the claim element. When used herein, “consisting essentially of” does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

[00493] In each instance herein, any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms.

[00494] It should be understood that the above description and the below examples provide exemplary arrangements, but the present invention is not limited to the particular methodologies, techniques, protocols, material, reagents, substances, etc., described herein and as such can vary. The terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention, which is defined solely by the claims. Aspects of the invention are provided in the independent claims. Some optional features of the invention are provided in the dependent claims.

[00495] All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer’s specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supersede any such material.

[00496] A better understanding of the present invention and of its advantages will be obtained from the following examples, offered for illustrative purposes only. The examples are not intended and should not be construed as to limit the scope of the present invention in any way.

[00497] **EXAMPLES**

[00498] **Example 1: MAGEB2 mRNA Expression and Immunization**

[00499] 1a: MAGEB2 mRNA Expression

[00500] An internal database was searched for MAGEB2 and MAGEA4 in ArrayStudio. Solid Tissue Normal samples were removed. For each gene, visualization of FPKM data across available tumor samples was depicted by selecting View → RNA-Seq Quantification → Gene FPKM. Results are summarized in Figures 2A and 2B, for MAGEB2 and MAGEA4, respectively. The box bounds the interquartile range (IQR) with a bold line indicating the median; the whiskers indicate the bounds of 1.5*IQR; the plus sign indicates the mean.

[00501] A similar database analysis was performed for MAGEB2 and MAGEA4 mRNA expression in normal tissue. Results are summarized in Figures 2C, 2D, and 2E. Numbers in parenthesis indicate sample size.

[00502] Example 1b: MAGEB2 Peptide Presentation Analysis by Mass Spectrometry

[00503] Qualitative and quantitative peptide presentation data for the MAGEB2 peptide were extracted from the XPRESIDENT database.

[00504] HLA-A*02 bound peptides were purified from shock-frozen human normal and tumor tissue samples by immunoaffinity chromatography. Isolated peptides were further separated and identified using nano-electrospray-ionization (nanoESI) liquid chromatography-mass spectrometry (LC-MS). Data processing was performed by combining different algorithms for sequence identification, spectral clustering, ion counting, retention time alignment, charge state deconvolution and normalization. The left panel depicts the combined results of these analyses for a total of 474 normal tissue and 539 tumor tissue samples showing presentation of the MAGEB2 peptide in a strongly tumor-associated manner (see Figure 2A, left panel). Tumor and normal samples are grouped according to organ of origin. Box-and-whisker plots represent normalized signal intensities over multiple samples and have been defined in the log space. Boxes display median, 25th and 75th percentile. Whiskers extend to the lowest data point still within 1.5 interquartile range (IQR) of the lower quartile, and the highest data point still within 1.5 IQR of the upper quartile. Lower part: The relative peptide detection frequency in every organ is shown as spine plot. Numbers below the panel indicate number of samples on which the peptide was detected out of the total number of samples evaluable for this analysis for each organ (N = 474 for normal samples, N = 539 for tumor samples). If the peptide has been detected on a sample but could not be quantified for technical reasons, the sample is included in this representation of detection frequency, but no dot is shown in the upper part of the figure. [adipose: adipose tissue; adrenal gl: adrenal gland; bladder: urinary bladder; bloodvess: blood vessel; esoph: esophagus; gall bl: gallbladder; intest. la: large intestine; intest. sm: small intestine; nerve cent: central nerve; nerve perith: peritheral nerve; parathyr: parathyroid gland; perit: peritoneum; pituit: pituitary; skel. mus: skeletal muscle; AML: acute myeloid leukemia; BRCA: breast cancer; CCC: cholangiocellular carcinoma; CLL: chronic lymphocytic leukemia; CRC: colorectal cancer; GBC: gallbladder cancer; GBM: glioblastoma; GC: gastric cancer; GEJC: gastro-esophageal junction cancer; HCC: hepatocellular carcinoma; HNSCC: head and neck squamous cell carcinoma; MEL: melanoma; NHL: Non-Hodgkin lymphoma; NSCLCaden: non-small cell lung cancer adenocarcinoma; NSCLCother: NSCLC samples that could not unambiguously be assigned to NSCLCaden or NSCLCsquam; NSCLCsquam: squamous cell non-small cell lung cancer; OC: ovarian cancer; OSCAR: esophageal cancer; PACA: pancreatic cancer; PRCA: prostate cancer; RCC: renal cell carcinoma; SCLC: small cell lung cancer; UBC: urinary bladder carcinoma; UEC: uterine and endometrial cancer.]

[00505] For a subset of 12 tumor tissues absolute quantitative presentation levels for the MAGEB2 peptide were determined as copies per cell (see Figure 2A right panel). This was accomplished by performing a set of additional experiments to determine the absolute amount of

peptide within a sample, the isolation efficiency of the peptide purification process and the total amount of cells within a sample. For this purpose different isotopically labeled versions of the MAGEB2 peptide were spiked into the sample during the peptide purification process and analyzed together with the natural MAGEB2 peptide using dedicated targeted mass spectrometry measurements.

[00506] Example 1c: Immunogen strategy and Titer analysis

[00507] The purified biotinylated MAGEB2 pMHC monomers were incubated with the neutravidin protein to generate pMHC tetramers. Each neutravidin protein can bind up to four biotin molecules and form avidin-biotin complexes. The biotinylated pMHC monomers were also coupled directly to the neutravidin coated microspheres to form pMHC-displaying microspheres. See representation in Figure 3. Depending on size of microspheres, there are roughly 1600-2000 neutravidin groups per microsphere for the bead that has an average diameter of about 0.1 μm . Both MAGEB2 pMHC tetramers and pMHC-displaying microspheres were adjuvated with QS21 or alum/CpG/poly(I:C) and were used as immunogens for XenoMouse immunization via subcutaneous injection.

[00508] At 4- and 8-weeks post immunization, serum samples were collected from animals and analyzed for titers against MAGEB2 pMHC. Identification of MAGEB2 immune response required depletion of titer against other components. In brief, 1:1000 serum dilution was incubated with control peptide pMHC at 300 $\mu\text{g/mL}$ to absorb irrelevant binders that recognize MHC molecules. The serum was then tested for binding of the MAGEB2 pMHC by FACS in the presence of control peptide pMHC. Animals with sera titers showing greatest Geomean Fold-change MAGEB2 over the irrelevant control peptide were selected for harvest and downstream hybridoma generation and screening. See Figure 3B.

[00509] **Example 2: Initial Screening of MAGEB2 scFv Binding Constructs**

[00510] Binding of pMAGE-HLA scFv constructs, generated from the XenoMouse, on peptide loaded T2 cells was evaluated by flow cytometry. T2 cells (DSMZ, ACC 598) were loaded with MAGEB2 peptide or nine different peptides sharing high sequence homology with the MAGEB2 peptide prior to incubation with scFv constructs containing bacterial lysates. Bound scFv constructs were detected with anti-Flag M2 (Sigma-Aldrich, F3165) and anti-mouse IgG-PE (Jackson ImmunoResearch, 115-116-071) and signals were analyzed by flow cytometry. Binding profiles of representative pMAGE-HLA specific scFv candidates are shown in Table 6.

[00511] Table 6: Binding profiles of representative pMAGE-HLA specific scFv candidates on peptide loaded T2 cells.

Clone	signal/background on peptide loaded T2 cells										
	MAGE E2	4A6	DP-93	5K	WFOF	63A	42F	CG92	CG13	5789F	
18089-D12	179	1.1	1.1	1.3	1.1	1.0	1.3	1.0	1.3	1.6	
18179-G12	42	0.8	1.1	1.3	0.9	0.9	1.3	0.8	1.2	0.9	
18179-C3	40	1.0	1.0	1.0	0.9	1.0	1.0	0.8	1.0	0.9	
18093-B11	119	1.2	1.0	1.1	1.2	1.3	1.3	1.0	1.2	1.1	
18182-G2	240	1.0	1.1	1.0	1.0	0.9	1.0	1.0	0.9	0.9	
18182-E1	151	0.9	0.9	1.0	0.9	0.9	1.0	0.9	0.8	1.0	
18182-B5	300	1.0	1.0	1.0	1.0	0.9	0.9	1.0	1.0	1.0	
18182-H9	303	1.0	1.1	1.2	1.1	1.6	1.0	1.0	0.9	1.1	
18182-E18	273	0.9	0.9	1.0	0.9	0.8	0.9	0.8	0.9	0.8	
18182-G8	282	1.1	1.0	1.1	1.0	0.9	1.0	0.9	0.9	1.0	
18182-E6	302	0.9	0.9	0.9	1.0	1.0	0.9	1.0	1.0	0.9	
18182-G18	305	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
18182-D12	208	0.8	0.8	1.0	0.9	0.8	0.9	1.0	0.8	0.9	
18182-A5	212	1.0	1.0	1.0	1.0	0.9	1.1	0.8	0.9	0.8	
18182-H12	208	1.2	1.0	1.0	1.2	0.9	1.0	1.0	1.1	1.0	
18182-E5	210	0.9	1.0	1.0	0.9	0.9	1.0	0.8	0.9	0.9	
18093-E7	209	1.0	1.2	1.4	1.1	1.0	1.0	1.0	1.1	1.1	
18093-B9	150	1.1	1.1	1.1	1.1	1.1	1.0	1.0	1.0	1.0	
18093-D11	79	1.2	1.1	1.2	1.1	1.0	1.1	1.0	1.1	1.1	
18093-C9	95	1.1	0.9	1.1	1.0	1.0	1.0	1.0	1.0	1.0	
18093-D8	98	1.0	1.2	1.3	1.1	1.0	1.0	0.9	1.0	1.0	
18093-F9	96	1.0	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	
18093-H11	32	1.0	1.0	1.1	1.1	0.8	0.9	0.9	1.0	0.9	
18093-B8	32	1.1	1.0	1.1	1.0	1.0	1.1	1.0	1.0	1.0	
18183-G9	300	0.9	1.1	1.0	1.0	0.9	1.0	1.0	1.0	1.0	
18179-B12	305	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	
18181-F1	305	1.0	1.1	1.1	1.1	0.9	1.1	1.1	1.1	1.0	
18181-A8	300	1.0	1.0	1.1	1.1	0.9	1.0	1.0	0.9	1.0	
18179-E1	308	1.0	1.0	1.1	1.0	1.0	0.9	1.0	0.9	1.0	
18179-B11	305	1.0	1.1	1.0	1.1	1.0	1.0	1.0	1.0	1.0	
18179-D7	301	1.0	1.1	1.1	1.0	1.0	1.0	1.1	1.0	1.0	
18179-A7	312	1.1	1.0	1.0	1.0	0.9	1.0	1.0	1.0	1.0	
18181-F3	312	0.9	1.1	1.0	1.1	1.0	1.0	1.1	0.9	1.0	
18179-H7	300	1.0	1.0	0.9	1.1	1.0	1.1	1.0	1.0	1.0	
18181-H7	229	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	
18181-B8	179	0.8	1.0	1.0	0.9	0.9	1.0	1.0	0.9	0.9	
18183-C9	140	1.0	0.9	1.0	1.1	0.9	1.0	1.0	0.9	1.1	
18181-G10	121	1.0	1.0	1.1	1.0	1.0	1.0	1.1	1.0	1.0	
18181-E2	100	1.0	1.0	1.1	1.1	1.0	1.1	1.0	1.1	1.1	
18093-B2	318	1.1	1.0	1.1	1.1	1.0	1.0	1.0	0.9	1.0	

[00512] Example 3: Evaluation of pMAGE-HLA HLE bispecific antibody constructs *in vitro* affinity and efficacy

[00513] Cell-based affinity of pMAGE-HLA bispecific antibody constructs was determined by fluorescence cytometry and nonlinear regression (one site - specific binding) analysis. MAGEB2 peptide loaded T2 cells were incubated with decreasing concentrations of pMAGE-HLA bispecific antibody constructs. Bound antibody constructs were detected by Alexa Fluor 488-conjugated anti-human IgG (Jackson ImmunoResearch, 109-547-003). Prior signal detection by fluorescence cytometry fixed cells were stained with DRAQ5. Respective equilibrium dissociation constant (Kd) values were calculated with the one site specific binding evaluation tool in the GraphPad Prism software. Cell activity of pMAGE-HLA HLE bispecific antibody constructs was evaluated in T cell-dependent cytotoxicity (TDCC) assays. Human PBMC were incubated at 10:1 with target cells expressing pMAGE-HLA complexes (U266B1 and DAN-G cells) in the presence of a dose range of antibody constructs. After 48 h

incubation, cell cytotoxicity was assessed using flow cytometry as a readout for cellular cytotoxicity. Results are depicted in Figures 4A-4B and Table 7.

[00514] Table 7: Binding affinities and efficacies of representative pMAGE-HLA HLE bispecific antibody constructs

Candidates x αCD3 x HLE	KD on MAGEB2 loaded T2 [nM]	EC50 [pM]	
		U266	DAN-G
MA 86-A4-N-F5 CC	51.8	135	4340
MA 88-B3-F9 CC	74.1	not active	not active
MA 5G-F28 CC	76.8	313	23743
MA 81-B9 CC	18.9	282	4035
MA 98-C7 CC	0.7	3.5	70.5
MA 03-D8 AS CC	0.5	0.3	15.2
MA 03-E11 AS CC	4.2	3.5	212
MA 09-E2 CC	0.7	2.0	68.7
MA 09-F12 CC	0.5	2.9	83.5
MA 09-G10 CC	0.8	12.6	90.8
MA 09-H7 CC	0.8	10.5	227
MA 09-H10 CC	0.6	3.2	103
MA 10-B5 CC	0.7	1.0	33.3
MA 10-D3 CC	1.1	8.8	187
MA 10-D6 CC	0.7	1.2	45.0
MA 10-G10 AS CC	1.7	2.9	141
MA 86-A4 CC	35.5	640	2858
MA 98-G12 AS CC	0.9	0.9	42.6
MA 03-C7 AS CC	1.5	1.2	89.8
MA 03-D12 AS CC	0.7	0.7	24.9
MA 03-E7 AS CC	0.5	0.6	8.5
MA 03-G10 AS CC	0.9	1.0	59.9
MA 03-G11 AS CC	1.3	2.4	73.7
MA 03-H12 AS CC	1.1	1.5	79.9
MA 09-C7 CC	0.9	12.8	374
MA 09-F11 CC	0.6	11.4	204
MA 09-G11 CC	0.6	6.7	170
MA 09-H11 CC	0.5	1.9	41.4
MA 10-G2 CC	1.0	2.8	126
MA 10-H1 CC	1.2	2.9	225
MA 10-H3 CC	0.7	1.3	111

[00515] EXAMPLE 4A: SCREENING OF SIMILAR PEPTIDE PANELS

[00516] SINGLE POINT

[00517] T2luc cells (luciferase expressing T2 cells generated at Amgen) were incubated with similar peptides, target specific peptide or DMOS/TFA control at 10uM final concentration for 2hrs at 37oC/5%CO2 in serum free media. Frozen or pre-activated primary human pan T-cells were washed and added to white-clear bottom 384-well assay plates at 20,000 cells/20uL in 10% ICM (Immune Cell Media). Pre-activated T-cells were prepared by seeding 2 x 10E6 cells/mL into 1ug/mL pre-coated TC flask anti CD3 (OKT3 clone, eBioscience, catalog # 160037) + 1ug/mL anti CD28 (CD28.2 clone, eBioscience, catalog # 16-0289-81) for 72hrs in 10% ICM at 37oC/5%CO2. Pre-activated T-cells were

expanded with 10ng/mL rhIL-2 (R&D Systems, cat# 202-IL-50). Peptide loaded T2luc cells were added to the primary T-cells at 2000 cells/20uL. MAGE-B2 pMHC BiTE® HLE molecules were added to the T-cells and peptide loaded T2luc cells at 10nM final concentration in 10% ICM and incubated for 48 or 24 hours (frozen or pre-activated respectively) at 37 deg C/5%CO2. T2luc cell viability was determined using Bio-Glo™ Luciferase Assay System (Promega cat# G7940) according to the manufacturer's recommendation. Luminescence was detected using EnVision® Multilable Plate Reader (Perkin Elmer). Percent viability was calculated using the following formula: % Viability = (Sample raw RLU value/Average DMSO/TFA control RLU) x 100. Figures 5A and 5B depict the response of MAGE-B2 pMHC BiTE® against 112 MAGE-B2 similar peptides, MAGE-B2 and relevant controls in 2 different T-cell donors. It was a striking result to achieve binding specificity to the MAGEB2 peptide-MHC complex, yet demonstrate minimal binding to other similar peptides-MHC complexes (e.g., those in Figure 1 and elsewhere herein).

[00518] POTENCY

[00519] T2luc cells were incubated with reactive similar peptides, target specific peptide or DMOS/TFA control at 10uM final concentration for 2hrs at 37oC/5%CO2 in serum free media. Frozen or pre-activated primary human pan T-cells were washed and added to white-clear bottom 384-well assay plates at 20,000 cells/20uL in 10% ICM (Immune Cell Media). Pre-activated T-cells were prepared by seeding 2 x 10E6 cells/mL into 1ug/mL pre-coated TC flask anti CD3 (OKT3 clone, eBioscience, catalog # 160037) + 1ug/mL anti CD28 (CD28.2 clone, eBioscience, catalog # 16-0289-81) for 72hrs in 10% ICM at 37oC/5%CO2. Pre-activated T-cells were expanded with 10ng/mL rhIL-2 (R&D Systems, cat# 202-IL-50). Peptide loaded T2luc cells were added to the primary T-cells at 2000 cells/20uL. MAGE-B2 pMHC BiTE® HLE molecules were added to the T-cells and peptide loaded T2luc cells at 25nM to 0.006pM final concentration in 10% ICM and incubated for 48 or 24 hours (frozen or pre-activated respectively) at 37oC/5%CO2. T2luc cell viability was determined using Bio-GLO Luciferase Assay System (Promega cat# G7940) according to the manufacturer's recommendation. Luminescence was detected using EnVision Multilable Plate Reader (Perkin Elmer). Percent viability was calculated using the following formula: % Viability = (Sample raw RLU value/Average DMSO/TFA control RLU) x 100. EC50 was determined using GraphPad Prism (non-linear regression curve fit analysis). Figures 6A and 6B depict the potency of MAGE-B2 pMHC BiTE® against MAGE-B2 and various reactive similar peptides.

[00520] **EXAMPLE 4B: SCREENING OF MAGEB2 9-MER PEPTIDES**

[00521] T2luc cells were incubated with MAGE-B2 9-mer peptides (i.e., single amino acid deletions from the full MAGEB2 10-mer peptide), target specific peptide, or DMOS/TFA control at 10uM final concentration for 2hrs at 37oC/5%CO2 in serum free media. Frozen primary human pan T-

cells were washed 3 times in sterile 10% ICM and added to white-clear bottom 384-well assay plates at 20,000 cells/20uL in 10% ICM (Immune Cell Media). Peptide loaded T2luc cells were added to the primary T-cells at 2000 cells/20uL. MAGE-B2 pMHC BiTE[®] HLE molecules were added to the T-cells and peptide loaded T2luc cells at 25nM to 0.006pM final concentration in 10% ICM and incubated for 48 hours at 37oC/5%CO2. T2luc cell viability was determined using Bio-Glo Luciferase Assay System (Promega cat# G7940) according to the manufacturer's recommendation. Luminescence was detected using EnVision Multilable Plate Reader (Perkin Elmer). Percent viability was calculated using the following formula: % Viability = (Sample raw RLU value/Average DMSO/TFA control RLU) x 100. EC50 was determined using GraphPad Prism (non-linear regression curve fit analysis). Figure 7 depicts the potency of MAGE-B2 pMHC BiTE[®] against the various MAGEB2 9-mer peptides.

[00522] EXAMPLES 5A—5E: BiTE[®] MOLECULE TDCC POTENCY ASSAYS ON CELL LINES AND PRIMARY CELLS

[00523] Methodologies for the TDCC assays performed in the following examples is described at the end of this section.

[00524] In Example 5A, BiTE[®] molecule activity was measured by TDCC assays on various cell lines with known MAGEB2 copies per cell (DANG, NCI-H1792, SK-MEL, SNU-475). Results are depicted in Figure 8.

[00525] In Example 5B, BiTE[®] molecule activity was measured by TDCC assays on cell lines with low/intermediate MAGEB2 expression. Results are depicted in Figure 9.

[00526] In Example 5C, BiTE[®] molecule activity was measured by TDCC assays on DAN-G MAGEB2 positive and DAN-G MAGEB2 negative cell lines. Results are depicted in Figure 10.

[00527] In Example 5D, BiTE[®] molecule activity was measured by TDCC assays on human primary cells (cardiac myocytes, endothelial cells, and epithelial cells). Results are depicted in Figure 11A.

[00528] In Example 5E, BiTE[®] molecule activity on MAGEB2(-) cells was evaluated by TDCC assay for various BiTE[®] molecules, many of which have comparable binding affinities to the pMAGE-HLA. Human T cells were co-cultured at ratios of 10:1 with HLA-A*02:01-positive tumor cells not expressing MAGEB2 (HEPG2 cells) in the presence of antibody constructs. After 48 h incubation, cell

cytotoxicity was assessed by flow cytometric determination of dead tumor cells. Results are depicted in Figure 11B.

[00529] In Example 5F, BiTE[®] molecule activity was measured by TDCC assays on various MAGEA4(+) / MAGEB2(-) cell lines. Results are depicted in Figure 12.

[00530] BiTE[®] Molecule TDCC Methods – For Adherent cells

[00531] BiTE[®] molecules - Indicated BiTE[®] molecule dilutions were prepared in complete RPMI media, cRPMI (RPMI 1640 supplemented with 10% FBS, Glutamax, non-essential amino acids, sodium pyruvate, HEPES, and penicillin/streptomycin). Target cells – Media of adherent target cells were aspirated, and cells were rinsed with PBS without calcium or magnesium. Corning CellStripper Dissociation Reagent was added, and flasks were incubated at 37°C to lift cells from flask. Cells were collected, washed with cRPMI, and resuspended at 1e5 cells/ml in cRPMI. Effector T cells - Frozen human pan T cells isolated from normal peripheral blood were thawed in warm cRPMI and centrifuged at 300g for 20 minutes. Cell pellets were resuspended at 1.25e6 cells/ml.

[00532] 2,500 target cells and 25,000 T cells (E:T 10:1) were co-cultured with diluted BiTE[®] molecule in 384 well plates. Samples are run in triplicate. Plates were incubated at room temperature for 20 minutes to allow cells to settle to bottom. Prepared MicroClima lids were added to the assay plates and plates were incubated at 37°C for 48 hours. For readouts, plates were gently washed with room temperature PBS with calcium and magnesium. After final wash, 20ul of PBS was added to each well. Promega Cell Titer Glo was added to wells and plates are placed on a shaker at room temperature for 10 minutes in the dark before luminescence of viable target cells are read from plates.

[00533] BiTE[®] Molecule TDCC Methods – For Suspension cells

[00534] BiTE[®] molecules and effector T cells were prepared as above. Suspension target cells were mixed thoroughly, washed with cRPMI, and resuspended at 1e6 cells/ml in serum-free RPMI 1640. Target cells were labeled with Invitrogen CFDA-SE dye for 5 minutes at 37°C in the dark at a final concentration of 2.5 uM. Cells were washed with cRPMI and resuspended at 1.25e5 cells/ml in cRPMI.

[00535] 10,000 target cells and 100,000 T cells (E:T 10:1) were co-cultured with diluted BiTE[®] molecule in 96 well plates. Samples were run in duplicate. Plates were incubated at room temperature for 20 minutes to allow cells to settle to bottom. Prepared MicroClima lids were added to the assay plates and plates were incubated at 37°C for 48 hours. For readout, cells were pelleted in plates by centrifugation and media was removed. Cells were resuspended with FACS Buffer (1% FBS in PBS) and

stained with ThermoFisher LIVE/DEAD Fixable Near-IR viability dye. Samples were acquired on BD Fortessa flow cytometer to determine labeled target cell viability.

[00536] BiTE® Molecule TDCC Methods – Human Primary Cells

[00537] BiTE® molecule TDCC assays with HLA-A*02:01-positive human primary cells: cardiac myocytes (PromoCell, Cat. No.: C-12810), dermal microvascular endothelial cells (PromoCell, Cat. No.: C-12212, renal proximal tubule epithelial cells (Lonza, Cat. No.: CC-2553) and HLA-A*02:01-positive pan T cells (PPA, Cat. No.: 15-00061).

[00538] Cardiac myocytes, endothelial cells, renal epithelial cells and T cells were carefully thawed and cultured in their recommended media over night at 37°C in a 5% CO₂ incubator. T cell media: 10% FCS in RPMI 1640; PromoCell's cardiac myocyte medium: basal medium, Cat. No.: C-22270, supplemented with the growth medium supplement pack, Cat. No.: C-39270. PromoCell's endothelial cell growth medium: basal medium MV, Cat. No.: C-22220, supplemented with the growth medium MV supplement pack, Cat. No.: C-39220. Lonza's renal epithelial cell medium: renal epithelial cell growth basal medium, Cat. No.: CC-3191, supplemented with the renal epithelial cell growth medium kit, Cat. No.: CC-4127.

[00539] Cardiac myocytes, endothelial cells and epithelial cells were either cultured alone or co-cultured with T cells at a ratio of 1 (1x10⁴ cells):10 in the presence or absence of BiTE® molecules for 48 hours at 37°C in a 5% CO₂ chamber. Cell culture assays were performed in a 1-to-1 media mix containing T cell medium and the corresponding media for myocytes, endothelial and epithelial cells without the supplement hydrocortisone.

[00540] Negative control assays were run with a BiTE® molecule specific for an antigen not expressed by healthy normal cells and positive controls were performed with a BiTE® molecule binding to a cell surface antigen with varying expression on healthy tissues. Cardiac myocytes, endothelial cells and epithelial cells cultured alone were lysed at the end of the culture period with Triton X-100 (maximal lysis). LDH release by dying cells into the assay supernatants was measured with Promega's LDH-Glo™ Cytotoxicity Assay Kit and monitored by a luminometer.

[00541] **EXAMPLE 6: Interaction of the MAGEB2 peptide with HLA-A*02 MHC**

[00542] Introduction

[00543] Bi-specific T cell engagers (BiTE®) specific to a MAGEB2 peptide (p) bound to HLA-A02 major histocompatibility complex (MHC) ("pMHC" when the peptide is bound to the MHC; alternatively "pMAGE-HLA") were successfully generated. The results presented here describe the interactions of the MAGEB2 10-mer peptide GGYDGEHSV (SEQ ID NO: 1) with the HLA-A02 MHC as

derived from the crystal structure of pMHC:N3H BITE® complex. Refer to the methods in Example 7 herein for this structure.

[00544] Results

[00545] **The 10-mer MAGEB2 peptide binds in the peptide binding groove of the MHC**

[00546] Crystal structure of pMHC:N3H

[00547] Coordinates are provided in Table 8.

[00548] The crystal structure of MAGEB2 pMHC:N3H has been determined at 1.76 Å. From the extracted pMHC coordinate file, the interactions of the MAGEB2 peptide to the MHC was determined to occupy the full peptide binding cleft in the MHC with the N- and C- terminal end of the peptide buried into the ends of the peptide cleft and the residues picking up several interactions across this peptide binding region.

[00549] The following is a list of residues involved in the interaction interface between the MHC and the peptide.

[00550] The core residues on HLA-A02 interaction interface with MAGEB2 peptide:

[00551] Met5, Tyr7, Phe9, Met45, Glu63, Arg65, Lys66, Val67, Ala69, His70, Thr73, Val76, Asp77, Thr80, Leu81, Tyr84, Arg97, Tyr99, Glu116, Tyr123, Ile124, Thr143, Lys146, Trp147, Ala150, Val152, Gln155, Leu156, Tyr159, Thr163, Trp167, and Tyr171.

[00552] The core residues on MAGEB2 interaction interface with HLA-A02 MHC:

[00553] Gly1, Val2, Tyr3, Asp4, Gly5, Glu6, Glu7, His8, Ser9 and Val10.

[00554] The following is a list of intermolecular bonded interactions between the MHC and the peptide.

[00555] The pairs of residues involved in intermolecular salt bridges and the distance cut-off as determined by PISA in angstroms (Å) are shown below in Table 9:

[00556] **Table 9.**

HLA-A02 MHC	MAGEB2 peptide	Length (in Å)
Arg65 NH1	Asp4 OD1	3.2
Arg65 NH1	Asp4 OD2	3.9
Arg65 NH2	Asp4 OD2	3.5
His70 ND1	Glu7 OE1	2.9
His70 ND1	Glu7 OE2	4.0
Lys146 NZ	Val10 O	2.8

Lys146 NZ	Val10 OXT	3.8
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[00557] The pairs of residues involved in intermolecular Hydrogen bonding and the distance cut-off as determined by PISA (in Å) are shown in Table 10:

[00558] Table 10-A.

HLA-A02 MHC	MAGEB2 peptide	Length (in Å)
Tyr159 OH	Gly1 O	2.6
Lys66 NZ	Val2 O	2.9
Gln155 NE2	Glu6 OE2	2.8
His70 N	Glu7 OE1	3.5
Thr73 OG1	Glu7 OE2	2.7
Lys146 NZ	Ser9 OG	3.7
Tyr84 OH	Val10 OXT	2.7
Thr143 OG1	Val10 OXT	2.8
Tyr171 OH	Gly1 N	2.6
Glu63 OE2	Val2 N	2.9
Tyr99 OH	Tyr3 N	3.0
Gln155 OE1	His8 NE2	2.8
Asp77 OD1	Val10 N	2.9

[00559] Specificity of MAGEB2 peptide to this HLA-A02 vis-à-vis other HLA-A02 subtypes

[00560] The table 10B below summarizes some of the residue position changes in other HLA-A02 subtypes as identified from our analyses.

[00561] Table 10-B

HLA-A02 residue	variant residues in other subtypes	Residue number (as in Structure)
F33	Y33	F9
Q67	R67	Q43
K90	N90	K66
T97	I97	T73
H98	D98	H74
V119	L119	V95
R121	M121	R97
Y123	C123, F123	Y99
W131	G131	W107

Y140	F140	Y116
K151	N151	K127
A173	T173	A149
V176	E176	V152
L180	W180	L156
A260	E260	A236

[00562] Figure 13A shows the MAGEB2 peptide-MHC interactions. Figure 13B shows the positions of variant residues in other HLA-A02 subtypes. From analyses of the structure examples (7, 8 and 9) and an in silico mutation analyses with the variant residues for each of the HLA-A02 subtype using PyMOL1, it seems to be highly likely that MAGEB2 peptide would be able to bind to most, if not all, of these subtypes in what is a fairly conserved binding pocket.

[00563] **Conclusion**

[00564] The MAGEB2 peptide makes canonical interactions with the HLA-A02 MHC in the peptide binding groove of MHC class I that is used for peptide binding and recognition. The peptide binds by burying its NH₂- and -COOH terminal ends into the two ends of the peptide groove and picking up key H-bonding and hydrophobic interactions with MHC, which is purported to account for the high affinity of binding and diversity of peptides that bind to class I MHC4. The MAGE-B2 10-mer peptide is one amino acid longer vis-à-vis the 9-mer peptides that mostly bind, and the longer peptide is accommodated in the same groove by bulging out the center part of the peptide from the pocket^{5,6}. The other interactions of the peptide with the MHC are through bonded, hydrophobic and van der

Waals interactions with the peptide core residues and its backbone to core residues in the MHC binding groove as listed above.

[00565] Methods

[00566] Reference the methods section in Example 7.

[00567]

[00568] Structure analyses

[00569] A free state structure of the MAGEB2 peptide bound MHC in the absence of BITE® binders was not attempted. In order to determine the interaction residues between MAGEB2 peptide and HLA-A02 MHC, the pMHC coordinates was extracted from the pMHC:N3H structure in PyMOL1 and this extracted coordinate file (pMHC only) was subject to extensive interface analyses using PISA2 (CCP4i3 package) as well as visual structure analyses using PyMOL. The core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the pMHC protein. The 5 Å core region cut-off distance allowed both atoms within a van der Waals radius and potential water-mediated hydrogen bonds in addition to hydrogen bonds, salt bridges and hydrophobic interactions. Furthermore, specific residue pairs from these core residues that are involved in electrostatic salt bridges or hydrogen bonding between the MHC and peptide (intermolecular interaction) with distances were also obtained from PISA and verified in PyMOL.

[00570] Bibliography

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[00571] EXAMPLE 7: Crystal Structure and Interaction Identification of the MAGEB2 peptide /HLA-A02 MHC/ Family 4 L7E BiTE® scFv complex

[00572] Introduction

[00573] Bi-specific T-cell engagers (BiTE®) specific to MAGEB2 peptide (p) bound HLA-A02 major histocompatibility complex (MHC) through engaging specific HLA interactions enabling MAGEB2 recognition were successfully generated. The following Examples 7, 8 and 9 describe how the crystal structures were obtained and the interactions that the family 4 BiTE® molecules make in order to identify and engage this pMHC specifically were defined.

[00574] Results

[00575] L7E scFv Heavy chain makes direct interactions with MAGEB2 peptide, light chain makes HLA and MAGEB2 interactions to identify and engage this complex

[00576] Coordinates are provided in Table 11.

[00577] The crystal structure of MAGEB2 pMHC:L7E has been determined at 1.9 Å. The scFv interactions with MAGEB2 peptide are from the heavy chain CDRs: CDR1, CDR2, CDR3 and the light chain CDR3. The light chain also interacts with HLA residues on the α-helix that form a part of the peptide binding groove to stabilize the molecule and this interaction.

[00578] The representations in Figures 14-16 show the key regions of the BiTE® and the surface of pMHC to capture the interacting interface of these molecules.

[00579] The core pMHC amino acid residues of the interaction interface with L7E were defined as pMHC residues that are within 5 Å of the L7E scFv BiTE®, listed below.

[00580] MHC interaction with heavy chain (HC): Arg65, Lys66, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Gln155.

[00581] MHC interaction with light chain (LC): Gly16, Arg17, Gly18, Glu19, Gln43, Arg65, Lys68, Ser71, Gln72, Arg75, Val76, Gly79, Thr80, Arg82, Gly83, Glu89, Lys146

[00582] MAGEB2 interaction with HC: Asp4, Gly5, Glu6, Glu7, His8, Ser9

[00583] MAGEB2 interaction with LC: Ser9

[00584] The core L7E scFv BiTE[®] amino acid residues of the interaction interface with pMHC were defined as L7E residues that are within 5 Å of the pMHC, listed below.

[00585] L7E HC interaction with MHC: Ser30, Ser31, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Val102, His103, Leu104, Gly105

[00586] L7E LC interaction with MHC: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, Leu95

[00587] L7E HC interaction with MAGEB2: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Lys100, Gly101, Val102, His103, Leu104

[00588] L7E LC interaction with MAGEB2: Trp90

[00589] The following is a list of intermolecular bonded interactions between the pMHC and the family 4 L7E BiTE[®]. The pairs of residues involved in intermolecular salt bridges and the distance cut-off as determined by PISA in angstroms (Å) are shown in Table 12:

[00590] Table 12.

pMHC	L7E BiTE [®]	Length (in Å)
p: Asp4 OD1	HC: Lys100 NZ	3.2
MHC: Arg75 NH1	LC: Asp49 OD1	2.8
MHC: Arg75 NH1	LC: Asp50 OD1	3.8
MHC: Arg75 NH2	LC: Asp50 OD2	3.1
MHC: Arg75 NH1	LC: Asp50 OD2	2.7
MHC: Lys68 NZ	LC: Asp52 OD1	2.9

[00591] The pairs of residues involved in intermolecular Hydrogen bonding and the distance cut-off as determined by PISA (in Å) are shown in Table 13:

[00592] Table 13.

pMHC	L7E BiTE [®]	Length (in Å)
p: Asp4 O	HC: Lys100 NZ	2.9
p: Gly5 O	HC: Lys100 NZ	3.0
p: Glu6 OE1	HC: Gly53 N	2.7
p: Glu7 N	HC: Lys100 O	2.9
p: Ser9 OG	LC: Trp 90 NE1	2.7/2.9*
MHC: Thr73 OG1	HC: His103 NE2	2.8

MHC: Ala149 O	HC: Ser54 OG	3.5
MHC: Arg75 NH2	LC: Gly28 O	2.8
MHC: Arg75 NH1	LC: Ser31 OG	3.7
MHC: Arg82 NH2	LC: Tyr 92 OH	3.3

**analysis in PyMOL. This is a notable water-mediated interaction. Not all water-mediated interactions are specifically denoted.*

[00593] Conclusions

[00594] The L7E BiTE[®] molecule makes notable interactions with both the peptide and HLA-A02 MHC through both the HC and LC of the BiTE[®]. The LC of family 4 L7E BiTE[®] make notable interactions on the MHC surface that seems to position the L7E HC for recognition of MAGEB2 peptide.

[00595] Methods

[00596] Purification, Complex formation of pMHC and family 4 BiTE[®] scFv and Crystallization

[00597] The L7E scFv BiTE[®] molecule was recombinantly over-expressed in mammalian cells and purified using affinity chromatography and SEC to yield a monomeric peak. The HLA-A02 (MHC) was over-expressed in E. coli and refolded and purified in the presence of MAGE-B2 peptide to generate the pMHC complex.

[00598] The ~25 kDa scFv BiTE[®] and the ~47 kDa pMHC was mixed in 1.2:1 molar ratio and the resultant pMHC complex was separated by size exclusion chromatography. This highly purified pMHC complex was concentrated and subject to sitting drop vapor diffusion crystallization trials. Crystals of pMHC:L7E was obtained in 0.1M MES monohydrate pH 6.5, 12% PEG20000.

[00599] Data collection and structure determination and analyses

[00600] Data for this structure was collected from a single crystal, flash-frozen at 100K in the presence of 20% glycerol in respective crystallization mother liquor, at the Advanced Light Source (ALS, Lawrence Berkeley National Laboratory) at beamline 5.0.1. All data were processed using DENZO1 or Mosflm2 and Aimless (CCP4i3 package).

[00601] L7E complex crystals grew in the P22121 space group with the unit cell dimensions of $a=44.208$, $b=108.086$, $c=163.569$ Å and $\alpha=\beta=\gamma=90^\circ$, with a single complex per asymmetric unit and diffracted to 1.9 Å resolution. The structure of pMHC:L7E was solved by molecular replacement with the program PHASER4 using an ensemble of the published 1HLA MHC structure⁵ and a model structure for scFv generated internally using Schrödinger⁶ as the starting search model. Following initial refinement using Phenix⁷, the pMHC, $\beta 2$ microglobulin domain and scFv chains were manually

corrected for best fit in density as much as possible with Coot8. The overall structure improved with iterative rounds of manual model building and refinement using Phenix.

[00602] The complex structures were subject to rigorous quaternary structural analyses, interface analyses and distance measurements. The core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the pMHC protein. The 5 Å core region cut-off distance allowed both atoms within a van der Waals radius and potential water-mediated hydrogen bonding. All amino acids meeting the distance criterion were further analyzed using PyMOL9 and the interface residues were obtained from the interface and quaternary structure analyses program PISA10 (CCP4i package) using the respective completed structure as input files.

[00603] Sequence alignment and analyses

[00604] The family 4 scFv BiTE® sequences used in structure determination were multiple sequence aligned for comparison using geneious11 software. The resulting alignment was annotated using the structural data.

[00605] Sequences of the pMHC and L7E scFv BiTE®

[00606] pMHC

[00607] >HLA_A02

[00608] MGSHSMRYFFTSVSRPGRGEPRFIAVGYYDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDG
ETRKVKAHSQTHRVDLGLRGYYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDGKDYIALKEDLRSWTAAD
MAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRLYENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAE
ITLTWQRDGEDQTQDTELVETRPAGDGTGFKWAADVVPVSGQEQRVTCHVQHEGLPKPLTLRWEP (SEQ ID NO:
18454)

>MAGEB2peptide

GVYDGEEHSV (SEQ ID NO: 1)

>β2microglobulin

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTKDEYA
CRVNHVTLSPKIVKWDRDM (SEQ ID NO: 18455)

scFv BiTE®

(L7E)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKCLEWVSTISGSGGGTYAASVKGRFTISRDN SKN
 TLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGGQGLTVTVSSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTA
 RITCGGNNIGSKSVHWYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYCQVWDYRT
 LDWVFGCGTKLTVLG (SEQ ID NO: 18456)

[00609] Example 7 Bibliography

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[00610] EXAMPLE 8: Crystal Structure and Interaction Identification of the MAGEB2 peptide /HLA-A02 MHC/ Family 4 BiTE® H6N scFv complex

[00611] Introduction

[00612] As described in Example 7.

[00613] Results

[00614] H6N scFv Heavy chain makes direct interactions with MAGEB2 peptide, light chain makes HLA and MAGEB2 interactions to identify and engage this complex

[00615] Coordinates are provided in Table 14.

[00616] The crystal structure of MAGEB2 pMHC:H6N (shown in Figure 17) has been determined at 1.96 Å. The H6N interactions with pMHC are similar to the family 4 L7E structure in Example 7. The H6N residue Asp62 in HC (Ala62 in L7E), potentially contributes to an energetically favorable LC CDR3 interaction as seen from the H6N secondary structure conformation in this region vis-à-vis L7E.

[00617] The 2 panel representations in Figure 18 show the key differences of the H6N BiTE® vis-à-vis L7E from Example 7. Left panel shows Asp62 which could form a stabilizing interaction of LC CDR2 and the right panel shows a different conformation for Lys100 in HC CDR3. Figures 19 and 20 show additional structural features of H6N and its interactions with the pMHC (pMAGE-HLA).

[00618] The core pMHC amino acid residues of the interaction interface with H6N were defined as pMHC residues that are within 5 Å of the H6N scFv BiTE®, listed below. The vast majority of H6N interactions show similarity with L7E showcasing common motifs of family 4 scFv and similar molecular basis for MAGEB2 recognition.

[00619] MHC interactions with heavy chain (HC): Arg65, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Glu154, Gln155.

[00620] MHC interactions with light chain (LC): Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Arg65, Lys68, Ser71, Gln72, Arg75, Val76, Gly79, Thr80, Arg82, Gly83, Glu89, Lys146

- [00621]** MAGEB2 interactions with HC: Asp4, Gly5, Glu6, Glu7, His8, Ser9
- [00622]** MAGEB2 interactions with LC: Ser9
- [00623]** The core H6N scFv BiTE[®] amino acid residues of the interaction interface with pMHC were defined as H6N residues that are within 5 Å of the pMHC, listed below.
- [00624]** H6N HC interactions with MHC: Ser30, Ser31, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Val102, His103, Leu104, Gly105
- [00625]** H6N LC interactions with MHC: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Phe66, Gly67, Trp90, Tyr92, Arg93, Leu95
- [00626]** H6N HC interactions with MAGEB2: Ser30, Ser31, His32, Ala33, Ser52, Gly53, Ser54, Lys100, Gly101, Val102, His103, Leu104
- [00627]** H6N LC interactions with MAGEB2: Trp90
- [00628]** The following is a list of intermolecular bonded interactions between the pMHC and the family 4 H6N BiTE[®].

[00629] The pairs of residues involved in intermolecular salt bridges and the distance cut-off as determined by PISA in angstroms (Å) are shown in Table 15:

[00630] Table 15.

pMHC	H6N BiTE [®]	Length (in Å)
MHC: Arg75 NH1	LC: Asp49 OD1	2.9
MHC: Arg75 NH1	LC: Asp50 OD1	3.8
MHC: Arg75 NH2	LC: Asp50 OD1	3.9
MHC: Arg75 NH1	LC: Asp50 OD2	2.9
MHC: Arg75 NH2	LC: Asp50 OD2	3.2
MHC: Lys68 NZ	LC: Asp52 OD1	3.0

[00631] The pairs of residues involved in intermolecular Hydrogen bonding and the distance cut-off as determined by PISA (in Å) are shown in Table 16:

[00632] Table 16.

pMHC	H6N BiTE [®]	Length (in Å)
p: Glu6 OE1	HC: Gly53 N	2.8
p: Glu7 N	HC: Lys100 O	2.9
p: Ser9 OG	LC: Trp 90 NE1	2.7/2.9*

MHC: Thr73 OG1	HC: His103 NE2	2.7
MHC: Ala149 O	HC: Ser54 OG	3.6
MHC: Glu89 OE1	LC: Asp26 ND2	2.6
MHC: Arg75 NH2	LC: Gly28 O	2.9
MHC: Arg75 NH2	LC: Lys30 O	3.4
MHC: Arg75 NH1	LC: Ser31 OG	3.7
MHC: Arg82 NH2	LC: Tyr 92 OH	3.3

**analysis in PyMOL. This is a notable water-mediated interaction. Not all water-mediated interactions are specifically denoted.*

[00633] Conclusions

[00634] The H6N BiTE[®] molecule makes notable interactions with both the peptide and HLA-A02 MHC through both the HC and LC of the BiTE[®]. The LC of family 4 H6N BiTE[®] make notable interactions on the MHC surface that seems to poise the H6N HC for key recognition of MAGEB2 peptide. Subtle differences although exist in recognition between the L7E and H6N BiTE[®] as indicated above. The positioning and recognition of HLA-A02 MHC by the LC of family 4 BiTE[®] molecules is a key characteristic (tables here and Example 7).

[00635] Methods

[00636] Purification, Complex formation of pMHC and H6N BiTE[®] scFv and Crystallization

[00637] The scFv BiTE[®] molecule H6N was recombinantly over-expressed in E. coli as inclusion bodies, refolded and purified by ion-exchange chromatography. The HLA-A02 (MHC) was over-expressed in E. coli and refolded and purified in the presence of MAGE-B2 peptide to generate the pMHC complex.

[00638] The ~25 kDa scFv BiTE[®] and the ~47 kDa pMHC was mixed in 1.2:1 molar ratio and the resultant pMHC complex was separated by size exclusion chromatography. This highly purified pMHC complex was concentrated and subject to sitting drop vapor diffusion crystallization trials. Crystals of pMHC:H6N was obtained in 0.1M MES monohydrate pH 6.5, 15% PEG6000, 5% MPD.

[00639] Data collection and structure determination and analyses

[00640] Data for this structure was collected from a single crystal, flash-frozen at 100K in the presence of 20% glycerol in respective crystallization mother liquor, at the Advanced Light Source (ALS,

Lawrence Berkeley National Laboratory) at beamline 5.0.2. Data was processed using DENZO1 or Mosflm2 and Aimless (CCP4i3 package).

[00641] Crystals of H6N complex grew in the P22121 space group with the unit cell dimensions of $a=44.068$, $b=106.329$, $c=162.508$ Å and $\alpha=\beta=\gamma=90^\circ$, with a single complex per asymmetric unit and diffracted to 1.96 Å resolution. The structure was solved by molecular replacement with the program PHASER4 using the previously solved pMHC:L7E structure (Example 7) as the starting search model. Following initial refinement using Phenix7, the pMHC, $\beta 2$ microglobulin domain and scFv chains were manually corrected for best fit in density as much as possible with Coot8. The overall structure improved with iterative rounds of manual model building and refinement using Phenix.

[00642] The structure was subject to rigorous quaternary structural analyses, interface analyses and distance measurements. The core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the pMHC protein. The 5 Å core region cut-off distance allowed both atoms within a van der Waals radius and potential water-mediated hydrogen bonding. All amino acids meeting the distance criterion were further analyzed using PyMOL9 and the interface residues were obtained from the interface and quaternary structure analyses program PISA10 (CCP4i package) using the respective completed structure as input files.

[00643] Sequence alignment and analyses

[00644] As described in Example 7.

[00645]

[00646] Sequences of the pMHC and H6N scFv BiTE[®] used in the structure

pMHC

>HLA_A

MGSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTH
RVDLGLTRGYYNQSEAGSHTVQRMYGCDVGSWDRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKW
EAAHVAEQLRAYLEGTCVEWLRRLYENGKETLQRTDAPKTHMTHHAVSDHEATLRWALSFPYAEITLTWQRDGED
QTQDTELVETRPAGDGTGFKWAAVVPSGQEQRYTCHVQHEGLPKPLTLRWEP (SEQ ID NO: 18454)

>MAGEB2peptide

GVYDGEESHSV (SEQ ID NO: 1)

> $\beta 2$ microglobulin

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWFSFYLLYYTEFTPTKDEYA
CRVNHVTLSPKIVKWDRDM (SEQ ID NO: 18455)

scFv BiTE®

(H6N)

EVQLLES GGGVLVQPGGSLRLSCAASGFTFS SHAMSWVRQAPGKCLEWVSTISGSGGGTYYADSVKGRFTISRDN SKN
 TLYLQMNSLR AEDTAVYYCATGKGVHLGFDYW GQGTLVTVSSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQTA
 RITCGGNNIGSKSVHWYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYCQVWDYRT
 LDWVFGCGTKLTVLG (SEQ ID NO: 18457)

[00647] **Bibliography**

[00648] See Example 7.

[00649] **EXAMPLE 9: Crystal Structure and Interaction Identification of the MAGEB2 peptide /HLA-A02 MHC/ Family 4 BiTE® N3H scFv complex**

[00650] **Introduction**

[00651] As described in Example 7.

[00652] **Results**

[00653] **N3H scFv Heavy chain makes direct interactions with MAGEB2 peptide, light chain makes HLA and MAGEB2 interactions to identify and engage this complex**

[00654] Coordinates are provided in Table 17.

[00655] The crystal structure of MAGEB2 pMHC:N3H (shown in Figure 21) has been determined at 1.76 Å. The major interactions recapitulate the family 4 structures presented in Examples 7 and 8. The residues in scFv HC position 62: ALA vs ASP, contribute to water-mediated LC CDR3 interaction.

[00656] The 2 panel representations in Figure 22 show the key differences of the N3H BiTE® vis-à-vis L7E (Example 7) and H6N (Example 8). Left panel shows the differing heavy chain (HC) residues in N3H: Tyr32, Ala50 and Ser84. The right panel shows differing light chain (LC) residues, all in CDR3: Ser93, Gly94, Gln95, Arg96 and Gln97.

[00657] The core pMHC amino acid residues of the interaction interface with N3H were defined as pMHC residues that are within 5 Å of the N3H scFv BiTE®, listed below. The vast majority of N3H interactions show similarity with L7E (Example 7) and H6N (Example 8) showcasing common motifs of family 4 scFv and similar molecular basis for MAGEB2 recognition.

[00658] MHC interactions with N3H HC: Arg65, Lys66, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Gln155.

[00659] MHC interactions with N3H LC: Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Arg65, Lys68, Ser71, Gln72, Arg75, Val76, Gly79, Thr80, Arg82, Glu89, Lys146

[00660] MAGEB2 interactions with N3H HC: Asp4, Gly5, Glu6, Glu7, His8, Ser9

[00661] MAGEB2 interactions with N3H LC: Ser9, Val10

[00662] The core N3H scFv BiTE[®] amino acid residues of the interaction interface with pMHC were defined as N3H residues that are within 5 Å of the pMHC, listed below.

[00663] N3H HC interactions with MHC: Ser30, Ser31, Tyr32, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, His103, Leu104, Gly105

[00664] N3H LC interactions with MHC: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Ser66, Gly67, Trp90, Tyr92, Gln95

[00665] N3H HC interactions with MAGEB2: Ser30, Ser31, Tyr32, Ala33, Ser52, Gly53, Ser54, Lys100, Gly101, Val102, His103, Leu104

[00666] N3H LC interactions with MAGEB2: Trp90, Gln95

[00667] The following is a list of intermolecular bonded interactions between the pMHC and the family 4 N3H BiTE[®].

[00668] The pairs of residues involved in intermolecular salt bridges and the distance cut-off as determined by PISA in angstroms (Å) are shown in Table 18:

[00669] **Table 18.**

pMHC	N3H BiTE [®]	Length (in Å)
p: Asp4 OD1	HC: Lys100 NZ	3.0
MHC: Arg75 NH1	LC: Asp49 OD1	2.9
MHC: Arg75 NH1	LC: Asp50 OD1	3.7
MHC: Arg75 NH1	LC: Asp50 OD2	2.8
MHC: Arg75 NH2	LC: Asp50 OD2	3.1
MHC: Lys68 NZ	LC: Asp52 OD1	3.1

[00670] The pairs of residues involved in intermolecular Hydrogen bonding and the distance cut-off as determined by PISA (in Å) are shown in Table 19:

[00671] Table 19.

pMHC	N3H BiTE®	Length (in Å)
p: Asp4 O	HC: Lys100 NZ	2.8
p: Glu6 OE1	HC: Gly53 N	2.8
p: Glu7 N	HC: Lys100 O	2.9
p: Ser9 OG	LC: Trp 90 NE1	2.8/3.1*
p: Ser9 OG	LC: Gln 95 OE1	2.8/3.1*
MHC: Thr73 OG1	HC: His103 NE2	2.8
MHC: Ala149 O	HC: Ser54 OG	3.5
MHC: Gln72 OE1	LC: His33 NE2	3.4
MHC: Glu89 OE2	LC: Asp26 ND2	2.7
MHC: Arg75 NH2	LC: Gly28 O	2.8
MHC: Arg75 NH1	LC: Ser31 OG	3.7
MHC: Arg82 NH2	LC: Tyr92 OH	3.4

*Analysis in PyMOL. As shown in Figure 23, these are 2 notable water-mediated interactions, coordinated by same water molecule. Mutations in LC CDR3 preserves a key HC-LC H-bond keeping Trp90 in place to pick up the same water-mediated H-bond. Gln95 now picks up another stabilizing interaction as well through the same water molecule. Distances denoted by ----- dash. Not all water-mediated interactions are denoted.

[00672] Another key feature of the Family 4 BiTE® molecules from the different structure examples (7, 8 and 9) are the interactions picked up by the LC on the HLA-A02 MHC (water molecules shown as grey spheres) as shown in Figure 24. This figure shows the interface of LC of family 4 BiTE® molecules and HLA-A02 and shows the interactions the LC makes with HLA-A02 (water shown as grey spheres). The LC interaction with HLA-A02 helps orient the HC and LC CDRs towards the MAGEB2 pMHC for specific recognition. The H-bond and salt bridged interactions between N3H LC and HLA-A02 are shown in the tables above. This is a key feature of the Family 4 BiTE® molecules as determined from the different structure examples (7, 8 and 9) and energy minimized family 4 models of other candidates (data not shown). In addition to these interactions, buried surface area (BSA) calculations also show several other residues (in HLA-A02 and N3H LC) to be involved, as indicated below and listed above.

MHC*	BSA*
Gly16	36.75
Arg17	15.07
Gly18	47.43
Glu19	29.24
Pro20	0.34
Gln43	12.10
Arg65	8.19
Ser71	5.76
Val76	50.47
Gly79	26.19
Thr80	26.71
Lys146	26.67

N3H LC*	BSA*
Asn25	10.62
Ser29	30.56
Lys30	5.64
Tyr48	52.63
Asn51	20.65
Arg53	0.29
Asn65	11.07
Ser66	20.43
Gly67	24.84
Trp90	28.64
Gln95	34.97

*These residues in the HLA-A02 and LC interaction face are largely common across family 4 BiTE® molecules with some variations in the calculated BSA.

[00673] Sequence alignment of the Family 4 BiTE® Molecules

[00674] Sequence alignment for family 4 BiTE® molecules demarcating the CDR's and portraying similarities albeit some sequence variations are shown in Figure 25. Grey shaded boxes highlight interactions with the pMHC. Note that not all of the interactions are captured in this comparison.

[00675] Conclusions

[00676] The family 4 BiTE® molecules, including N3H, make notable interactions with both the peptide and HLA-A02 MHC through both the HC and LC. The LC picks up key interactions on the MHC surface through its CDR1 and CDR2 as well as some other regions, that position the HC for recognition of MAGEB2 peptide. Subtle differences exist in recognition between the different BiTE® molecules as indicated (Examples 7, 8 and 9). In addition to the Trp90 interaction with the peptide, N3H LC CDR3 contributes an additional favorable water mediated interaction via Gln95. The positioning of the LC for recognition of HLA-A02 MHC and MAGEB2 peptide recognition mostly by the HC is a notable characteristic. Of note is that all structures also show a small surface groove or cleft formed due to the MAGEB2 binding to HLA-A02 in the binding pocket, which together with the protruding MAGEB2 peptide conformation presents a complementary and remarkable surface for the family 4 BiTE® molecules to specifically recognize and bind.

[00677] Methods

[00678] Purification, Complex formation of pMHC and N3H BiTE® scFv and Crystallization

[00679] The scFv BiTE[®] molecule N3H was recombinantly over-expressed in *E. coli* as inclusion bodies, refolded and purified by ion-exchange chromatography. The HLA-A02 (MHC) was over-expressed in *E. coli* and refolded and purified in the presence of MAGE-B2 peptide to generate the pMHC complex.

[00680] The ~25 kDa scFv BiTE[®] and the ~47 kDa pMHC was mixed in 1.2:1 molar ratio and the resultant pMHC complex was separated by size exclusion chromatography. This highly purified pMHC complex was concentrated and subject to sitting drop vapor diffusion crystallization trials. Crystals of pMHC:N3H was obtained in 0.1M Trisodium citrate pH 5.5, 20% PEG3000.

[00681] Data collection and structure determination and analyses

[00682] Data for this structure was collected from a single crystal, flash-frozen at 100K in the presence of 20% glycerol in the above crystallization mother liquor, at the Advanced Light Source (ALS, Lawrence Berkeley National Laboratory) beamline 5.0.2. Data was processed using DENZO1 or Mosflm2 and Aimless (CCP4i3 package).

[00683] Crystals of H6N complex grew in the P22121 space group with the approximate unit cell dimensions of $a=44$, $b=108$, $c=162$ Å and $\alpha=\beta=\gamma=90^\circ$, with a single complex per asymmetric unit and diffracted to 1.76 Å resolution. The structure was solved by molecular replacement with the program PHASER4 using the previously solved pMHC:L7E structure (example 7) as the starting search model. Following initial refinement using Phenix7, the pMHC, $\beta 2$ microglobulin domain and scFv chains were manually corrected for best fit in density as much as possible with Coot8. The overall structure improved with iterative rounds of manual model building and refinement using Phenix.

[00684] The structure was subject to rigorous quaternary structural analyses, interface analyses and distance measurements. The core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the pMHC protein. The 5 Å core region cut-off distance allowed both atoms within a van der Waals radius and potential water-mediated hydrogen bonding. All amino acids meeting the distance criterion were further analyzed using PyMOL9 and the interface residues were obtained from the interface and quaternary structure analyses program PISA10 (CCP4i package) using the respective completed structure as input files.

[00685] Sequence alignment and analyses

[00686] As described in Example 7, data presented here.

[00687] Sequences of the pMHC and N3H scFv BiTE[®] used in the structure

pMHC

>HLA_A

MGSHSMRYFFTSVSRPGRGEPRIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTH
 RVDLGLTRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKW
 EAAHVAEQLRAYLEGTCVEWLRRLRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFPYAEITLTWQRDGED
 QTQDTELVETRPAGDGTQKWA AVVVPSGQEQRYTCHVQHEGLPKPLTLRWEP (SEQ ID NO: 18454)

>MAGEB2peptide

GVYDGEEHSV (SEQ ID NO: 1)

>B2microglobulin

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWFSFYLLYYTEFTPTEKDEYA
 CRVNHVTLSPKIVKWDRDM (SEQ ID NO: 18455)

[00688] scFv BiTE®

(N3H)

MKEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKCLEWVSAISGSGGGTYAASVKGRFTISRDN
 KNTLYLQMSSLRAEDTAVYYCATGKGVHLGFDYWGGQTLTVSSGGGGSGGGGSGGGGSSYVLTQPPSVSVAPGQ
 TARITCGGNNIGSKSVHWYQQKPGQAPVMVVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWD
 YSGQRQVFGCGTKLTVLG (SEQ ID NO: 18458)

[00689] Bibliography

[00690] See Example 7.

[00691] **Example 10: Crystal Structure and Interaction Identification of the MAGEB2 peptide /HLA-A02 MHC/ Family 7 H6H BiTE® Fab version 10B5 complex**

[00692] Introduction

[00693] Bi-specific T-cell engagers (BiTE®) specific to MAGEB2 peptide (p) bound HLA-A02 major histocompatibility complex (MHC) through engaging specific interactions enabling MAGEB2 recognition were successfully generated. This example describes how a crystal structure was obtained and defines the interactions that the family 7 molecule makes in order to identify and engage this pMHC specifically. The recognition by family 7 is distinct from any of the family 4 examples previously described (see Examples 7, 8 and 9 herein) and further exemplifies differing modes of specific recognition by these molecules.

[00694] Results

[00695] H6H Fab version 10B5 Heavy chain makes direct interactions with MAGEB2 peptide, light chain makes critical HLA interactions to identify and engage this complex

[00696] Coordinates are provided in Table 77 herein.

[00697] The crystal structure of MAGEB2 pMHC:10B5 Fab has been determined at 2.02 Å and is represented in Figure 28. The major interactions in recognition of MAGEB2 peptide by this molecule of family 7 are distinct from all the family 4 structures presented in Examples 7, 8 and 9 herein.

[00698] The 2 panel representations in Figure 29 show the differences between recognition of the family 4 N3H BiTE® as compared to this family 7 10B5 Fab (H6H BiTE®). The left panel of Figure 29 shows the N3H heavy chain (HC) and some light chain (LC) in MAGEB2 recognition. The right panel of Figure 29 shows the HC and LC of family 7 and the role of 10B5 HC CDR's in MAGEB2 recognition on mostly the N-terminal part of the peptide rather than the mid-region as in family 4 molecules. Also, the LC of 10B5 is completely on the other side and only contributes to MHC interactions and stability.

[00699] The core pMHC amino acid residues of the interaction interface with H6H were defined as pMHC residues that are within 5 Å of the 10B5 Fab, listed below.

[00700] MHC with H6H HC: Glu55, Glu58, Tyr59, Asp61, Gly62, Glu63, Arg65, Lys66, Ala69, Ala158, Gly162, Thr163, Glu166, Trp167, Arg170

[00701] MHC with H6H LC: Gln54, Glu55, Gly56, Pro57, Glu58, Tyr59, Asp61, Trp167, Arg170

[00702] MAGEB2 with H6H HC: Gly1, Val2, Asp4, Gly5, Glu6, Glu7

[00703] The core 10B5 Fab amino acid residues of the interaction interface with pMHC were defined as H6H residues that are within 5 Å of the pMHC, listed below.

[00704] H6H HC to MHC: Trp33, Arg50, Arg52, Ser55, Tyr56, Gly57, Thr59, Tyr103, Gly105, Ser106, Tyr107, Tyr108, Asn109, Tyr110, Phe111, Ser112

[00705] H6H LC to MHC: Ser30, Ser31, Tyr32, Ala50, Ser67, Thr91, Tyr92, Ser93, Met94, Phe96

[00706] H6H HC to MAGEB2: Ser30, Asn31, Arg54, Ser55, Tyr56, Ser104, Gly105, Ser106, Tyr110

[00707] There are no H6H LC residues within the distance requirements that directly contribute to the MAGEB2 peptide interacting interface which is a notable difference in recognition as compared to family 4 molecules.

[00708] The following is a list of intermolecular bonded interactions between the pMHC and the family 7 H6H BiTE® – 10B5 Fab.

[00709] The pairs of residues in Table 74 below are involved in intermolecular salt bridges and the distance cut-off as determined by PISA in angstroms (Å) is shown:

[00710] Table 74.

pMHC	10B5 Fab	Length (in Å)
MHC: Glu58 OE1	HC: Arg50 NH2	3.8
MHC: Glu58 OE2	HC: Arg50 NH2	3.0
MHC: Glu58 OE2	HC: Arg50 NH1	2.7
MHC: Asp61 OD2	HC: Arg52 NH1	3.3
MHC: Asp61 OD2	HC: Arg52 NH2	2.3

[00711] The pairs of residues in the table below are involved in intermolecular Hydrogen bonding and the distance cut-off as determined by PISA (in Å) is shown (bb- backbone) in Table 75 below.

[00712] Table 75.

pMHC	N3H BiTE®	Length (in Å)
p: Asp4 OD2	HC: Ser106 N (bb)	2.9
MHC: Glu63 OE1	HC: Tyr110 OH	2.6
MHC: Glu63 N (bb)	HC: Tyr110 OH	3.3
MHC: Arg65 NH1	HC: Thr59 OG1	3.3
MHC: Arg65 NH1	HC: Tyr56 O (bb)	3.8
MHC: Ala158 O (bb)	HC: Tyr103 OH	3.5
MHC: Thr163 OG1	HC: Ser106 N (bb)	3.9
MHC: Glu166 OE2	HC: Tyr108 OH	3.8
MHC: Glu54 NE2	LC: Ser30 OG	2.9
MHC: Glu55 OE1	LC: Tyr32 OH	2.6
MHC: Arg170 NH1	LC: Ser31 OG	2.8
MHC: Arg170 NH2	LC: Ser30 OG	3.4
MHC: Arg170 NH2	LC: Ser31 OG	3.1

[00713] Figure 30 shows some of the water-mediated bonding network. In the figure, water is represented as black spheres, distances are shown (black dashed line, distances in Å), MHC is shown as vacuum electrostatic surface representation (greyscale), and the residues of the MAGEB2 peptide are shown in light grey and heavy chain CDR's of 10B5 are shown as dark grey. The critical water-mediated interactions are shown in this figure. The several water molecules mediate key H-bond's bridging the peptide bound MHC to the HC CDR's of 10B5.

[00714] Another key feature is the complementary surface of the HC to the pMHC surface that facilitates this unique recognition. Figure 31 shows the vacuum electrostatic surfaces, pMHC (left panel) and the HC CDR's (right panel) in grayscale.

[00715] **Conclusions**

[00716] The family 7 BiTE® molecule H6H Fab version (10B5) makes critical direct and water-mediated interactions with the peptide through the HC, and with the HLA-A02 MHC through both the

HC and LC. There are key differences in recognition between the different BiTE[®] molecules as indicated (see family 4 examples 7, 8 and 9 as compared to this family 7 example).

[00717] **Methods**

[00718] **Purification, Complex formation of pMHC and 10B5 Fab (H6H BiTE[®]) and Crystallization**

[00719] The Fab version of H6H BiTE[®] represented by 10B5 was recombinantly expressed and purified by chromatography. The HLA-A02 (MHC) was over-expressed in *E. coli* and refolded and purified in the presence of MAGE-B2 peptide to generate the pMHC complex.

[00720] The ~50 kDa 10B5 Fab and the ~47 kDa pMHC was mixed in 1:1 molar ratio and the resultant pMHC complex was separated by size exclusion chromatography. This highly purified pMHC:Fab complex was concentrated and subjected to sitting drop vapor diffusion crystallization trials. Crystals of pMHC:10B5 Fab was obtained in 10% v/v 2-Propanol, 0.1M Sodium citrate tribasic pH 5.0, 26% PEG 400.

[00721] **Data collection and structure determination and analyses**

[00722] Data for this structure was collected from a single crystal, flash-frozen at 100K in the presence of 20% glycerol in the above crystallization mother liquor, at the Advanced Light Source (ALS, Lawrence Berkeley National Laboratory) beamline 5.0.2. Data was processed using DENZO¹ or Mosflm² and Aimless (CCP4i³ package).

[00723] Crystals of pMHC:10B5 Fab complex grew in the C222₁ space group with the approximate unit cell dimensions of a=98, b=193, c=109 Å and $\alpha=\beta=\gamma=90^\circ$, with a single complex per asymmetric unit and diffracted to 2.02 Å resolution. The structure was solved by molecular replacement with the program PHASER⁴ using the previously solved pMHC structure (only the pMHC part from example 7) and Fab model structure (Schrödinger⁶) as the starting search model. Following initial refinement using Phenix⁷, the pMHC and $\beta 2$ microglobulin domain were manually corrected for best fit in density as much as possible with Coot⁸. The Fab heavy and light chains were subject to subsequent iterations of refinement following extensive manual model building based on the experimental data and the sequences of 10B5. The overall complex structure improved with iterative rounds of manual model building and refinement using Phenix.

[00724] The structure was subject to rigorous quaternary structural analyses, interface analyses and distance measurements. The core interaction interface amino acids were determined as being all amino acid residues with at least one atom less than or equal to 5 Å from the pMHC protein. The 5 Å core region cut-off distance allowed both atoms within a van der Waals radius and potential water-mediated hydrogen bonding. All amino acids meeting the distance criterion were further analyzed using PyMOL⁹ and the interface residues were obtained from the interface and quaternary

structure analyses program PISA¹⁰ (CCP4i package) using the respective completed structure as input files.

[00725] Sequences of the pMHC and 10B5 Fab (version of H6H BiTE®) used in the structure

[00726] pMHC

>HLA_A

MGSHSMRYFFTSVSRPGRGEPRIAVGVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTH
RVDLGLTLRGYYNQSEAGSHTVQRMYGCDVGS DWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKW
EAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQRTDAPKTHMTHHAVSDHEATLRCWALSFP AEITLTWQRDGED
QTQDTELVETRPAGDGT FQKWA AVVVP SGQE QRYTCHVQHEGLPKPLTLRWEP (SEQ ID NO: 18454)

>MAGEB2peptide

GVYDGEEHSV (SEQ ID NO: 1)

>B2microglobulin

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYA
CRVNHVTL SQPKIVKWDRDM (SEQ ID NO: 18455)

[00727] 10B5 Fab (Fab version of family 7 H6H BiTE®)

>10B5Fab_HC

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVGRIRSRSYGGTTDYAAPVKGRFTISRD
DSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWVGQGT TVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
CLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDH
HHHHHHHHH (SEQ ID NO: 18459)

>10B5Fab_LC

DIQMTQSPSSLSASVGDRTITCRTSQSISSYLNWYQKPKGRAPKLLIFAASSLQGGVPSRFSGSGSGTDFTLTISLQP
EDFATYYCQQTYSMPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO: 18460)

- [00728] **Bibliography**
[00729] See Example 7.

[00730] **Example 11: Anti-tumor activity of a MAGEB2 BiTE® molecule**

[00731] To evaluate the anti-tumor activity of representative BiTE® molecules, an *in vivo* tumor experiment was performed using the following criteria.

[00732] Test system: Female NOD/SCID mice subcutaneously injected with human HCT-116 colon carcinoma cells

[00733] Effector cells: *In vitro* expanded and activated human CD3+ T cells (Day 13)

[00734] Treatment start: After tumors had reached a volume of ~ 200 mm³ (Day 16); Once weekly (q7d); 4 administrations

[00735] Treatment:

2 control groups (w/ and w/o T cells)

2 BiTE® molecules: N3H and H6H at 2 dose levels each: 2.0 and 0.2 mg/kg

[00736] Route of administration: Intravenous bolus injections

[00737] PK analysis: Following initial treatment at

0.5, 8, 24, 48, 120, 168 hours post injection; (n=3 animals of main study/time point)

168, 240, 312 hours post injection; (n=4 additional animals following single dosing)

[00738] **Animal care**

[00739] Female non-obese diabetic, severe combined immunodeficient (NOD SCID) mice were obtained from Charles River Laboratories (Sulzfeld, Germany). Studies were performed at Amgen Research (Munich) GmbH in accordance with the German Animal Welfare Law with permission from the responsible local authorities, in accordance with the standards of the Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC). Mice were cared for in accordance with the Guide for the Care and Use of Laboratory Animals, 8th Edition. Mice were housed in individual ventilated caging systems on sterilized aspen bedding. Animal rooms were set to maintain a temperature of 22°C ± 2°C, relative humidity of 55 ± 20%, and intermittent light and dark cycles of 12 hours. Sterile food and sterile water were made freely available throughout the studies. Cages were changed weekly inside an engineered cage changing station.

[00740] **Antitumor efficacy study in an HCT-116 colon carcinoma xenograft model**

[00741] Sublethal irradiated (2 Gy) female NOD/SCID mice were implanted subcutaneously with HCT-116 cells (5×10^6 /mouse) on day 1. On day 9, all animals received a single intravenous dose of anti-asialo GM1 antibody (50 μ L of a 1:2.5 dilution/mouse) into the lateral tail vein, in order to deplete remaining natural killer (NK) cells. As the anti-MAGEB2 N3H molecule does not cross-react to mouse CD3, activated human T cells were administered to mice bearing xenograft tumors (2×10^7 /mouse) on day 13 (see below for details). On day 16, when the tumors reached approximately 200 mm³, treatment was initiated. Because of the extended half-life, N3H (at dose levels of 2.0 or 0.2 mg/kg/admin) or vehicle control was administered once weekly by bolus IV injection on days 16, 23, 30 and 37. After the initial dose on day 16, blood samples were collected from the periorbital venous plexus for pharmacokinetic (PK) analysis (see below for details). Tumor volume was measured by calipers (DCS-1, Plexx B.V.) 3 times a week and progress was evaluated by intra- and intergroup comparison of tumor volumes (TV). The study was terminated on day 45.

[00742] All statistical analyses were performed using GraphPad Prism version 7.02. Data were analyzed by one-way analysis of variance (ANOVA), and differences in experimental results for tumor growth were assessed by Dunnett's post-hoc test for comparison against a control group. A p value of < 0.05 was considered to be statistically significant. The statistical significance is reported as follows: * = $p < 0.05$; ** = $p < 0.01$; *** = $p < 0.001$.

[00743] The following criteria were used to quantify the anti-tumor activity.

[00744] (i) Tumor eradication is achieved, when no measurable tumors are present at study end.

[00745] (ii) If the TV of a given animal or group is smaller as compared to the TV of the same animal or group at treatment start, a tumor regression (TR) is achieved and calculated as follows:

[00746]
$$TR [\%] = 100 - \left(\frac{100 \times TV_{\text{after treatment}}}{TV_{\text{at treatment start}}} \right).$$

[00747] (iii) The tumor growth inhibition TGI [%] is determined in case the TV of an animal or group equals or exceeds the TV at treatment start and is calculated relative to the growth of control group 2 using the formula:

[00748]
$$TGI [\%] = 100 - \left(\frac{100 \times \Delta TV_{\text{treated animal/group}}}{\Delta TV_{\text{control animal/group}}} \right), \text{ with}$$

[00749]
$$\Delta TV = TV_{\text{at observation}} - TV_{\text{at treatment start}}.$$

[00750] T cell expansion and activation

[00751] Normal peripheral blood CD3⁺ T cells from a healthy donor (#2336) were isolated from a LeukoPak through negative selection and cryopreserved by vendor (AllCells LLC, Alameda, CA, USA) prior to shipment. In order to obtain sufficient human T cells from a single donor for use in one mouse xenograft study, cells were activated and expanded for 10 days using ImmunoCult™ Human CD3/CD28 T Cell Activator (# 10970), ImmunoCult™-XF T Cell Expansion Medium (# 10981) and Human Recombinant IL-2 (# 78036.3, all STEMCELL, Cologne, Germany) in accordance with the manufacturer's instructions. The cell suspension was split on day 3, 6 and 8 of expansion. On the day of injection, cells were resuspended, pooled, centrifuged, washed twice with DPBS and adjusted to a concentration of 1×10^8 cells/mL in RPMI 1640 (#FG1215, Gibco/ Fisher Scientific GmbH, Schwerte, Germany). Cell viability was 93% as evaluated by flow cytometry. T cell activation was assessed by flow cytometric analysis of CD25 cell surface expression, and T cell expansion was measured by the T cell count over time.

[00752] Blood sampling

[00753] For peri-orbital blood sampling, animals were placed under anesthesia with 3-4% isoflurane (CP Pharma, Burgdorf, Germany; #798-932) using an Isotec3 isoflurane evaporator (Voelker GmbH, Kaltenkirchen, Germany). Blood was taken by rupture of the peri-orbital sinus with heparinized MiniCAPS capillaries (5 µL, Hirschmann Laborgeräte, Eberstadt, Germany, #6122437). Approximately 100 µL of blood was sampled into MiniCollect® Clot Activator and Gel Tubes (Greiner Bio One, Frickenhausen, Germany, #450472) and allowed to coagulate for 45 minutes at room temperature. Samples were centrifuged at 3000 x g for 10 minutes at room temperature in an Eppendorf centrifuge (Type 5424R, Hamburg, Germany) and serum (50 µL per blood sample) was separated from blood cells via a pipette. Serum was stored at -20°C and after 24 h at -80°C. N3H concentration in mouse serum was analyzed by an electrochemiluminescence-based immunoassay developed at Amgen Research (Munich) GmbH.

[00754] Quantification of mouse serum levels

[00755] Serum levels were quantified using an electrochemiluminescence-based immunoassay (ECL-Assay) at BA, ARM. Mouse serum samples were stored at -80°C prior to analysis. Samples were first pre-diluted in 100% NOD/SCID serum, if applicable, followed by a 1:10 dilution in Casein Blocker (Thermo Scientific, 37532, 1% in TBS) to reach a final dilution of 1:10 to 1:500. For immobilization of analytes streptavidin microplates (Mesoscale Discovery; L55SA-1) were coated with 30 µL MAGE-B2 pMHC-Biotin at 5 µg/mL in PBS and incubated overnight at 5 ± 3 °C, followed by a wash step with 3x 300 µL PBS/0.05% Tween-20 and blocking with 150 µL Casein Blocker (Thermo Scientific, 37532, 1% in TBS) for 60 min at 25 ± 2 °C on a rotational shaker (700-750 rpm). After a second wash step (3x 300 µL PBS/0.05% Tween-20) 30 µL of standard, QC or study samples were added to each well and incubated for 60 ± 20 min at 25 ± 2 °C on a rotational shaker (700-750 rpm). Standard samples, QC and study samples were tested in duplicates. Subsequently, plates were washed once more (3x 300 µL PBS/0.05% Tween-20), followed by addition of 25 µL detection antibody anti-anti-CD3-SulfoTAG (clone 1C1.1) at 1 µg/mL in Casein Blocker (Thermo Scientific, 37532, 1% in TBS) and incubation for 60 ± 20 min at 25 ± 2 °C on a rotational shaker (700-750 rpm). After a last wash (3x 300 µL BS/0.05% Tween-20) Read Buffer (Mesoscale Discovery; R92TG-2; 150 µL/well) was added and the plate was read on a QuickPlex SQ120 (Mesoscale Discovery).

[00756] Data analysis was performed using SoftMaxPro (version 6.4.1). Mean ECL values were applied for standard curve fitting against the nominal concentrations using a 5-Parameter Fit (weighting: 1/y²). Analyte concentrations in serum samples were calculated from the standard curve and multiplied with the respective dilution factor.

[00757] The quantitation limits for each assay run were derived from an acceptable recovery of quality control samples (low control 1 ng/mL; high control 160 ng/mL; prepared in 10 % serum). This confirmed an LLOQ of 10 ng/mL and an ULOQ of 1600 ng/mL analyte in 100 % serum. Samples with higher serum concentrations were diluted into the dynamic range of the assay. All samples were quantified within the dynamic range of the assay.

[00758] PK Data Analysis

[00759] Noncompartmental analysis (NCA) was performed on the individual serum concentration-nominal time data using Phoenix WinNonlin (Version 6.4.0.768, Pharsight Corporation) to estimate the following TK parameters:

[00760] The maximum observed concentration (C_{max}) was taken directly from the concentration-time data.

[00761] The area under the concentration-time curve from time zero to the time of the last quantifiable concentration (AUC_{last}) was calculated by the linear trapezoidal method, where data permitted.

[00762] The clearance (CL) was calculated by dividing the dose with the AUC_{inf} , where data permitted.

[00763] The terminal half-life ($t_{1/2}$) was determined by log-linear regression from the terminal elimination phase of the concentration-time curve, where data permitted.

[00764] PK data is summarized in graphical formats in Figure 36 herein. The left panel is data for the N3H molecule and the right panel is data for the H6H molecule.

[00765] CONCLUSIONS

[00766] As represented in Figures 32-35 herein, treatment of animals with tumors resulted in a clear inhibition of tumor growth from both the N3H molecule (Figures 32 and 33) and the H6H molecule (Figures 34 and 35) as compared to appropriate controls.

[00767] Table 20-A. Experimental Plan and Treatment Schedule

Group	Mice/ Group	Target Cells / Mouse (SC)	Effector Cells / Mouse (IP)	Treatment	Dose Level (mg/kg)	Dose Volume (mL)	RoA	Treatment Days
1	5	5×10^6 HCT-116/LUC	-	Vehicle	0	0.1	IV	16, 23, 30, 37
2	10	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	Vehicle	0	0.1	IV	16, 23, 30, 37
3	10	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	N3H	2	0.1	IV	16, 23, 30, 37
3b*	4	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	N3H	2	0.1	IV	Single shot, D16

4	10	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	N3H	0.2	0.1	IV	16, 23, 30, 37
4b*	4	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	N3H	0.2	0.1	IV	Single shot, D16
5	10	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	H6H	2	0.1	IV	16, 23, 30, 37
5b*	4	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	H6H	2	0.1	IV	Single shot, D16
6	10	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	H6H	0.2	0.1	IV	16, 23, 30, 37
6b*	4	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	H6H	0.2	0.1	IV	Single shot, D16
7**	8	5×10^6 HCT-116/LUC	2×10^7 CD3 ⁺ T cells	AMG CNTRL	1	0.1	IV	23, 30, 37, 44
-	55 + 16	5×10^6 HCT-116/LUC	Additional animals used for staging					
Σ	110	7.5×10^8 (with 20% surplus)	$>1.8 \times 10^9$ (with surplus)					

[00768] Serum was sampled from 3-4 animals/group/timepoint as indicated in the following Table 20-B.

[00769] Table 20-B. Serum sample overview

Day of experiment	Time point p.i. [h]	Group	Animals	Eye	Serum Quantity
16	0.5	3	36, 37, 59	right	50 µL
		4	11, 42, 43		
		5	38, 83, 89		
		6	04, 30, 51		
	8	3	06, 32, 104		
		4	26, 39, 57		
		5	01, 13, 15		
		6	14, 63, 65		
17	24	3	55, 66, 69	right	50 µL
		4	82, 98, 10		
		5	24, 27, 07		
		6	34, 56, 68		
18	48	3	36, 37, 59	left	50 µL
		4	11, 42, 43		

		5	38, 83, 89		
		6	04, 30, 51		
21	120	3	06, 32, 104		
		4	26, 39, 57		
		5	01, 13, 15		
		6	14, 63, 65		
23	168	3	55, 66, 69		
		4	82, 98, 10		
		5	24, 27, 07		
		6	34, 56, 68		

h = hours; p.i. = post injection

[00770] Table 20-C. Serum sample overview (single shot, long time PK)

Day of experiment	Time point p.i. [h]	Group	Animals	Eye	Serum Quantity
23	168	3B	46, 49, 102, 105	right	50 µL
		4B	05, 23, 106, 107		
		5B	53, 64, 86		
		6B	62, 76, 80, 99		
26	240	3B	46, 49, 102, 105	left	
		4B	05, 23, 106, 107		
		5B	53, 64, 86		
		6B	62, 76, 80, 99		
29	312	3B	46, 49, 102, 105	right	
		4B	05, 23, 106, 107		
		5B	53, 64, 86		
		6B	62, 76, 80, 99		

h = hours; p.i. = post injection

[00771] **Example 12: BLCL killing assay—Maximum IL-2 production by HLA-A*02:06 and HLA-A*02:07 expressing BLCLs**

[00772] This experiment was performed to determine whether the binding molecules of the invention bind to the pMAGE-HLA target when the MAGEB2 peptide of SEQ ID NO: 1 is complexed with different HLA-A serotypes.

[00773] B-lymphoblastoid cell lines (BLCL) target cells were harvested and resuspended at 1e6 cells/ml in media (RPMI 1640 with 15% fetal bovine serum and 1mM sodium pyruvate). BLCLs were peptide pulsed with MAGEB2 peptide at 50uM for 4 hours at 37C or left unpulsed. After incubation, target cells were resuspended at 1e5 cells/ml without washing off peptide. BiTE® molecule dilutions were prepared ranging from 5e4 pM to 20 pM for co-culture with peptide pulsed BLCLs. Only 5e4 pM and 20 pM of BiTE® dilution were used for co-culture with unpulsed BLCLs as negative controls. Effector cells were human pan T cells and resuspended at 1.25e6 cells/ml. 25,000 T cells and 2,500 target cells (E:T 10:1) were co-cultured with diluted BiTE® in 384 well plates. After 72 hours, supernatant was harvested and stored at -20C until assayed for IL-2 with PerkinElmer IL-2 (human) AlphaLISA Detection Kit. BLCL 165 is HLA-A*02:01 negative. HG01786 is HLA-A*02:01 positive. 1346-8357 is HLA-A*02:06/01:01 positive and T7526 is HLA-A*02:06/02:07 positive.

Cell Line Name	IHW Reference	A1	A2
1346-8357	IHW01080	A*02:06	A*01:01
T7526	IHW09076	A*02:06	A*02:07
HG01786 (+)	#12	A*02:01	
165 (-)		A*02:01 Negative Line	

[00774] Results of this experiment are depicted in Figure 27 and indicate that the three different binding molecules (H6H, N3H, Y8P) do bind to the pMAGE-HLA complex where the HLA is an HLA-A*01:01 and/or HLA-A*02:06 and/or an HLA-A*02:07.

[00775] **Example 13: MAGEB2 BiTE® Molecule TDCC: MAGEB2 Peptide Titration on Various Different HLA-A2 Cells**

[00776] The purpose of this experiment was to titrate MAGEB2 peptide onto HLA-A2 T2 cells with various HLAs in TDCC assays with the MAGEB2 N3H BiTE® molecule and evaluate cell killing.

[00777] TDCC Assay Overview

[00778] Donor pan T cells: RG1872

[00779] E:T of 10:1

[00780] 25,000 pan T cells

[00781] 2500 target cells

[00782] Samples run in triplicate

[00783] Incubate plates at 37°C for 48hrs

[00784] Readout: luminescence signal via BioGlo

[00785] Calculations

[00786] Values normalized to Target Cell Only values for each peptide concentration

[00787] EC50 values calculated without unpulsed values

[00788] Unpulsed values labeled as 0 on plots

[00789] Methods

[00790] CD3e and HLA-A*02:01 were knocked out in T2.luciferase cells to generate D5.H6-E1 T2.luc (D5) cells that do not express the HLA-A*02:01 allele. These D5 cells were used to generate cells that express the different HLA-A family alleles that were assayed. For the T cell-dependent cellular cytotoxicity assay, target cells were resuspended at 1e6 cells/ml in media (RPMI 1640 with 10% fetal bovine serum, 1mM sodium pyruvate, 100U/ml penicillin/streptomycin, 2mM Glutamax, 10mM HEPES, and 1X MEM NEAA). Cells were pulsed with MAGEB2 peptide at 8 10-fold MAGEB2 peptide dilutions starting at 50uM for 2 hours at 37C and then peptides were washed off. Target cells including unpulsed cells were resuspended at 1e5 cells/ml. MAGEB2 N3H BiTE® molecule was used at 5e4 pM and EGFRvIII BiTE® molecule was used at 1e4 for co-culture with peptide pulsed cells. Effector cells were human pan T cells and resuspended at 1.25e6 cells/ml. 25,000 pan T cells and 2,500 target cells (E:T 10:1) were co-cultured with N3H BiTE® in 384 well plates and run in triplicate. After 48 hours incubation at 37C, luminescence signal was assayed using Bio-Glo reagent. Values were normalized to target cell only values for each peptide concentration for each cell line for specific cytotoxicity calculations.

[00791] Results are depicted graphically in Figures 37-39, and summarized below in Table 76. N3H BiTE® exhibits dose-dependent killing on MAGEB2 peptide titrated onto various T2 HLA-A2 family allele knock-in cells. A*02:05 resulted in lower EC50 compared to T2.luc or A*02:01 rescue and A*02:06 appears similarly potent to A*02:01. A*02:07 resulted in an approximately 2 log higher peptide EC50 concentration compared to A*02:01, which is in line with previous results with N3H BiTE® titrated against this cell line pulsed at a high concentration. At the highest peptide pulse concentration (50uM), A*02:05 and A*02:06 increased HLA-A2 MFI by 2-to-3-fold compared to unpulsed cells.

Table 76

Cell Line ID #	HLA-A Allele	EC50 (M)	Max Killing (%)
T2.Luc	A*02:01	3.43e-9	97.73
D5	N/A	N/A	0.35
1	A*02:01:01:01	5.24e-9	96.91
4	A*02:05:01:01	2.59e-10	98.20
5	A*02:06:01:01	1.23e-9	98.29
6	A*02:07:01:01	3.54e-7	82.83

[00792] Example 14: Homology model generation and analysis of MAGEB2 peptide /HLA-A02 MHC/ Family 4 scFvs

[00793] Introduction

[00794] Homology models of several lead scFvs specific for MAGEB2 peptide (p) bound HLA-A02 major histocompatibility complex (MHC) belonging to family 4 were successfully generated. These “*in silico*” structures are useful to further identify key amino acid residues that play a role in binding of the molecules of the invention to the MAGEB2 pMHC. Homology models were generated utilizing a structural computational approach, utilizing the known crystal structure of one family 4 scFv (L7E) in complex with its pMHC target and generally following the workflow set forth in Figure 40 herein. Following the creation of the homology models, predictive mutagenesis algorithms were used to propose alternative mutations at each key residue target binding position and these results are summarized in Figures 47-50 herein.

[00795] Homology modeling of scFv N3H correlates well with its crystal structure.

[00796] A homology model for scFv N3H was generated following the procedure outlined in the methods below, superimposing with its crystal structure with an RMSD of 0.3 Å (full atom). The region of highest correlation was in the apical regions of the scFv (i.e. away from the target binding site). See Figure 41 herein. This result supported the validity of models subsequently generated.

[00797] Models for several Family 4 scFvs show interactions within the binding interface consistent with varying degrees of stability.

[00798] The homology model for the WT, L6A, N3H and Y8P scFvs was energy minimized and the target binding interface analyzed for the presence of cavities surrounding key residues engaged in binding to the MAGEB2 pMHC. Figure 42 herein is representative of the results of this analysis. The models indicate varying degrees of contacts and residual cavities upon complex formation, which may translate in different thermostability and affinity. N3H and L6A show smaller cavities, indicating potentially better binding, whereas Y8P and WT, harboring larger cavities, may be less stable.

[00799] A closer look at the interactions between the scFvs and the MAGE B2 suggests that the VH and VL portion of the scFv play different roles: the former contacts primarily the peptide, while the latter is engaged in stabilizing the HLA portion of the target receptor. Key determinants of binding have therefore been identified in VL residues: 92, 95, 96 and 97, and position 97 playing a central role in binding. The interaction of those key hotspots was assessed in the context of the four homology models generated (including the parental molecule), as shown in Figures 43-46 herein.

[00800] VL position 92: Parental residue is a SER, while in all the four models created the residue at position 92 is mutated to TYR, which occupies a cavity (originally present in WT) and engages in hydrogen bonds with three surrounding residues (SER, ARG and LYS) belonging to the target or VL itself.

[00801] VL position 95: Parental residue is an ASP. Mutated to GLN or LEU in different models, LEU appears to be more stable and yields more favorable interaction energies.

[00802] VL position 96: Parental residue is a HIS. Mutated to ASP, GLN or ARG. The ARG (Y8P) appears to be in a non-favorable position Both GLN and ASP engage in charged contacts (GLN appears most energetically favorable).

[00803] VL position 97: Parental residue is a VAL. Mutated to HIS, GLN and TRP. This position serves as bridging region between the VH:VL and HLA.

[00804] Interaction energies were calculated utilizing Schrodinger as described in the Methods below and were correlated with observed T_m. The energies have various degrees of predictive power due to insufficient degrees of variation between experiments.

[00805] **Table 100. Energetics vs. WT (B3K)**

Molecule	ΔG – interaction Ab:Ag (kcal/mol)	Δ stability (kcal/mol)	dVdW (kcal/mol)	Observed T _m (C)
L7E	-388	-35	-12	53.5
L6A	-466	-148	-33	56.4
N3H	-480	-233	-21	57.1
Y8P	-450	-170	-18	57.5
G2H	-481	-145	-35	57.0
L8M	-488	-138	-22	52.7
G2B	-466	-165	-21	54.5
Q4R	-471	-151	-43	56.9
Q4Z	-465	-108	-23	53.5
T1C	-214	-101	-33	54.1

Stability metrics from models show correlation with observed T_m.

[00806] Conclusions

[00807] Homology models were generated for selected Family 4 scFvs and show high correlation with at least one corresponding crystal structure (N3H). Structural analysis supports the notion that key residues on the light chain (LC) contact the HLA while the heavy chain (HC) appears to play a role in stabilizing the peptide via specific amino acid contacts. Energetic and interaction analysis provides insights into possible key determinants of binding and stability, including the presence of specific voids within the interface. Structural modeling and predictive mutagenesis were also used to broaden the analysis, providing additional mutations for key determinants of binding that are likely to play an equally important role.

[00808] Methods

[00809] The existing crystal structure of L7E was utilized as basis for the creation of homology models of the parental as well as three additional scFv variants. The complex for all models was optimized by rotameric search along residues at the interface, extending spherically 7 Å around each residue and followed by energy minimization. Initial model correction was performed using Coot/Pymol, homology modeling, minimization and energetic analysis was performed using the Schrodinger suite and predictive mutagenesis was done using MOE 2019.02. The modeling workflow is summarized in Figure 40 herein.

[00810] **Example 15: Effect of test articles on human T cell mediating killing of patient-derived organoids (PDXOs)**

Table 101: Abbreviations for Example 15

PDXO	Patient-derived xenograft organoid
ELISA	Enzyme-linked immunosorbent assay
NSCLC	Non Small Cell Lung Cancer
SCLC	Small Cell Lung Cancer
LUTM	Lung Tumor Medium
CRTM	Colonrectal Tumor Medium
PBS	Phosphate Buffer Saline
FACS	Fluorescence-activated Cell Sorting
RPMI	Roswell Park Memorial Institute
FBS	Fetal Bovine Serum
Cat #.	Catalog number
hPBMC	Human peripheral blood mononuclear cell
min	Minute
hr	Hour
RT	Room Temperature

[00811]

[00812] **Objectives**

[00813] This study aimed to evaluate the capacity of test molecules to retarget human T cells on patient-derived xenograft organoids (PDXOs) in order to induce their killing, as assessed by the enzyme-linked immunosorbent assay (ELISA) and flow cytometry.

[00814] **Materials**

[00815] **Human peripheral blood mononuclear cell (hPBMC)**

[00816] The frozen PBMCs from 1 donor (coded as LP200601B) were obtained and used for 4.2.

[00817] **PDXOs**

[00818] Table 102. Organoid information

No.	Model_Name	Race	Cancer Type	Subtype	Culture Medium
1	LU1206	Asian	Lung Cancer	NSCLC, SCC	LUTM
2	CR5088	Western	Colonrectal Cancer	NA	CRTM

[00819] Reagents**[00820] Table 103. Major reagents used in this study**

Item	Supplier	Cat#
Advanced DMEM/F12	Life Technologies	12634028
DMEM	Hyclone	SH30243.01
RPMI1640	Gibco	A1049101
Matrigel GFR, Phenol Red-free	Corning	356231
Organoid culture media LUTM, CRTM	Crownbio	
Coculture medium	Crownbio	
PBMC	Allcells	PB006-C
TrypLE™ Express	Life Technologies	12605010
2-ME	Gibco	21985-023
FBS	Gibco	100991-148
EDTA	Gibco	15575-038
PBS	Hyclone	SH30256.01
CFSE	eBioscience	65-0850-84
IL-2 ELISA Kit	R&D	D2050
IFN γ ELISA Kit	R&D	DIF50
Granzyme B ELISA Kit	R&D	DGZB00
HLA-A2 antibody	BD	558570

[00821] Note:**[00822]** Complete T cell Medium: RPMI 1640 with 10% FBS, 1% P/S and 55 μ M 2-ME**[00823]** Coculture medium: Complete T cell Medium / LUTM (1:1) + 5% MG or Complete T cell Medium / CRTM (1:1) + 5% MG**[00824] Test articles**

[00825] Table 104 Test Articles supplied by Sponsor

Name	M.W. Da	Stocking Conc.		Storage
N3H	104636.6	5 mg/mL	47.8 μ M	-80°C
H6H	105934.1	5 mg/mL	47.2 μ M	-80°C
W5C	106863.0	1 mg/mL	9.4 μ M	-80°C
Q9R	54385.6	1 mg/mL	18.4 μ M	-80°C

[00826] Other Equipment**[00827] Table 105. Other equipment used in this study.**

Item	Supplier	Cat#
6 Well Clear TC-Treated Multiple Well Plates	Corning	3516
12 Well Clear TC-Treated Multiple Well Plates	Corning	3512
96-Well Ultra-Low Attachment Microplate	Corning	3340
20 μ m cell filters	PluriSelect	43-50020-03
70 μ m cell filters	Greiner	542070
CO2 Water Jacketed Incubator	Thermo Scientific	

[00828] Procedures**[00829] HLA-A2 screening**

[00830] The selected organoids models, LU1206B and CR5088B, were thawed and cultured in the corresponding medium, LUTM and CRTM, until they reached 2-3 wells of 6 well plate. The organoids (20-100 μm in size) were harvested and counted, and 1×10^5 organoids were used for HLA-A2 staining, and then dissociated into single cell by TryLE digestion. The TryLE activity was stopped by adding the wash medium and then centrifuged at 300g for 5mins. The organoid cells were washed twice and counted by trypan blue exclusion assay to get an estimation of the single cells/organoid for later coculture use. All cells were transferred to labeled FACS tubes. 2 mL of FACS buffer was added to each tube and cells were re-suspended gently. Tubes were then centrifuged at 300g for 5 mins and then discarded the supernatant. The wash steps were repeated 2x. Anti-human HLA-A2 antibody diluted in FACS buffer was added to each sample and incubated at RT for 30 mins in the dark. Cells were washed twice with 2ml of FACS wash buffer, centrifuged and then decanted supernatant. Cells were resuspended in 100 μL of FACS staining buffer. 5 μL of 7-AAD staining solution was added to each sample, and incubated for 10 mins before analysis. The data are analyzed by Kaluza.

[00831] Redirected T cell killing for organoids

[00832] Organoid seeding

[00833] Expanded the selected organoid models (LU1206B and CR5088B) to $1-2 \times 10^6$ organoids (20-70 μm in size). On the day of the experiment, collected the organoids into the labeled centrifuge tubes, counted the organoid numbers. Resuspended the desired number of organoid (2500 organoid/well) with 5 ml of PBS. Prepared 2x CFSE solution (4 μM) in PBS (pre-warmed to RT), added 5 ml of 2x CFSE solution to 5 ml of organoid suspension to a final concentration of 2 μM according to CFSE cell labeling kit, incubated at RT for 5 mins. Stopped labeling by adding 40 ml of pre-chilled medium (RPMI1640+10% FBS), and then centrifuged at 300g, 4 ° C for 5 mins. Supernatant was discarded and then the wash step was repeated. Resuspended the organoid in the coculture medium and seeded 90 μL of organoids suspension to each well (2500 organoid/well) of 96-well ultra low attachment U bottom plate.

[00834] hPBMCs preparation

[00835] Frozen hPBMC were used for the coculture. Thawed the frozen hPBMCs rapidly using a water bath at 37°C and immersed the cryotubes with gentle agitation. Added pre-warmed complete T cell medium to 12ml and centrifuged at 2000rpm for 5 min RT. Repeated the wash again and centrifuged at 2000rpm for 5 min RT. Removed the medium and resuspended the hPBMC in coculture medium and counted the cell number by trypan blue exclusion assay.

[00836] Cytotoxicity assay

[00837] Added 90 μ l of hPBMCs with desired cell numbers to corresponding E:T ratios (E: effector cells, T:target cells). Prepared the antibody solution (1:100 dilution), treated the cells with 20 μ l antibody solution per well (final concentration is 50,000pM). Incubated the cells at 37° C for 48hrs, checked the medium color and cell status every day. After incubation, centrifuged the 96-well plate at 300g for 5min, then collected 80ul of the supernatant for the ELISA analysis of on IL-2, IFN- γ and Granzyme B by following the instruction from the kit. Transferred the cells with care to 96-V bottom plate and combine 2 wells into 1 sample and 3 samples for each treatment. Dissociated the organoids into single cell with 50-100 μ l TrypLE, incubated the organoids at 37 ° C until the cells were getting dissociated by several rounds of pipetting. Added 100-150 μ l of RPMI 1640 to stop TrypLE digestion, centrifuged at 300g, 5 min, discarded the supernatant. Transferred all cells in 200 μ L FACS buffer to labeled FACS tube, centrifuged at 300g for 5 mins at 4°C. Added 1 μ L Fixable Viability Dye eFluor™ 780 to the cells and incubate at 4°C for 30 mins in the dark. Added 2 mL FACS buffer to each well and re-suspended cells gently. Centrifuged the plates at 300g for 5 mins at 4°C and discarded the supernatant. Repeated the wash steps. Resuspended the cells in 200 μ L of FACS buffer and analyzed on a flow cytometer. The data are analyzed by Kaluza.

[00838] Data analysis

[00839] ELISA data are analyzed by GraphPad Prism . FACS data are analyzed by Kaluza. All statistics were performed using Prism 8, version 8.3.0. The comparison between treatment and control group was performed by the Student's *t*-test.

[00840] Results

[00841] LU1206B

[00842] HLA-A2 expression in LU1206B

[00843] 1×10^5 organoids were digested into single cell suspension with TrypLE and HLA-A2 expression was analyzed by using flow cytometry.

[00844] ELISA of IFN- γ , IL-2 and Granzyme B

[00845] The supernatant from coculture of LU1206B with hPBMC was collected and IFN- γ , IL-2 and Granzyme B in the supernatant was measured by ELISA. The production of the three cytokines in the coculture is shown in Figure 51A herein.

[00846] CR5088B

[00847] HLA-A2 expression in CR5088B

[00848] 1×10^5 organoids were digested into single cell suspension with TrypLE and HLA-A2 expression was analyzed by using flow cytometry.

[00849] **6.2.2 ELISA of IFN- γ , IL-2 and GranzymeB in CR5088B**

[00850] The supernatant from coculture of CR5088B with hPBMC was collected and IFN- γ , IL-2 and Granzyme B in the supernatant was measured by ELISA. The production of the three cytokines in the coculture is shown in Figure 51B herein.

[00851] Summary

[00852] In the LU1206B coculture assay, the production of IFN- γ , IL-2 and Granzyme B in N3H- and H6H groups was dramatically increased as compared to the W5C group (a negative control molecule) at both E/T ratios. Such an increase was also observed in the Q9R group, serving as a positive control. A small killing effect on LU1206B was observed in N3H and H6H groups. In the CR5088B coculture assay, N3H- and H6H groups showed a much higher production of IFN- γ , IL-2 and Granzyme B as compared to the W5C control group. A small killing effect was observed in the N3H and Q9R groups at both E/T ratios and in the H6H groups at higher E/T ratios. This data indicates proper targeting and associated effects by both the N3H and H6H molecules.

[00853] Example 16: TDCC assays against DAN-G Cells

[00854] BiTE[®] molecule-induced redirected lysis and T cell activation against MAGEB2 pMAGE-HLA expressing target cells was determined in cytotoxicity assays by flow cytometry (Becton, Dickinson and Company (BD), FACSCanto II).

[00855] The MAGE-B2-positive tumor cell line DAN-G (German Collection of Microorganisms and Cell Cultures GmbH (DSMZ), Cat.No. ACC 249) and the tumor cell line DAN-G knocked-out for MAGE-B2 were labelled with the fluorescent membrane dye DiO (Invitrogen, Cat.No. V22886) according to the manufacturer's instructions. Human T cells (1×10^5) were co-cultured with DiO labelled tumor cells (1×10^4) and serial dilutions of the MAGE-B2 BiTE[®] molecules H6H and N3H in 96 well flat bottom plates. Co-cultures were performed at 37°C in a 5% CO₂ incubator for 48 hours. Following incubation, adherent cells were detached by Trypsin/EDTA (Gibco, Cat. No. 15400054) and pooled with non-adherent cells. Flow cytometric analysis was performed to investigate tumor cell lysis and T cell activation on pooled cells. Tumor cells were identified as DiO-positive cells. Redirected lysis of DiO-positive tumor cells was determined by measurement of PI incorporation. T cells were identified by antibodies directed to CD4 (BD, Cat. No. 651849/566703) and CD8 (BD, Cat. No. 560179); their activation status was monitored by antibodies directed to the extracellular proteins CD25 (BD, Cat. No. 555432) and CD69 (BD, Cat. No. 557745). Antibody staining was performed for 30 minutes at 4 - 8°C in the dark. Percentages of tumor cell lysis and up-regulation of CD25, CD69 on T cells were plotted against the logarithm of BiTE[®] molecule concentrations. Data demonstrating proper targeting and cell killing by the BiTE[®] molecules is summarized in Figures 52A (for N3H) and 52B (for H6H) herein.

[00856] Example 17: *In vivo* efficacy of MAGEB2 BiTE® molecules

[00857] The aim of the study is the evaluation of BiTE® molecules that target a pMAGE-HLA, specifically, one complexed with a MAGEB2 peptide, and their efficacy on NCI-H2023 human NSCLC xenograft tumor formation and the pharmacokinetic properties in female NXG mice.

[00858] Experimental Schedule

[00859] Day -1: Prearrangement: assign to cages, earmark, shave, take first body weight; tumor and PBMC cell mix injection, group allocation (w/o irradiation)

[00860] Day 3: Treatment start – planned q7dx3

[00861] Start of PK

[00862] First Tumor Volume measurement

[00863] Day X: Study end

[00864] Table 106: Study Design

Group	Mice/ Group	Cell Injection				Treatment		
		NCI-H2023 Tumor Cells / Mouse	hu PBMC Effector Cells / Mouse	E:T Ratio	Matrigel* 1.5 mg / Mouse	Treatment	RoA	Dosing Schedule
1	8	5x10 ⁶	2.5x10 ⁶	1:2	Yes	Vehicle	IV	Days 3, 10, 17
2	8	5x10 ⁶	2.5x10 ⁶	1:2	Yes	N3H 2 mg/kg	IV	Days 3, 10, 17
3	8	5x10 ⁶	2.5x10 ⁶	1:2	Yes	N3H 0.2 mg/kg	IV	Days 3, 10, 17
4	8	5x10 ⁶	2.5x10 ⁶	1:2	yes	N3H 0.02 mg/kg	IV	Days 3, 10, 17
Σ	32	~2x10 ⁸ with 20% surplus	~1x10 ⁸ with 20% surplus					

[00865] * Reduced Growth Factor Basement Membrane Extract, Path Clear® (Matrigel) will be adjusted to a final concentration of ~7.5 mg/mL (~1.5 mg/mouse when injected 200 µL).

Table 107: Test Species

Species/Strain:	Mouse / NOD-Prkdcscid-IL2rgTm1/Rj “NXG”
Number/Sex:	32 / female
Vendor:	Janvier
Age at arrival:	7 weeks
Weight at start of experiment:	tbd
Age at start of experiment:	tbd
Subject's disease status:	Immunocompromised mice with SC injected cell mix of NCI-H2023 tumor cells and human PBMC effector cells
Animal care:	ARM animal facility
Animal housing:	Single-sex groups will be housed free of specific pathogens (SPF according to FELASA recommendations; Mahler et al, 2014) in IVC's under sterile and standardized environmental conditions: target temperature of $22 \pm 2^{\circ}\text{C}$; target relative humidity of $55 \pm 10\%$; 12 hour light-dark cycle, ad libitum food and drinking water.

[00866] Necessary Material

[00867] 4.1 Basement Membrane Extract (Matrigel) for *In Vivo* Growth of Tumor Cells

[00868] Matrigel will be used for adequate *in vivo* growth of NCI-H2023 cells. Reduced Growth Factor Basement Membrane Extract, Path Clear® (Matrigel; Cat. No. 3433-005-01; R&D Systems, Inc., Minneapolis).

Table 108: Formulation of Cell Mix For *In Vivo* Injection

Tumor Cell Suspension			PBMC Cell Suspension			Matrigel*		DPBS		Final Injection Volume	
Number of Cells per Mouse	Volume Per mouse (μL)	Minimal Total Volume (μL)	Number of Cells per Mouse	Volume Per Mouse (μL)	Minimal Total Volume (μL)	Vol. Per Mouse (μL)	Min. Total Vol. (μL)	Vol. Per Mouse (μL)	Min. Total Vol. (μL)	Per Mouse (μL)	Min. Total Vol. (μL)
5×10^6	50	2000	2.5×10^6	50	2000	90	3600	10	400	200	8000

* Calculated for a Matrigel concentration between 16 and 17.5 mg/mL

[00869] Target Cells

- [00870] Human non small lung cancer cell line NCI-H2023
- [00871] Mycoplasma test is performed on: tbd, test: lotno. and cells should be negative
- [00872] Before injection:
- [00873] Cells will be counted, centrifuged, washed with cold DPBS and adjusted to a concentration of 1×10^8 cells/mL. Cell viability will be determined. Cells will be filtered through a cell strainer (70 μ m) to ensure homogenous cell suspension (w/o clumps) after trypsinization. Cells will be stored on ice prior to injection
- [00874] Matrigel (Reduced Growth Factor Basement Membrane Extract, Path Clear®) will be used. Tumor cells will be mixed with human 1) PBMC (E:T ratio = 1:2) and 2) Matrigel. Tumor-target cell mix will be SC injected in a final volume of 200 μ L/mouse into the right dorsal flank. Cell line used will be NCI-H2023 (HuNSCLC) at 1×10^8 cells/ml.

[00875] Effector Cells

- [00876] Human PBMC isolated from Buffy coat of donor. On the day of injection, human PBMC will be counted and washed 2x with cold DPBS. Cell number will be adjusted to 5×10^7 cells/mL. If necessary, filter cells through a cell strainer to avoid cell clumps. Cells will be stored on ice prior to injection. Before injection: human PBMC will be mixed with tumor cells (E:T = 1:2) and Matrigel as described above. Cells will be SC injected in a final volume of 200 μ L/mouse into the right dorsal flank.

[00877] Treatment

- [00878] Animals will receive the MAGEB2 BiTE® construct or control vehicle by IV injection into the lateral tail vein. Mice will be treated as described herein. The dose volume will be kept constant to a total of 100 μ L per mouse, per injection. The BiTE® molecule will be diluted in the corresponding vehicle to the appropriate concentration (c) according to the most recently determined group mean body weight. The dose concentration is calculated using the formula:

$$c \left[\frac{\mu g}{\mu l} \right] = \frac{dose \left[\frac{\mu g}{kg} \right] \times mean BW [kg]}{dose volume [\mu l]}$$

- [00880] Treatment duration: q7dx3 (days 3, 10, 17)

[00881] Table 109: Test / Control Items

Item	Specified	Concentration	Formulation
Vehicle	Solution suitable for dilution of test item and <i>in vivo</i> use; treatment solution for control groups	-	25 mM L-lysine monohydrochloride, 0.002% (w/v) polysorbate 80 in 0.9% (w/v) sodium chloride pH 6.8 (next retest: Jan 2022)
N3H BiTE®	Half-life extended BiTE® molecule (scFc) directed against human MAGE B2 pMAGE-HLA	5.04 mg/mL	10 mM L-glutamic acid, 9.0% sucrose, 0.010% polysorbate 80, pH 4.2

[00882] Data Collection

[00883] During the course of the study, all animals will be observed daily for general appearance, activity, behavior and survival. Abnormalities or discrepancies will be noted in the appropriate sheet in the study file. Additionally, a Score Sheet will be used for stress evaluation of every mouse and stored in the appropriate study file. Scoring frequency is done as defined in the Score Sheet. Body weight will be determined 2-3x/week or more often if required and recorded via Vivo Manager Software. Tumor size will be determined with an external caliper 2-3x/week or more often if required and tumor volume will be calculated using the formula: $TV = \frac{height \times width^2}{2}$. Data will be recorded via Vivo Manager Software.

[00884] Sampling

[00885] After the 1st treatment, serum sampling for standard PK analysis planned: maximal 10% of blood volume will be sampled within 2 weeks by alternating retro-orbital rupture of the sinus plexus and processed to serum. Two animals per group per bleeding time point.

[00886] Table 110: Sampling Information

Day of experiment	Time point p.i.	Group	Animals	Eye	Serum Quantity
3	30 min / 0.0125 day	2, 3, 4	1, 2	right	50 µL
3	8 h / 0.33 day	2, 3, 4	3, 4	right	50 µL
4	24 h / 1 day	2, 3, 4	5, 6	right	50 µL
5	48 h / 2 days	2, 3, 4	1, 2	left	50 µL
8	120 h / 5 days	2, 3, 4	3, 4	left	50 µL
10	168 h / 7 days*	2, 3, 4	5, 6	left	50 µL

p.i.: post injection

[00887] At study end, data will be analyzed and summarized in graph format to further demonstrate the therapeutic effect of the anti-pMAGE-HLA (MAGEB2) BiTE® molecules in an *in vivo* setting.

[00888] SEQUENCES

[00889] Table 21: Misc. Sequences

SEQ ID NO:	Molecule	SEQUENCE
22	Fc monomer-1 +c/-g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
23	Fc monomer-2 +c/-g/delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP
24	Fc monomer-3 -c/+g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
25	Fc monomer-4 -c/+g/delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP
26	Fc monomer-5 -c/-g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
27	Fc monomer-6 -c/-g/delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYGSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP
28	Fc monomer-7 +c/+g	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK
29	Fc monomer-8 +c/+g/delGK	DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYNSTYRCVSVLTVLHQDWLNGKEYKCKV

		SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSP
31	CD3 ϵ binder VL	QTVVTQEPSTLVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIG GTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGG GTKLTVL
32	CD3 ϵ binder VH	EVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWWVRQAPGKGLEWVA RIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRH GNFGNSYVSWWAYWGQGLTVSS
33	CD3 ϵ binder scFv	EVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWWVRQAPGKGLEWVA RIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRH GNFGNSYVSWWAYWGQGLTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWWQKPGQAPRGLIGGTKFLAPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

Table 30
BiTE-scFc Full Sequences

iPS#	Ab	Type	BiTE_scFc
iPS:2768827	MA_79- G12_CC_x_I2C0x_scFc_(K1F)_transl ation	NA	<i>No seq available</i>
		AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGAEVKKPGASVKVSKASG YTFTRNGLSWVRQAPGQCLEWMGWISGYNGDTNYAQKLQGRGTMITD TSTSTAYMELRSLRSDDTAVYYCARGRATFDYWGQGLVTVSSGGGGS GGGGGGGGSELVMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQK PGKVPKLLISAASTLQSGVPSRFSGSGGTDFTLTISLQPEDVATYYCQK YNSAPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGF TFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLVT VSSGGGGGGGGGGGGGQTVVTQEPSTVSPGGTVTLTSGSSTGAVTS GNYPNWVQKPGQAPRLIGGTFLAPGTPARFSGSLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHEAL HNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGSDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 2966)
		NA	<i>No seq available</i>

iPS:2306869	MA_79- H7_CCx_I2C0x_scFc_(Q4C)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISR DDSKNTLYLQMNSLKTEDTAVYYCTTPSYSGSYYNFVSMDVWVGQGT VTVSSGGGGGGGGGSELQMTQSPSSLASVGDVVTTCRTSQSISS YLNWFQKPGKAPKLLIFAASSLQSGVPSRFGSGSGTDFLTITISLQPEDF ATYYCQQSYSSPFTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNSYISYWAYW GQGTLVTVSSGGGGGGGGGSGGSGQTVVTQEPSTVSPGGTTLTTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLLGGKA ALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTC CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV SVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 2967)
		NA	No nuc. seq. available

iPS:2768829 MA_81- E7_CCx_I2C0x_scFc_(O8Y)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGPGLVKPSETLSLTCTVSGD SISSRYYWGWIRQPPGKCLEWIGSIYYSGSTYYNPSLKSRTISVDTSKN QFSLKLSVTAADTA VY YCARGIFGVITYFDYWGQGLTVTVSSGGGSG GGSGGGGSELVMTQTPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA WYQQKPGQPPKLLIYWASTRESGVPDFSGSGGTDFTLTISSLQAEDEV VYYCQYYSTPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNSYISYWAYW GQGLTVTVSSGGGSGGGGSGGSGQTVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPP CPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSN KALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS C SVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDV S HEDPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQV S LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFS C SVMHEALHNHYTQKSLSLSPGK
	NA	(SEQ ID NO: 2968) <i>No nuc. seq. available</i>

		MA_81- iPS:2768830_F9_CCx_I2C0x_scFc_(I6I)_translatio n	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGPMLVKPTQTLTLCTFSGF SFTTHKMGVDWIRQPPGKCLEWLALIYWNDDKRYSPSLQSLTITKDT KNQVVLTMNMDPVDATYYCAYRRYNWNYENWFDPPWGQGLVTVS SGGGSGGGSGGGSELQMTQSPSSLASVGDVVTITCRASQISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPFTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGSGGGSGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSS GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDV DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
				(SEQ ID NO: 2969)
			NA	No nuc. seq. available

iPS:2768831 MA_81- H7_CC_xl2C0x_scFc_(M5O)_translat ion	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGPGLVKPSQTLSTCTVSGD SISSNPYYWSWIRQHPGKCLEWIGYISYSGITNYPNPSLKSRTMSVDTSKN QFSLKLTSLTAADTA VYYCAREKMWFGVLNYYGMDVWGGQTTVTVS SGGGGSGGGGGGGSELVMTQTPLSLVTPGEPASISCRSSQSLHRNG YNYLDWYLQKPGQSPQLLIYLGSNRASGVPDFRSGSGGTDFTLKISRVE AGDVGVYYCMQALQTPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQP GGSLLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISY WAYWGQGLVTVSSGGGGGGGGGSGQTVVTQEPSTLVSPGGTVT LTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSL GGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGSG GGGGGGGGDKTHTCPCPAPELGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 2970) <i>No nuc. seq. available</i>
	NA	

MA_82- iPS:2768832 B5_CCx_I2C0x_scFc_(B3K)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYTADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGG GSGGGGGGGSELVLTQPPSVVAPGQTARITCGGNNIGSKSVHWYQQ KPGQAPVLVYDDNDRPSGIPERFSGNFGNTATLIISRVEAGDEADYYC QVWDSDDHVVFSGGTLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGNSYISYWAYWGQ GTLVTVSSGGGGGGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSS GAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGLTVLGGGGDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPETVTCVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPETVTCVVDV DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
	NA	(SEQ ID NO: 2971) <i>No nuc. seq. available</i>

iPS:2768833	MA_89- B2_CCx_I2C0x_scFc_(N1M)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGRCLEWVSTISISGGSTNYADSVKGRFTISRDN NTLYLQMNSLRAEDTAVYYCAKDGSGGWFPKLLHYGLDVWGQGTITVT VSSGGGSGGGGGGGSELQMTQSPSSLSASVGDRTTTCQASQDISNY LNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISLQPEDF ATYYCQQSYSIPLTFGCCTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFNSYISYWAYW GQGTLVTVSSGGGSGGGGGGSGGSGQTVVTQEPSTVSPGGTIVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKA ALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTC CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV SVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQV LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 2972)
		NA	No nuc. seq. available

185

iPS:2768836	MA_93- B11_CCx_I2C0x_scFc_(N7N)_translat ion	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVKPGGSLRLSCAASG FTFSDYYMSWIRQAPGKCLEWVSYSKSGSTIYADSVKGRFTISRDN AKNSLYLQMNSLRAEDTAVYYCATYNYGHFDYWGGQTLTVTSSGGGSG GGSGGGGSELVLTQPPSVSAPGQTARITCGNNIGSKSVHWYQQKPG QAPLVVYDDSDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVW DSSSDHHVVFSGGTLTVSGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTIS RDDSNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGGQTL VTVSSGGGGGGGGGSGGQTVVTQEPSTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGLLGGKAALTL S GVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG V EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE W ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHE ALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGSD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 2974)

Table 31
BiTE-scFc Fv#1 (MAGEB2) VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:2768827	MA_79-G12_CC_x_I2C0x_scFc_(K1F)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RASQGISNYLA (SEQ ID NO: 2975)	AASLQS (SEQ ID NO: 3011)	QKYNAPFT (SEQ ID NO: 3047)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2306869	MA_79-H7_CCx_I2C0x_scFc_(Q4C)_translation	AA	RTSQSISSYLN (SEQ ID NO: 2976)	AASLQS (SEQ ID NO: 3012)	QQSYSSPFT (SEQ ID NO: 3048)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768829	MA_81-E7_CCx_I2C0x_scFc_(O8Y)_translation	AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 2977)	WASTRES (SEQ ID NO: 3013)	QQYYSPTLT (SEQ ID NO: 3049)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768830	MA_81-F9_CCx_I2C0x_scFc_(I6I)_translation	AA	RASQSISSYLN (SEQ ID NO: 2978)	AASLQS (SEQ ID NO: 3014)	QQSYSTPFT (SEQ ID NO: 3050)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768831	MA_81-H7_CC_xI2C0x_scFc_(M5O)_translation	AA	RSSQSLHRNGYNYLD (SEQ ID NO: 2979)	LGSNRAS (SEQ ID NO: 3015)	MQALQTPWT (SEQ ID NO: 3051)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768832	MA_82-B5_CCx_I2C0x_scFc_(B3K)_translation	AA	GGNIGSKSVH (SEQ ID NO: 2980)	DDNDRPS (SEQ ID NO: 3016)	QVWDSSDHVV (SEQ ID NO: 3052)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768833	MA_89-B2_CCx_I2C0x_scFc_(N1M)_translation	AA	QASQDISNYLN (SEQ ID NO: 2981)	AASLQS (SEQ ID NO: 3017)	QQSYSIPLT (SEQ ID NO: 3053)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768835	MA_89-D12_CCx_I2C0x_scFc_(V4C)_translation	AA	RASQGISNYLA (SEQ ID NO: 2982)	AASLQS (SEQ ID NO: 3018)	QKYNAPFT (SEQ ID NO: 3054)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:2768836	MA_93-B11_CCx_I2C0x_scFc_(N7N)_translation	AA	GGNIGSKSVH (SEQ ID NO: 2983)	DDSDRPS (SEQ ID NO: 3019)	QVWDSSDHVV (SEQ ID NO: 3055)

Table 32
BiTE-scFc Fv#1 (MAGEB2) VH CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:2768827	MA_79-G12_CC_x_I2C0x_scFc_(K1F)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RNGLS (SEQ ID NO: 2984)	WISGYGDTNYAQKLOG (SEQ ID NO: 3020)	GRATFDY (SEQ ID NO: 3056)
	MA_79	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available

iPS:2306869	MA_17-H7_CCx_I2C0x_scFc_(Q4C)_translation	AA	NAWMS (SEQ ID NO: 2985) <i>No nuc. seq. available</i>	RIKSKTYGGTTDYAAPVKG (SEQ ID NO: 3021) <i>No nuc. seq. available</i>	PSYSGSYNYFVSMDV (SEQ ID NO: 3057) <i>No nuc. seq. available</i>
iPS:2768829	MA_81-E7_CCx_I2C0x_scFc_(O8Y)_translation	AA	SSRYWYG (SEQ ID NO: 2986) <i>No nuc. seq. available</i>	SIYYSGSTYNNPSLKS (SEQ ID NO: 3022) <i>No nuc. seq. available</i>	GIFGVITYFDY (SEQ ID NO: 3058) <i>No nuc. seq. available</i>
iPS:2768830	MA_81-F9_CCx_I2C0x_scFc_(I6I)_translation	AA	THKMGVD (SEQ ID NO: 2987) <i>No nuc. seq. available</i>	LIYWNDDKRYSPSLQS (SEQ ID NO: 3023) <i>No nuc. seq. available</i>	RRYNNWYENWFDY (SEQ ID NO: 3059) <i>No nuc. seq. available</i>
iPS:2768831	MA_81-H7_CC_xI2C0x_scFc_(M5O)_translation	AA	SNPYWYS (SEQ ID NO: 2988) <i>No nuc. seq. available</i>	YISYSGITNYNPSLKS (SEQ ID NO: 3024) <i>No nuc. seq. available</i>	EKMWFGLNYYYGMDV (SEQ ID NO: 3060) <i>No nuc. seq. available</i>
iPS:2768832	MA_82-B5_CCx_I2C0x_scFc_(B3K)_translation	AA	SHAMS (SEQ ID NO: 2989) <i>No nuc. seq. available</i>	AISGGGTTYADSVKG (SEQ ID NO: 3025) <i>No nuc. seq. available</i>	GKGVHLGFDY (SEQ ID NO: 3061) <i>No nuc. seq. available</i>
iPS:2768833	MA_89-B2_CCx_I2C0x_scFc_(N1M)_translation	AA	SYAMS (SEQ ID NO: 2990) <i>No nuc. seq. available</i>	TISISGGSTNYADSVKG (SEQ ID NO: 3026) <i>No nuc. seq. available</i>	DGSGGWPKLLHYGLDV (SEQ ID NO: 3062) <i>No nuc. seq. available</i>
iPS:2768835	MA_89-D12_CCx_I2C0x_scFc_(V4C)_translation	AA	TYGMH (SEQ ID NO: 2991) <i>No nuc. seq. available</i>	VISYDGSNKYYADSVKG (SEQ ID NO: 3027) <i>No nuc. seq. available</i>	GQLLTGY (SEQ ID NO: 3063) <i>No nuc. seq. available</i>
iPS:2768836	MA_93-B11_CCx_I2C0x_scFc_(N7N)_translation	AA	DYVMS (SEQ ID NO: 2992) <i>No nuc. seq. available</i>	YISKSGSTIYADSVKG (SEQ ID NO: 3028) <i>No nuc. seq. available</i>	YNYGHFDY (SEQ ID NO: 3064) <i>No nuc. seq. available</i>

Table 33
BiTE-scFc Fv#2 (CD3) VL CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:2768827	MA_79-G12_CC_x_I2C0x_scFc_(K1F)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2993) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3029) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3065) <i>No nuc. seq. available</i>
iPS:2306869	MA_79-H7_CCx_I2C0x_scFc_(Q4C)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2994) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3030) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3066) <i>No nuc. seq. available</i>
iPS:2768829	MA_81-E7_CCx_I2C0x_scFc_(O8Y)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2995) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3031) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3067) <i>No nuc. seq. available</i>
NA 01		NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>

iPS:276883 0	MA_81- F9_CCx_I2C0x_scFc_(I6I)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2996) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3032) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3068) <i>No nuc. seq. available</i>
iPS:276883 1	MA_81- H7_CC_xI2C0x_scFc_(M5O)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2997) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3033) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3069) <i>No nuc. seq. available</i>
iPS:276883 2	MA_82- B5_CCx_I2C0x_scFc_(B3K)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2998) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3034) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3070) <i>No nuc. seq. available</i>
iPS:276883 3	MA_89- B2_CCx_I2C0x_scFc_(N1M)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 2999) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3035) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3071) <i>No nuc. seq. available</i>
iPS:276883 5	MA_89- D12_CCx_I2C0x_scFc_(Y4C)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3000) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3036) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3072) <i>No nuc. seq. available</i>
iPS:276883 6	MA_93- B11_CCx_I2C0x_scFc_(N7N)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3001) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3037) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3073) <i>No nuc. seq. available</i>

Table 34

BiTE-scFc Fv#2 (CD3) VH CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276882 7	MA_79- G12_CC_x_I2C0x_scFc_(K1F)_transla tion	NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>
iPS:230686 9	MA_79- H7_CCx_I2C0x_scFc_(Q4C)_transla tion	AA	KYAMN (SEQ ID NO: 3002) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3038) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3074) <i>No nuc. seq. available</i>
iPS:276882 9	MA_81- E7_CCx_I2C0x_scFc_(O8Y)_transla tion	AA	KYAMN (SEQ ID NO: 3003) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3039) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3075) <i>No nuc. seq. available</i>
iPS:276883 0	MA_81- F9_CCx_I2C0x_scFc_(I6I)_transla tion	AA	KYAMN (SEQ ID NO: 3004) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3040) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3076) <i>No nuc. seq. available</i>
iPS:276883 1	MA_81- H7_CC_xI2C0x_scFc_(M5O)_transla tion	AA	KYAMN (SEQ ID NO: 3005) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3041) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3077) <i>No nuc. seq. available</i>
NA 05		NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>

iPS:276883 2	MA_89- B5_CcX_12C0x_scFc_(B3K)_translation	AA	KYAMN (SEQ ID NO: 3007) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3043) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3079) <i>No nuc. seq. available</i>
iPS:276883 3	MA_89- B2_CcX_12C0x_scFc_(N1M)_translation	AA	KYAMN (SEQ ID NO: 3008) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3044) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3080) <i>No nuc. seq. available</i>
iPS:276883 5	MA_89- D12_CcX_12C0x_scFc_(Y4C)_translation	AA	KYAMN (SEQ ID NO: 3009) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3045) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 3081) <i>No nuc. seq. available</i>
iPS:276883 6	MA_93- B11_CcX_12C0x_scFc_(N7N)_translation	AA	KYAMN (SEQ ID NO: 3010)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3046)	HGNFGNSYISYWAY (SEQ ID NO: 3082)

Table 35
BTE=seF Variable Region Sequences (MAGB2)

IPs	Ab	Type	IC Region	HC Region	IC Region	HC Region	IC (CD)	HC Region
IPs:276882 7	MA 79- G12_Cc_x12C0x_seFc (K1F)_transla tion	NA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS ASTLQSGVPSHFSGSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC TKLEIK (SEQ ID NO: 3083)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3092)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3101)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3110)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3110)	
IPs:230686 9	MA 79- H7_Cc_x12C0x_seFc (Q4C)_transla tion	NA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS SSLSQSGVPSHFSGSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC VEIK (SEQ ID NO: 3084)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3093)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3102)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3111)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3111)	
IPs:276882 9	MA 81- E7_Cc_x12C0x_seFc (O8V)_transla tion	AA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS PKPLLYLQNSRASQVPSHFSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC STPLTGGCTKVEIK (SEQ ID NO: 3085)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3094)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3103)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3112)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3112)	
IPs:276883 0	MA 81- F9_Cc_x12C0x_seFc (I6I)_transla tion	NA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS ASSLSQSGVPSHFSGSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC KVEIK (SEQ ID NO: 3086)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3095)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3104)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3113)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3113)	
IPs:276883 1	MA 81- H7_Cc_x12C0x_seFc (N8O)_transla tion	AA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS QLLYLQNSRASQVPSHFSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC TPWTFGGCTKVEIK (SEQ ID NO: 3087)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3096)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3105)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3114)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3114)	
IPs:276883 2	MA 82- H5_Cc_x12C0x_seFc (B3K)_transla tion	NA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS DNDPSQIPERFSGNSONTATLISRVEAGDEADYYCQVWDSSSDHHV GGGKTLTVL (SEQ ID NO: 3088)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3097)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3106)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3115)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3115)	
IPs:276883 3	MA 89- B2_Cc_x12C0x_seFc (N1M)_transla tion	AA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS ASSLSQSGVPSHFSGSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC TKVEIK (SEQ ID NO: 3089)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3098)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3107)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3116)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3116)	
IPs:276883 5	MA 89- D12_Cc_x12C0x_seFc (Y4C)_transla tion	AA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS ASTLQSGVPSHFSGSGSGTDFLTLSLQPEDVATYYCQKNSAPFTFGC TKVEIK (SEQ ID NO: 3090)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3099)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3108)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3117)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3117)	
IPs:276883 6	MA 92- B11_Cc_x12C0x_seFc (N7N)_transla tion	AA	EVLTQPSLSASVGDVATTCGASGDSNYLAWVOOKPGKVPKLLYLS DSDPSQIPERFSGNSONTATLISRVEAGDEADYYCQVWDSSSDHHV VFGGKTLTVS (SEQ ID NO: 3091)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3100)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3109)	QTVVYTPBRLTNSFGTVTLTCGSGTGAVTSGNPNWVOOKPGQAPRGE IGOTKFLAPGTAPARESGLLGOKAALTLSCQVPEDEABEYCYVLWYSNRW VFGGKGLTVL (SEQ ID NO: 3118)	EVLTQSGGGLVQPGGSLKLSAASGFTFNKYAMNWVROA YCARAGATPDYWGQGLTVTVSS (SEQ ID NO: 3118)	

$\partial_t \phi + u \cdot \nabla_x \phi = -\operatorname{div}_x (\sigma \nabla_x \phi) + \sum_{j=1}^N \partial_j \phi \frac{\partial \sigma}{\partial x_j}$ [illegible]

Sequence Listing

IPS:27683 2	MA_S2 BS_CCS_12Cp_wFC_(B3N)_transid1	VIH3-73/D3-3-3RFSJH4	3153	K-----YAMW	3207	WTRDAPCNLEWVA	3261	RIESTK-HWATTTAGSYVD	3315	RFTTSDDGNFATLQNNHATDGNATVYCVR	3369	HBNFBNB	-----YISWAL	3423	WQZTUATVSS	3477
IPS:27683 3	MA_S9 B1_CCS_12Cp_wFC_(N1M)_transid1	VIH3-73/D3-3-3RFSJH4	3154	K-----YAMW	3208	WTRDAPCNLEWVA	3262	RIESTK-HWATTTAGSYVD	3316	RFTTSDDGNFATLQNNHATDGNATVYCVR	3370	HBNFBNB	-----YISWAL	3424	WQZTUATVSS	3478
IPS:27683 4	MA_S9 D13_CCS_12Cp_wFC_(N4C)_transid1	VIH3-73/D13-3-3RFSJH4	3155	K-----YAMW	3209	WTRDAPCNLEWVA	3263	RIESTK-HWATTTAGSYVD	3317	RFTTSDDGNFATLQNNHATDGNATVYCVR	3371	HBNFBNB	-----YISWAL	3425	WQZTUATVSS	3479
IPS:27683 5	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3156	K-----YAMW	3210	WTRDAPCNLEWVA	3264	RIESTK-HWATTTAGSYVD	3318	RFTTSDDGNFATLQNNHATDGNATVYCVR	3372	HBNFBNB	-----YISWAL	3426	WQZTUATVSS	3480
IPS:27683 6	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3157	H CDRI	3211	WTRDAPCNLEWVA	3265	RIESTK-HWATTTAGSYVD	3319	H PR3	3373	H CDRI	-----YISWAL	3427	H PR4	3481
IPS:27683 7	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3158	H CDRI	3212	WTRDAPCNLEWVA	3266	RIESTK-HWATTTAGSYVD	3320	H PR3	3374	H CDRI	-----YISWAL	3428	H PR4	3482
IPS:27683 8	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3159	H CDRI	3213	WTRDAPCNLEWVA	3267	RIESTK-HWATTTAGSYVD	3321	H PR3	3375	H CDRI	-----YISWAL	3429	H PR4	3483
IPS:27683 9	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3160	H CDRI	3214	WTRDAPCNLEWVA	3268	RIESTK-HWATTTAGSYVD	3322	H PR3	3376	H CDRI	-----YISWAL	3431	H PR4	3484
IPS:27683 10	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3161	H CDRI	3215	WTRDAPCNLEWVA	3269	RIESTK-HWATTTAGSYVD	3323	H PR3	3377	H CDRI	-----YISWAL	3432	H PR4	3485
IPS:27683 11	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3162	H CDRI	3216	WTRDAPCNLEWVA	3270	RIESTK-HWATTTAGSYVD	3324	H PR3	3378	H CDRI	-----YISWAL	3433	H PR4	3486
IPS:27683 12	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3163	H CDRI	3217	WTRDAPCNLEWVA	3271	RIESTK-HWATTTAGSYVD	3325	H PR3	3379	H CDRI	-----YISWAL	3434	H PR4	3487
IPS:27683 13	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3164	H CDRI	3218	WTRDAPCNLEWVA	3272	RIESTK-HWATTTAGSYVD	3326	H PR3	3380	H CDRI	-----YISWAL	3435	H PR4	3488
IPS:27683 14	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3165	H CDRI	3219	WTRDAPCNLEWVA	3273	RIESTK-HWATTTAGSYVD	3327	H PR3	3381	H CDRI	-----YISWAL	3436	H PR4	3489
IPS:27683 15	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3166	H CDRI	3220	WTRDAPCNLEWVA	3274	RIESTK-HWATTTAGSYVD	3328	H PR3	3382	H CDRI	-----YISWAL	3437	H PR4	3490
IPS:27683 16	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3167	H CDRI	3221	WTRDAPCNLEWVA	3275	RIESTK-HWATTTAGSYVD	3329	H PR3	3383	H CDRI	-----YISWAL	3438	H PR4	3491
IPS:27683 17	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3168	H CDRI	3222	WTRDAPCNLEWVA	3276	RIESTK-HWATTTAGSYVD	3330	H PR3	3384	H CDRI	-----YISWAL	3439	H PR4	3492
IPS:27683 18	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3169	H CDRI	3223	WTRDAPCNLEWVA	3277	RIESTK-HWATTTAGSYVD	3331	H PR3	3385	H CDRI	-----YISWAL	3440	H PR4	3493
IPS:27683 19	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3170	H CDRI	3224	WTRDAPCNLEWVA	3278	RIESTK-HWATTTAGSYVD	3332	H PR3	3386	H CDRI	-----YISWAL	3441	H PR4	3494
IPS:27683 20	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3171	H CDRI	3225	WTRDAPCNLEWVA	3279	RIESTK-HWATTTAGSYVD	3333	H PR3	3387	H CDRI	-----YISWAL	3442	H PR4	3495
IPS:27683 21	MA_S2 B11_CCS_12Cp_wFC_(N7N)_transid1	VIH3-73/D3-3-3RFSJH4	3172	H CDRI	3226	WTRDAPCNLEWVA	3280	RIESTK-HWATTTAGSYVD	3334	H PR3	3388	H CDRI	-----YISWAL	3443	H PR4	3496

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[illegible]

PS-270833	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-13D13-3BRF3JH4	B	3332	K.....Y..R	3385	P.....A	3640	T..R...Y..D...D	3694	M.....V	3745	Y..S..WA	3802		3816
PS-270834	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-13D13-3BRF3JH4	B	3333	K.....Y..R	3386	P.....A	3641	T..R...Y..D...D	3695	M.....V	3746	Y..S..WA	3803		3817
PS-270835	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-13D13-3BRF3JH4	B	3334	K.....Y..R	3388	P.....A	3642	T..R...Y..D...D	3696	M.....V	3747	Y..S..WA	3804		3818
PS-230460	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3335	H..CDRI	3390	H..PR2	3643	H..CDR2	3697	H..PR3	3751	H..CDR3	3805	H..PR4	3819
PS-270836	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3336	H..CDRI	3391	H..PR2	3644	H..CDR2	3698	H..PR3	3752	H..CDR3	3806	H..PR4	3820
PS-270837	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3337	H..CDRI	3392	H..PR2	3645	H..CDR2	3699	H..PR3	3753	H..CDR3	3807	H..PR4	3821
PS-270838	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3338	H..CDRI	3393	H..PR2	3646	H..CDR2	3700	H..PR3	3754	H..CDR3	3808	H..PR4	3822
PS-270839	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3339	H..CDRI	3394	H..PR2	3647	H..CDR2	3701	H..PR3	3755	H..CDR3	3809	H..PR4	3823
PS-270840	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3340	H..CDRI	3395	H..PR2	3648	H..CDR2	3702	H..PR3	3756	H..CDR3	3810	H..PR4	3824
PS-270841	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3341	H..CDRI	3396	H..PR2	3649	H..CDR2	3703	H..PR3	3757	H..CDR3	3811	H..PR4	3825
PS-270842	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3342	H..CDRI	3397	H..PR2	3650	H..CDR2	3704	H..PR3	3758	H..CDR3	3812	H..PR4	3826
PS-270843	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3343	H..CDRI	3398	H..PR2	3651	H..CDR2	3705	H..PR3	3759	H..CDR3	3813	H..PR4	3827
PS-270844	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3344	H..CDRI	3399	H..PR2	3652	H..CDR2	3706	H..PR3	3760	H..CDR3	3814	H..PR4	3828
PS-270845	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3345	H..CDRI	3400	H..PR2	3653	H..CDR2	3707	H..PR3	3761	H..CDR3	3815	H..PR4	3829
PS-270846	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3346	H..CDRI	3401	H..PR2	3654	H..CDR2	3708	H..PR3	3762	H..CDR3	3816	H..PR4	3830
PS-270847	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3347	H..CDRI	3402	H..PR2	3655	H..CDR2	3709	H..PR3	3763	H..CDR3	3817	H..PR4	3831
PS-270848	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3348	H..CDRI	3403	H..PR2	3656	H..CDR2	3710	H..PR3	3764	H..CDR3	3818	H..PR4	3832
PS-270849	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3349	H..CDRI	3404	H..PR2	3657	H..CDR2	3711	H..PR3	3765	H..CDR3	3819	H..PR4	3833
PS-270850	NA, SP [B, CC, 12Cn, uFc, (N10), translation on PstI]	VRH3-15D13-3BRF3JH6	B	3350	H..CDRI	3405	H..PR2	3658	H..CDR2	3712	H..PR3	3766	H..CDR3	3820	H..PR4	3834

Table 22			
BiTE-scFc Full Sequences			
iPS#	Ab	Type	BiTE_scFc
iPS:2306866	MA_03- C7_AS_CC_x_12C0_x_scFc_(G2H)_tr anslation	NA	(SEQ ID NO: 34) MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYTAAASVKGRTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFEDYWGQGLVTVSSGGG GSGGGGGSSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQ KPGQAPVMVVDNDNRPSGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYERPAMVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNTATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLLVTVSSGGGGGGGGGGGSGTQVTVTQPSLTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGKTLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEVESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 35)
		NA	(SEQ ID NO: 36)

iPS#	Ab	Type	BITE_scFc
iPS:2306861	MA_03- D8_AS_CC_x_12C0_x_scFc_(L7E)_tr anslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSTISGGGGTYAASVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGSSVLTQPPSV/APGQTARITCGNNIGSKSVHWYQQ KPGQAPV/MVVDNDNRPSPGIPERFSGSNFGNTATLIISRVEAGDEADYYC QVWDYRTLWDVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVVFCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 37)
		NA	(SEQ ID NO: 38)

iPS#	Ab	Type	BITE_scFc
iPS:2307360	MA_03-D8_CC_x_I2C0_x_scFc_(H6N)_transl ation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSTISGGGGTYADSVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGSGGGSSVLTQPPSV/APGQTARITCGNNIGSKSVHWYQQ KPGQAPV/MVVDNDNRPSPGIPERFSGSNFGNTATLIISRVEAGDEADYYC QVWDYRTLWDVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGSGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGSGGGGGSGGGGGSGGGGGSGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 39)
		NA	(SEQ ID NO: 40)

iPS#	Ab	Type	BITE_scFc
iPS:2306862	MA_03- D12_AS_CC_x_I2C0_x_scFc_(L6A)_t ranslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYAAASV/KARFTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGSSVYLTQPPSV/APGQTARITCGNNIGSKSVHWYQQ KPGQAPV/MVVDNDNRPSGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYLRQQVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 41)
		NA	(SEQ ID NO: 42)

iPS#	Ab	Type	BITE_scFc
iPS:2306860	MA_03- E7_AS_CC_x_I2C0_x_scFc_(L6M)_tr anslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGVVQPGRSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYAASGKGRFTISRDN KNTLYLQMNSLRAEDTAAYYCVTGKGVHLGFDYWQQGTLVTVSSGGG GSGGGSGGGSSVLTQPPSV/APGQTARITCGNNGSKSVHWYQQ KPGQAPVMVVDNDNRPSGIPERFSGNSNGNTATLTISRVEAGDEADYYC QVWDYNNMNVWVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYW GQGTLVTVSSGGGGSGGGGSGQTIVTQEPSLTVSPGGTVTLTCGS STGAVTSGNYPNVVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGKA ALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSC SVMHEALHNHYTQKSLSLSPGKGGGGSGGGGGSGGGGGSGGGGGSGG GGGSDK'THTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQV LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 43)
		NA	(SEQ ID NO: 44)

iPS#	Ab	Type	BITE_scFc
iPS:2307361	MA_03- E11_AS_CC_x_I2C0_x_scFc_(G2B)_t ranslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYNAASV/KGRFTISRDNS KNTLYLQMNSLRAEDTAAYYCVTGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGSSVYLTQPPSV/APGQTARITCGNNGSKSVHWYQQ KPGQAPV/MVVDNDNRPSPGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYYSNRAVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGSGTQVVTQEPSLTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 45)
		NA	(SEQ ID NO: 46)

iPS#	Ab	Type	BITE_scFc
iPS:2306863	MA_03- G10_AS_CC_x_12C0_x_scFc_(N3H)_t ranslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKCLEWVSAISGGGGTYAAASV/KGRFTISRDNS KNTLYLQMSSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGSSVLTQPPSV/APGQTARITCGNNIGSKSVHWYQQ KPGQAPV/MVVDNDNRPSPGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYSGQRQVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDK RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWL GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 47)
		NA	(SEQ ID NO: 48)

iPS#	Ab	Type	BITE_scFc
iPS:2306865	MA_03- G11_AS_CC_x_12C0_x_scFc_(O4R)_t ranslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGGLVKPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYAAASV/KGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCATGKGVHLNFDYWGGQTLVTVSSGGG GSGGGGGSSVLTQPPSV/APGQTARITCGNNIGSKSVHWYQQ KPGQAPVLVYDDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYC QVWDYLLPGQVFGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 49)
		NA	(SEQ ID NO: 50)

iPS#	Ab	Type	BITE_scFc
iPS:2307362	MA_03- H12_AS_CC_x_12C0_x_scFc_(K5A)_t ranslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYNAASV/KGRFTISRDNS KNTLYLQMNSLRAEDTAAYYCVTGKGVHLGFDYWGGQTLVTVSSGGG GSGGGGGSSVYLTQPPSV/APGQTARITCGGNNIGSKSVHWYQQ KPGQAPVMVVDNDNDRPSGIPERFSGSNFGNTATLTISRVEAGDEADYYC QVWDYVTPRWVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGQTVVTVQEPSLTVSPGGTVTLTCGSS TGAVTSGNYPNVVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 51)
		NA	(SEQ ID NO: 52)

205

iPS#	Ab	Type	BITE_scFc
iPS:2306868	MA_09- E2_CC_x_I2C0_x_scFc_(V8T)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISR DDSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFVMDVWGQGT VTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTITTCRTSQSISS YLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGGTDFTLTISLQPED FATYYCQQSYSSPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNGFNSYISYWAY WGQGTLVTVSSGGGGGGGGGGGGQTVVTQEPSLTVSPGGTVTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLLGGK AALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGS GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 55)
		NA	(SEQ ID NO: 56)

iPS#	Ab	Type	BITE_scFc
iPS:2307364	MA_09-F11_CC_x_I2C0_x_scFc_(L6Q)_translation	AA	MDMRVPAQLLGLLLWLRGARQCITLKESGPMMLVKPTQTLTLTCTFSGF SFTTHKMGVDWIRQPPGKCLEWLAIIYWNDDKRYSPSLQSRLTITKDT KNQVVLMTNMDPVDATYYCAYRRYNWNYENWFDWPGQGTLLVTVS SGGGSGGGSGGGSDIQTQSPDSLASVGDRTTITCQASQDISNYLN WYQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISSLPEDFAT YYCQQSYMWPITFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGSGGGGGGSGTQVTVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 57)
		NA	(SEQ ID NO: 58)

208

209

iPS#	Ab	Type	BITE_scFc
iPS:2307367	MA_09- G10_CC_x_I2C0_x_scFc_(C4K)_trans lation	AA	MDMRVPAQLLGLLLWLRGARQCITLKESGPTLVKPTQTLTLCTFSGFS FTTHKMGVDWIRQPPGKCLEWLAGHIYDDKRYSPSLQSRLTITKDTSKN QVVLMTNMDPVDTATYCYARRYNWNYENWFDPWGGTLVTVSSG GGSGGGGGGGSDIQMTQSPSSLSASVGDRTITCQASQDISNYFNWY QQKPGKAPKLLIYAASSLSQSGVPSRFSGSGTDFLTITSSLPQEDFATYY CQQSYITPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGGGGGGGGSGTQVVTQEPSLTVSPGGTVLTCGSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAALTL SGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVM HEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTC LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 63)
		NA	(SEQ ID NO: 64)

iPS#	Ab	Type	BITE_scFc
iPS:2307368	MA_09- G11_CC_x_I2C0_x_scFc_(Y9Q)_trans lation	AA	MDMRVPAQLLGLLLWLRGARQCITLKESGPMMLVKPTQTLTLTCTFSGF SFTTHKMGVDWIRQPPGKCLEWLALIYWNDKRYSPSLQSRLTITKDT KNQVVLMTNMDPVDATYYCAYRRYNWNYENWFDWPGQGTLVTVS SGGGSGGGSGGGSDIQTQSPSSLSASVGDRTITCRASQFISSYLN WYQQKPGKAPKLLIYAASSLQSGVPSRFSGRSGTDFLTITSLQPEDFAT YYCQQSYQSPITFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNGFNSYISYWAYWGGQ GTLVTVSSGGGGSGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APELLGGPSVFLFPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVTLVHQQDWLNGKEYCKKVSNA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPKPKDTLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVHQQDWLNG KEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFC SVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 65)
		NA	(SEQ ID NO: 66)

iPS#	Ab	Type	BITE_scFc
iPS:2307369	MA_09- H7_CC_x_I2C0_x_scFc_(T3S)_translation	AA	MDMRVPAQLGLLLWLRGARQCITLKESGPALVKPTQTTLTCTFSGFS FTTHKMGVDWIRQPPGKCLEWLALYWNDDKRYSPSLQSRLLTITKDTSK NQVLTMTNMDPVDATYYCAYRRYNWNYENWFDWPWGQGLVTVSS GGGGGGGGGGGGDIQMTQSPSSLSASVGDRTITTCQASQDISNYLNW YQKPGKAPKLLIYAASSLQSGVPSRFSGSGGTDFTLTISLQPEDFATY YCQSYFPVVEFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNGFNSYISYWAYWGQ GTLVTVSSGGGGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APELLGGPSVFLPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVTLVHQQDWLNGKEYCKKVSNA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSV MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVTLVHQQDWLNG KEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 67)
		NA	(SEQ ID NO: 68)

213

214

iPS#	Ab	Type	BITE_scFc
iPS:2306867	MA_10- B5_CC_x_I2C0_x_scFc_(H6H)_transl ation	AA	MDMRVPAQLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIRSRSYGGTTDYAAPVKGRFTISRD DSKNTLFLQMNSLKTEDAVYYCTTPSYSGSYNYFVMDVWVGQGTIV TVSSGGGGGGGGGGGSDIQMTQSPSSLSASVGDRTITTCRTSQTSSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFGSGSGTDFLTITSLQPEDF ATYYCQQTYSMPFTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNGFNSYISYWAY WGQGTIVTVSSGGGGGGGGGGGSGTQTVVTQEPSLTVSPGGTVTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGS GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 73)
		NA	(SEQ ID NO: 74)

iPS#	Ab	Type	BITE_scFc
iPS:2307372	MA_10-B6_CC_x_I2C0_x_scFc (I3O)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIKSKTYGGTTDYAAPVKGRFTISR DDSKNTLYLQMNLSKTEDTAVYYCTTPSYSGSYNYFVSMDVWGQGT VTVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTITTCRTSQSISS YLNWYQQKPGRAPKLLIFAASSLQGGVPSRFSGSGGTDFTLTISLQPED FATYYCIQAYTSPFTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLSKTEDTAVYYCVRHGNGFNSYISYWAY WGQGTLVTVSSGGGGGGGGGGGGQTVVTQEPSLTVSPGGTVTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 75)
		NA	(SEQ ID NO: 76)

iPS#	Ab	Type	BITE_scFc
iPS:2307373	MA_10-D3_CC_x_I2C0_x_scFc_(O6B)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKCLEWVGRITSSRYGGTTDYAAPVKGRFTISRD DSKNTLFLQMNSLKTEDAVYYCTTPSYSGSYNYFVMDVWVGQGTTV TVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITICRTSQTSSISSY LNWYQQKPGRAPKLLIFAAASSLQGGVPSRFSGSGSGTDFLTITSLQPEDF ATYYCQQTYSMPFTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNGFNSYISYWAY WGQGTLVTVSSGGGGGGGGGGSGTQTVVTQEPSLTVSPGGTVTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGS GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 77)
		NA	(SEQ ID NO: 78)

Angen Proximity - Confidential

Anger Property - Confidential

iPS#	Ab	Type	BITE_scFc
iPS:2307376	MA_10- G5_CC_x_I2C0_x_scFc_(S9O)_transl ation	AA	MDMRVPAQLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIVSSTYGTTDYAAPVKGRFTISR DSKNTLYLQMNSLKTEDAVYYCTTPSYSGSYNYFVMDVWQGTTV TVSSGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRTSQSISSY LNWYQQKPGRAPKLLIFAASSLQGGVPSRFGSGSGTDFLTLSLQPEDF ATYYCQQTYSMPFTFGGCKVDIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNLLKTEDAVYYCVRHGNGFNSYISYWAY WQGGLTVTVSSGGGGGGGGGGGSGTQTVVTQEPSLTVSPGGTVTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 83)
		NA	(SEQ ID NO: 84)

iPS#	Ab	Type	BITE_scFc
iPS:2307377	MA_10- G10_AS_CC_x_12C0_x_scFc_(T11)_tr anslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGTYNAASV/KGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGSGGGSSVLTQPPSV/APGQTARITCGNNGSKSVHWYQQ KPGQAPVMVVDNDNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYVAPRHVFGCGTKLTVLSGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGSGGGGSGTQVTVTQEPSLTVSPGGTVTLTCGSS TGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGSGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNL GKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 85)
		NA	(SEQ ID NO: 86)

iPS#	Ab	Type	BITE_scFc
iPS:2307378	MA_10- G10_CC_x_I2C0_x_scFc_(B3A)_trans lation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYNADSVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGSSVYLTQPPSV/APGQTARITCGNNGSKSVHWYQQ KPGQAPVMVVDNDNRPSPGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYVAPRHVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK RFTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGQTVVTVQEPSLTVSPGGTVTLTCGSS TGAVTSGNYPNVVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 87)
		NA	(SEQ ID NO: 88)

iPS#	Ab	Type	BITE_scFc
iPS:2307379	MA_10- H1_CC_x_I2C0_x_scFc_(T9K)_transl ation	AA	MDMRVPAQLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRITSGIYGGTTDYAAPVKGRFTISRD DSKNTLYLQMNSLKTEDTAVYYCTTPSYSGSYNYFVSMDVWQGQTTV TVSSGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRTSQSISSY LNWYQQKPGRAPKLLIFAAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDF ATYYCQQTYSMPFTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAY WQGQTLVTVSSGGGGGGGGGGGSGTQTVVTQEPSLTVSPGGTVTLTCG SSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGK AALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVVS NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGS GGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 89)
		NA	(SEQ ID NO: 90)

iPS#	Ab	Type	BITE_scFc
iPS:2307380	MA_10- H3_CC_x_I2C0_x_scFc_(M9L)_transl ation	AA	MDMRVPAQLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIRSRPYGGTTDYAAPVKGRFTISR DSKNTLYLQMNLSLKTEDAVYYCTTPSYSGSYNYFVSMVMDVWQGTTV TVSSGGGGGGGGGGSDIQMTQSPSSLSASVGDRTVITCRTSQSISSY LNWYQQKPGRAPKLLFAASSLQGGVPSRFGSGSGTDTLTITSLQPEDF ATYYCQQTYSPPFTGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVK DRFTISRDDSKNTAYLQMNLSLKTEDAVYYCVRHGNFGNSYISYWAYW GQGTLVTVSSGGGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGS STGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLGGA ALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSC SVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG GGGSDK'THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV HEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREEMTKNQV LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 91)
		NA	(SEQ ID NO: 92)

iPS#	Ab	Type	BITE_scFc
iPS:2307381	MA_81-B9_CC_x_I2C0_x_scFc (U4L)_translation	AA	MDMRVPAQLGLLLWLRGARCVQLQESGPGLVKPSSETLSLTCTVSGD SISSRYWGWIRQPPGKCLEWIGSIYSGSTYYPNPSLKSRVTISVDTSKN QFSLKLSVTAADTA VYYCARGIFVITYFDYWGQGTLVTVSSGGGSG GGSGGGSDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA WYQQPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVA VYYCQQFYSTPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDK RFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGSGGGGGGSGTQVTVTQEPSTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGG GGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWL GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 93)
		NA	(SEQ ID NO: 94)

iPS#	Ab	Type	BITE_scFc
iPS:2307382	MA_86-A4_CC_x_I2C0_x_scFc_(K2W)_transl ation	AA	MDMRVPAQLLGLLLWLRGARCVQLVESGGGVVQPGRLRLSCAASG FTFSTYGMHWVRQAPGKCLEWVAVISYDASNKYAESVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCARGQLLTGYWGQGTLLTVSSGGGGSG GGGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPG KVPKLLIYAASLTQSGVPSRFSGSGTDFTLTISLQPEDFATYYCQKYN SAPFTGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTF NKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLTVTS SGGGGGGGGGGSGTQVVTQEPSTVSPGGTVLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHN HYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNKATKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV SCVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 95)
		NA	(SEQ ID NO: 96)

iPS#	Ab	Type	BITE_scFc
iPS:2307383	MA_86-A4-N-F5_CC_x_I2C0_x_scFc_(M4H)_transl ation	AA	MDMRVPAQLLGLLLWLRGARQCQQLVESGGGVVQPGRLRLSCAASG FTFSTYGMHWVRQAPGKCLEWVAVISYDAETVKYAESVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCARGQLLTGYWQGQTLVTVSSGGGGSG GGGGGGSDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQQKPG KVPKLLIYAASLTQSGVPSRFSGSGTDFTLTISLQPEDVATYYCQKYN SAPFTGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTF NKYAMNWRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLLVTVS SGGGGGGGGGGSGQTIVTQEPSTVSPGGTVLTCGSSTGAVTSGN YPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDGVEVHN AKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHN HYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNATKPKCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY SDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF SCVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 97)
		NA	(SEQ ID NO: 98)

228

iPS#	Ab	Type	BITE_scFc
iPS:2306864	MA_98- C7_CC_x_I2C0_x_scFc_(Y8P)_translation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSSISGGGTYYAASVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGSGGGSSVLTQPPSVSVAPGQTARITCGNNGSKSVHWYQQ KPGQAPVMVVDNDNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYC QVWDYSPLRHVFGGKTLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNGFNSYISYWAYWGQ GTLVTVSSGGGGSGGGSGGGSQTVVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTPARFSGSLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKKVSNA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSV MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKKVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSVPMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 101)
		NA	(SEQ ID NO: 102)

iPS#	Ab	Type	BITE_scFc
iPS:2307385	MA_98- G12_AS_CC_x_12C0_x_scFc_(Q4Z)_t ranslation	AA	MDMRVPAQLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSHAMSWVRQAPGKCLEWVSAISGGGGTYNAASV/KGRFTISRDN KNTLYLQMNSLRAEDTAAYYCVTGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGSSVYLTQPPSV/APGQTARITCGGNNIGSKSVHWYQQ KPGQAPV/MVVDNDNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYC QVWDYFSMTHVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWG QGTLVTVSSGGGGGGGGGGGQTVVTVQEPSLTVSPGGTVTLTCGSS TGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCS VMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 103)
		NA	(SEQ ID NO: 104)

iPS#	Ab	Type	BITE_scFc
iPS:2307386	MA_SG-F28_CC_x_I2C0_x_scFc_(D9R)_transl ation	AA	MDMRVPAQLGLLLWLRGARQCQQLQESGPGLVKPSQTLSTCTVSG DSISSNPPYYWSWIRQHPGKCLEWIGYISYSGITNYPNPSLKSRVTMSVDTSK NQFSLKLTSLTAADTAVYYCAREKMWFGVLNYYGMDVWQGTTVTV SSGGGGGGGGGGSDIVMTQTPLSLPVTPEPASISCRSSQSLHRS YNYLDWYLQKPGQSPQLLIYLSNRASGVPDRFSGSGSDFTLKISRVE AGDVGVYYCMQALQTPWTFGCGTKVEIKSGGGGSEVQLVESGGGLVQP GGSLKLSCAAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGGGTLVTVSSGGGGGGGGGGGSGTQTVVTQEPSTVSPGGT LTCGSSGTGAVTSGNYPNWVQKPGQAPRGLIGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK KVSNAKALPAIEKTIKSKAKGPQREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGG GGGGGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTIKSKAKGPQREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 105)

Table 38
BiTE-scFc Full Sequences

iPS#	Ab	Type	BiTE_scFc
iPS:2768797	MA_12- E12_CCx_I2C0_x_scFc_(J7J)_translat ion	NA	<i>No seq available</i>
		AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVKPGGSLRLSCAASG FTFSTYSMNWVRQAPGKCLEWVSSISSSSYIYADSVKGRFTISRDNK NSLYLQMNSLRDEDTAVYYCARDRIAVATYFDNWVGQGLTVTVSSGGGG SGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYCCQQ YANSPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGF TFNKYAMNWVRQAPGKGLEWVARIRSKYNNTATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVT VSSGGSGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSGTGAVTS GNYPNWVQKPGQAPRLIGGKFLAPGTPARFSGSLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHEAL HNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGGSGGGSDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVK FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 3875)
		NA	<i>No seq available</i>

iPS:2768793	MA_13- D12_CCx_I2C0_x_scFc_(S4S)_transla tion	AA	MDMRVPAQLLGLLLWLRGARCQVQLVESGGGVVQGRSLRLSCAASG FTFSSYGMHWVRQAPGKCLEWVALISYDGSSKYYADSVKGRFTISRDN KNTLDLQMNLSRAEDTAVYYCARSPDYVWGSYRNYYYGMDVWVWQG TTVTVSSGGGGGGGGGSSQA VVTQEPSLTVSPGGTVTLTCGSSSTG AVTSGHYPYWFQKPGQAPRTLIDTSNKHSWTPARFSGSLLGGKAALT LSGAQPEDEAEYYCFLSYSGARNWVFGCGTKLTVLSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYN NYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLVTVSSGGGGGGGGGGGSGQTVVTQEPSLTV SPGGTVTLTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGKFLAPGTP ARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL GGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWL NGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGS GGGGGGGGGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 3876)
		NA	No nuc. seq. available

iPS:2768801 MA_24- C9_CCx_I2C0x_scFc_(M6S)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASG YAFSKSWMNWVKQRPKCLEWIGRIYPGDGTNYNGKFKGKAALTAD KSSNTANMQLNSLTSEDAVYFCARDGVFYAPLAYWGQGLTVTVSSGG GGSGGGGGGGSELVMTQSPSSLAHSVGEKITMSCKSSQSLLYSSNQKN YLAWYQQKPGQSPKLLIYWASTRESGVDPDRFTGSGGTDFTLTISSVKAE DLAVYYCQQYYSYPYTFGCGTKLELKS GGGGSEVQLVESGGGLVQP GGS LKLSCAASGFTENKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWA YWGGQGLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTLTC GSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGG KAAATLSGVQPEDEAEYCYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLSKLTVDKSRWQQGNVF SCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WNLGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFYLSKLT VDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 3878) <i>No nuc. seq. available</i>
	NA	

iPS:2768805	MA_24- G6_CCx_I2C0_x_scFc_(M9Z)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASD YTFESKSWMNWVKQRPGECEWIGRVPWPGDGDTTYNEKFKGKATLTAD KSSRTAYMQLSSLTSEDSAVYFCARGNYFGSSEAYFDYWGGQTRVTVSS GGGGSGGGGGGGSELVLTQSPAIMSASPGQKVTTTCSASSNVNIHWY QQKLGSSPKLWIYDTSKLAPGVPARFSGSGSGTSYSLTISSMEAEADAASYF CHQWSSYPPTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWGGGT LVTVSSGGGGGGGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAATL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPCAP ELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSV HEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMHENHNHYTQKSLSLSPGK
			(SEQ ID NO: 3879)
		NA	No nuc. seq. available

MA_31- iPS:2768809 H8_CCx_I2C0_x_scFc_(F3H)_translat ion	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASG YAFSSWMNWWVKQRPCKCLEWIGRIYPGDGTNYNGKFKDKATLTADK SSNTAYMQLSSLTSEDSAVYFCARRQLNHVFAMDYWGQGTSTVTVSSGG GGSGGGGGGGSELQMTQSPASLSASVGETVTTTCRASGNIHNYLAWY QQKQKSPQLLVYNAKTLAGGVPSRFSGGSGTQFSLKINSLOPEDFGSY YQHHYGTPLTFGCGTKLELKS GGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDAVYVCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGGGGGSGGGSQT VVTQEPSLTVSPGGTVTLTCGSS GAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPETVTCVVVDV DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 3880)
		No nuc. seq. available
	NA	

	MA_32- A8_CCx_I2C0_x_scFc_(J6Z)_translati on iPS:2768813	AA	MDMRVPAQLLGLLLWLRGARCQVQLVQSGAEVKKPGASVKVSCKAS GYTFTSYDINWVRQATGQCLEWMGMNPNNGNTGYAQKFQGRVTMTTR NTSISTAYMELSSLRSEDVAVYYCARGGGYNGYDYGMDVWVGQGTIVT VSSGGGGGGGGGGSDIVMTQSPLSLPVSPGEPASISCRSSQSLLYSN GYNVVDWYLYQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISKV EAEDVGYYCMQALQTPPTFGCGTRLEIKSGGGGSEVQLVESGGGLVQP GGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISY WAYWGQGLVTVSSGGGGGGGGGSGGSGTIVVTQEPSLTVSPGGTVT LTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGSG GGGGGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 3881)
		NA	No nuc. seq. available

MA_32- C3_CCx_I2C0x_scFc_(L2A)_translati on iPS:2768795	AA MDMRVPAQLLGLLLWLRGARCQVQLQQWAGAGMLKPSETLSLTC AVYGGFSGYYNWIRQPPGKCLEWIGEINHSGSTNYNPSLKSRVTISVDTSK NQFSLKSSVTAADTAVYCARGGYSYGYDYGMDVWQGTTVTTVSS GGGGSGGGGGSDIVMTQSPLSLPTPGEPASISCRSSQSLLYSNGYN YLDWYLQKPGSQPLLILYLSNRASGVDRFSGSGGTDFTLKISRVEAE DVGYYCMQALQTPPTFGCGTKVDIKSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGGGGGGSGQTVVVTQEPSLTVSPGGTVTLTC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGG KAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPPCPAPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLTVDKSRWQQGNV SCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG SGGGGSKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WNLNGKEYKCKVSNKALPAPIEKTSISKAKGQPREPVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFFLYSKLT VDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: **) No nuc. seq available (SEQ ID NO: **)
	NA (SEQ ID NO: **) No nuc. seq available (SEQ ID NO: **)

iPS:2768815	MA_48- D12_CCx_I2C0x_scFc_(B4P)_translat ion	AA	MDMRVPAQLLGLLLWLRGARCQVQLVESGGGVVQGRSLRLSCAASG FTFRSYRMHWVRQAPGKCLEWVAVISYDGGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREQWPNYYGMDVWGQGTITVTVSS GGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAV YYCQQYGSSPLTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGSLKLSLC AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV MHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGGSGGGSGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 3882)

Table 39
BTE-scFc Fv#1 (MAGEB2) VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:276879 7	MA_12- E12_CCx_I2C0_x_scFc_(J7D)_transla tion	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RASQSVSSSYLA (SEQ ID NO: 3883)	GASSRAT (SEQ ID NO: 3915)	QQYANSPLT (SEQ ID NO: 3947)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276879 3	MA_13- D12_CCx_I2C0_x_scFc_(S4S)_transl ation	AA	GSSTGAVTSGHYPY (SEQ ID NO: 3884)	DTSNKHS (SEQ ID NO: 3916)	FLSYSGARNWV (SEQ ID NO: 3948)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276880 1	MA_24- C9_CCx_I2C0x_scFc_(M6S)_translat ion	AA	KSSQSLLYSSNQKNYLA (SEQ ID NO: 3885)	WASTRES (SEQ ID NO: 3917)	QQYYSPYPT (SEQ ID NO: 3949)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276880 5	MA_24- G6_CCx_I2C0_x_scFc_(M9Z)_transl ation	AA	SASSNVNYIH (SEQ ID NO: 3886)	DTSKLAP (SEQ ID NO: 3918)	HOWSSYPPT (SEQ ID NO: 3950)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276880 9	MA_31- H8_CCx_I2C0_x_scFc_(F3H)_transla tion	AA	RASGNHNYLA (SEQ ID NO: 3887)	NAKTLAG (SEQ ID NO: 3919)	QHYYGTPLT (SEQ ID NO: 3951)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276881 3	MA_32- A8_CCx_I2C0_x_scFc_(J6Z)_translat ion	AA	RSSQSLLYSNGYNYVD (SEQ ID NO: 3888)	LGSNRAS (SEQ ID NO: 3920)	MQALQTPPT (SEQ ID NO: 3952)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276879 5	MA_32- C3_CCx_I2C0x_scFc_(L2A)_translat ion	AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 3889)	LGSNRAS (SEQ ID NO: 3921)	MQALQTPPT (SEQ ID NO: 3953)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276881 5	MA_48- D12_CCx_I2C0x_scFc_(B4P)_transla tion	AA	RASQSVSSSYLA (SEQ ID NO: 3890)	GASSRAT (SEQ ID NO: 3922)	QQYGSPLT (SEQ ID NO: 3954)

Table 40
BTE-scFc Fv#1 (MAGEB2) VH CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:276879 7	MA_12- E12_CCx_I2C0_x_scFc_(J7D)_transla tion	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	TYSMN (SEQ ID NO: 3891)	SISSSSYIYADSVKG (SEQ ID NO: 3923)	DRIAVATYFDN (SEQ ID NO: 3955)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
IPS:276879 3	MA_13- D12_CCx_I2C0_x_scFc_(S4S)_transl ation	AA	SYGMH (SEQ ID NO: 3892)	LISYDSSKYYADSVKG (SEQ ID NO: 3924)	PYDYVWGSYRNYYGMDV (SEQ ID NO: 3956)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available

iPS:276880 1	MA_24- C9_CCx_I2C0x_scFc_(M6S)_translat ion	AA	KSWMN (SEQ ID NO: 3893) <i>No nuc. seq. available</i>	RIYPGDGDTNNGKFKG (SEQ ID NO: 3925) <i>No nuc. seq. available</i>	DGVFYAPLAY (SEQ ID NO: 3957) <i>No nuc. seq. available</i>
iPS:276880 5	MA_24- G6_CCx_I2C0_x_scFc_(M9Z)_transl ation	AA	KSWMN (SEQ ID NO: 3894) <i>No nuc. seq. available</i>	RVWPGDGDITTYNEKFKG (SEQ ID NO: 3926) <i>No nuc. seq. available</i>	GNYSSEAYFDY (SEQ ID NO: 3958) <i>No nuc. seq. available</i>
iPS:276880 9	MA_31- H8_CCx_I2C0_x_scFc_(F3H)_transla tion	AA	SSWMN (SEQ ID NO: 3895) <i>No nuc. seq. available</i>	RIYPGDGDTNNGKFKD (SEQ ID NO: 3927) <i>No nuc. seq. available</i>	RQLNHVAFMDY (SEQ ID NO: 3959) <i>No nuc. seq. available</i>
iPS:276881 3	MA_32- A8_CCx_I2C0_x_scFc_(J6Z)_translat ion	AA	SYDIN (SEQ ID NO: 3896) <i>No nuc. seq. available</i>	WMNPNSGNTGYAQKFG (SEQ ID NO: 3928) <i>No nuc. seq. available</i>	GGYSNGYDYGMDV (SEQ ID NO: 3960) <i>No nuc. seq. available</i>
iPS:276879 5	MA_32- C3_CCx_I2C0x_scFc_(L2A)_translat ion	AA	GYWYN (SEQ ID NO: 3897) <i>No nuc. seq. available</i>	EINHSSTNYPNPKS (SEQ ID NO: 3929) <i>No nuc. seq. available</i>	GGYSYGYDYGMDV (SEQ ID NO: 3961) <i>No nuc. seq. available</i>
iPS:276881 5	MA_48- D12_CCx_I2C0x_scFc_(B4P)_transla tion	AA	SYRMH (SEQ ID NO: 3898) <i>No nuc. seq. available</i>	VISYDGGNKYYADSVKG (SEQ ID NO: 3930) <i>No nuc. seq. available</i>	EQWPNYYGYMDV (SEQ ID NO: 3962) <i>No nuc. seq. available</i>

Table 41

BiTE-scFc Fv#2 (CD3) VL CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276879 7	MA_12- E12_CCx_I2C0_x_scFc_(J7D)_transla tion	NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>
iPS:276879 3	MA_13- D12_CCx_I2C0_x_scFc_(S4S)_transl ation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3899) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3931) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3963) <i>No nuc. seq. available</i>
iPS:276880 1	MA_24- C9_CCx_I2C0x_scFc_(M6S)_translat ion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3900) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3932) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3964) <i>No nuc. seq. available</i>
iPS:276880 5	MA_24- G6_CCx_I2C0_x_scFc_(M9Z)_transl ation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3901) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3933) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3965) <i>No nuc. seq. available</i>
iPS:276880 9	MA_31- H8_CCx_I2C0_x_scFc_(F3H)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3902) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3934) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3966) <i>No nuc. seq. available</i>
NA	NA	NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>

iPS:276881 3	MA_32- A8_CCx_I2C0_x_scFc_(J6Z)_translat ion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3904) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3936) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3968) <i>No nuc. seq. available</i>
iPS:276879 5	MA_32- C3_CCx_I2C0x_scFc_(L2A)_translat ion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3905) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3937) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3969) <i>No nuc. seq. available</i>
iPS:276881 5	MA_48- D12_CCx_I2C0x_scFc_(B4P)_transla tion	AA	GSSTGAVTSGNYPN (SEQ ID NO: 3906) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 3938) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 3970) <i>No nuc. seq. available</i>

Table 42
BiTE-scFc Fc#2 (CD3) VH CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276879 7	MA_12- E12_CCx_I2C0_x_scFc_(J7J)_transla tion	NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>
iPS:276879 3	MA_13- D12_CCx_I2C0_x_scFc_(S4S)_transl ation	AA	KYAMN (SEQ ID NO: 3907) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3939) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3971) <i>No nuc. seq. available</i>
iPS:276880 1	MA_24- C9_CCx_I2C0x_scFc_(M6S)_translat ion	AA	KYAMN (SEQ ID NO: 3908) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3940) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3972) <i>No nuc. seq. available</i>
iPS:276880 5	MA_24- G6_CCx_I2C0_x_scFc_(M9Z)_transl ation	AA	KYAMN (SEQ ID NO: 3909) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3941) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3973) <i>No nuc. seq. available</i>
iPS:276880 9	MA_31- H8_CCx_I2C0_x_scFc_(F3H)_transla tion	AA	KYAMN (SEQ ID NO: 3910) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3942) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3974) <i>No nuc. seq. available</i>
iPS:276881 3	MA_32- A8_CCx_I2C0_x_scFc_(J6Z)_translat ion	AA	KYAMN (SEQ ID NO: 3911) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3943) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3975) <i>No nuc. seq. available</i>
iPS:276879 5	MA_32- C3_CCx_I2C0x_scFc_(L2A)_translat ion	AA	KYAMN (SEQ ID NO: 3912) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3944) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3976) <i>No nuc. seq. available</i>
iPS:276881 5	MA_48- D12_CCx_I2C0x_scFc_(B4P)_transla tion	AA	KYAMN (SEQ ID NO: 3913) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3945) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3977) <i>No nuc. seq. available</i>
iPS:276881 5	MA_48- D12_CCx_I2C0x_scFc_(B4P)_transla tion	AA	KYAMN (SEQ ID NO: 3914) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 3946) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 3978) <i>No nuc. seq. available</i>

[illegible]

IPSR	Parent region sequences	Type	LC Y-region	Fwd (MAGCB3)	HC Y-region	LC Y-region	Rev (CDB)	HC Y-region
IPSPs:276879	MA_12- E12_CcX_12C0_x_scFc_(J7D)_transla- tion	NA	537,768, 549, 550,551,552	559,768, 552, 553,554,555	559,768, 552, 553,554,555	559,768, 549, 550,551,552	557,768, 549, 550,551,552	557,768, 549, 550,551,552
		AA	EIVLTQSPGTL SLSPGERATL SCRAQSQSVSSYLAWYQKPGQAPRLIYGASSRATGIPDRFSGSGSDFTLTI SRLEPDEFAVYYCQYANSPILTFGCGLTKEIK	QVQLVESGGGLVKPGGSLRLSCAASGFTFTSYSMNW VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA NAKSNLYLQMSLRDIEDTAVYYCARDRIAIVTVD NWGGQTLVTSSS (SEQ ID NO: 3979) 557,768, 552, 553,554,555	QVQLVESGGGLVKPGGSLRLSCAASGFTFTSYSMNW VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA NAKSNLYLQMSLRDIEDTAVYYCARDRIAIVTVD NWGGQTLVTSSS (SEQ ID NO: 3987) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 4003) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4003) 557,768, 552, 553,554,555	
		NA						
IPSPs:276879 3	MA_13- D12_CcX_12C0_x_scFc_(S4S)_transla- tion	AA	QAVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGHYPY WFQPKQGPAPRLIYDTSNKHSHWTPARFSGSLLGK AALLTSCAQPEDEAEYYCFLSYSGARNWVFGCGTKL IVL	QVQLVESGGGVQPGGSLRLSCAASGFTTSYGMH WVRAAPKGLIEWVARIRSYDGSKYVADSVKGRFTIS RDNSKNTLYLQMSLRADTAVYYCARSPDYVW GSTRNYYLGMDFWGGQITVTSSS (SEQ ID NO: 3980) 557,768, 552, 553,554,555	QVQLVESGGGVQPGGSLRLSCAASGFTTSYGMH WVRAAPKGLIEWVARIRSYDGSKYVADSVKGRFTIS RDNSKNTLYLQMSLRADTAVYYCARSPDYVW LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 3996) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 4005) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4004) 557,768, 552, 553,554,555	
		NA						
		NA						
IPSPs:276880 1	MA_24- C9_CcX_12C0x_scFc_(M6S)_transla- tion	NA	ELVMTQSPSSLASVNGEKITMSCKSQSLLYSSNQKN YLAWYQKPGQPKLLIYAGSTRGSGVDPRTFGSG GDTFLTSSVKAEDLAVYYCQYYSYTPTFGCGLT LELK (SEQ ID NO: 3981) 557,768, 552, 553,554,555	VQLLEQSGPEL VQPGASVKISCKASGYAFSKSWAN WQKRPQKCLEWIGRIYDPGDITNYNGKFKDAITL LTADKSNITANMQLSITSDSAVYTCARDGVYFAP LAYWGGQTLVTSSS (SEQ ID NO: 3989) 557,768, 552, 553,554,555	VQLLEQSGPEL VQPGASVKISCKASDYTFSKSWAN WQKRPQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 3997) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4005) 557,768, 552, 553,554,555		
		NA						
		AA	ELVLTQSPALMSAPGQKVITITCSASSNNYHIVYQK KLGSPPKIWIYDTSKLAGNPAPRFGSGSGTFSYLTIS SMEAEDAASYTCQWSSYTPPTFGCGTKLEIK (SEQ ID NO: 3982) 557,768, 552, 553,554,555	VQLLEQSGPEL VQPGASVKISCKASDYTFSKSWAN WQKRPQKCLEWIGRIYDPGDITNYNEKFKGKATL LTADKSNITAYMQLSITSDSAVYTCARGNTFGSS EAYPDYWGQGTITVTSSS (SEQ ID NO: 3990) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 3998) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4006) 557,768, 552, 553,554,555		
IPSPs:276880	MA_31- IB_CcX_12C0_x_scFc_(F3H)_transla- tion	NA	ELMTQSPASLSASVGEIVTITCRASGNHNTLAWY QKQKQSPQLLYVYNAKTLAGVPSRFGSGSGTQFS LKINSLQPEDEAYYYCQHHYGTPLTFGCGLTLEK (SEQ ID NO: 3983) 557,768, 552, 553,554,555	VQLLEQSGPEL VQPGASVKISCKASGYAFSSSWANN WQKRPQKCLEWIGRIYDPGDITNYNGKFKDAITL ADKSNITAYMQLSITSDSAVYTCARRQLNHVFA MDYWGQGTITVTSSS (SEQ ID NO: 3991) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 3999) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4007) 557,768, 552, 553,554,555		
		NA						
		AA	DIVMTQSPSLIPLVTPGPEPASICRSQSLLYSNGNYVL DWYLRQKQSPQLLYLGSNRASGVDPDRFSGSGGT DTFLTKISVEAEDVGVYYCMQALQTPPTFGCGTKVD IK (SEQ ID NO: 3984) 557,768, 552, 553,554,555	QVQLVQSGAEVKKPGASVKVSCKASGYTFITSDYN DWYLRQKQSPQLLYLGSNRASGVDPDRFSGSGGT TMTNRTSISATYMLSLTSDSAVYTCARGGGYNY GYDYGMDVWGQGTITVTSSS (SEQ ID NO: 3992) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 4000) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4008) 557,768, 552, 553,554,555		
IPSPs:276881 3	MA_32- A8_CcX_12C0_x_scFc_(J6Z)_transla- tion	NA						
		AA	DIVMTQSPSLIPLVTPGPEPASICRSQSLLYSNGNYVL DWYLRQKQSPQLLYLGSNRASGVDPDRFSGSGGT DTFLTKISVEAEDVGVYYCMQALQTPPTFGCGTKVD IK (SEQ ID NO: 3985) 557,768, 552, 553,554,555	QVQLVQSGAEVKKPGASVKVSCKASGYTFITSDYN DWYLRQKQSPQLLYLGSNRASGVDPDRFSGSGGT TMTNRTSISATYMLSLTSDSAVYTCARGGGYNY GYDYGMDVWGQGTITVTSSS (SEQ ID NO: 3993) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 4001) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4009) 557,768, 552, 553,554,555		
		NA						
IPSPs:276881	MA_48- D12_CcX_12C0x_scFc_(B4P)_transla- tion	AA	EIVLTQSPGTL SLSPGERATL SCRAQSQSVSSYLAWYQKPGQAPRLIYGASSRATGIPDRFSGSGSDFTLTI SRLEPDEFAVYYCQYQYSSGSPILTFGCGLTKEIK	QVQLVESGGGVQPGGSLRLSCAASGFTFSRYRHH WVRAAPKGLIEWVARISYDYGKNYVADSVKGRFTIS RDNSKNTLYLQMSLRADTAVYYCAREQWPNY YTGMDYWGQGTITVTSSS (SEQ ID NO: 3986) 557,768, 552, 553,554,555	QVQLVESGGGVQPGGSLRLSCAASGFTFSRYRHH WVRAAPKGLIEWVARISYDYGKNYVADSVKGRFTIS RDNSKNTLYLQMSLRADTAVYYCAREQWPNY YTGMDYWGQGTITVTSSS (SEQ ID NO: 4002) 557,768, 552, 553,554,555	QTVVLTQPSLTVSPGGITVLTCGSSGTGAVTSGNPWN VQPKQGPAPRGLIGGKTKLAPGTARFSGSLLGKAA LTLISGVQPEDEAEYYCVLIWYSNRWVFGGTKLTVL (SEQ ID NO: 4010) 557,768, 552, 553,554,555	EVQLVESGGGLVQPGGSLKLSCAASGFTPNKYAMN WVRAAPKGLIEWVARIRSKYNNTAVYYADSVKDR FTSRDSDSKNTAYLQMNLLTIEDTAVYYCVRHGNF (SEQ ID NO: 4010) 557,768, 552, 553,554,555	

$\partial_t \phi + \nabla_x \cdot (\phi v) = -\nabla_x \cdot (\phi v)$

KAPPA VARIABLE									
Genotype	K_FRI	SEQ ID NO	K_CDH1	SEQ ID NO	K_FRI	SEQ ID NO	K_CDH3	SEQ ID NO	K_FRI
MA_12- PS:216879 D12_Cc12C_x_wFC (J73), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_13- PS:216880 D13_Cc12C_x_wFC (J84), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_14- PS:216881 D14_Cc12C_x_wFC (J95), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_15- PS:216882 D15_Cc12C_x_wFC (J106), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_16- PS:216883 D16_Cc12C_x_wFC (J117), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_17- PS:216884 D17_Cc12C_x_wFC (J128), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_18- PS:216885 D18_Cc12C_x_wFC (J139), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_19- PS:216886 D19_Cc12C_x_wFC (J150), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_20- PS:216887 D20_Cc12C_x_wFC (J161), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_21- PS:216888 D21_Cc12C_x_wFC (J172), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_22- PS:216889 D22_Cc12C_x_wFC (J183), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_23- PS:216890 D23_Cc12C_x_wFC (J194), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_24- PS:216891 D24_Cc12C_x_wFC (J205), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_25- PS:216892 D25_Cc12C_x_wFC (J216), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_26- PS:216893 D26_Cc12C_x_wFC (J227), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_27- PS:216894 D27_Cc12C_x_wFC (J238), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_28- PS:216895 D28_Cc12C_x_wFC (J249), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_29- PS:216896 D29_Cc12C_x_wFC (J260), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_30- PS:216897 D30_Cc12C_x_wFC (J271), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_31- PS:216898 D31_Cc12C_x_wFC (J282), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_32- PS:216899 D32_Cc12C_x_wFC (J293), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_33- PS:216900 D33_Cc12C_x_wFC (J304), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_34- PS:216901 D34_Cc12C_x_wFC (J315), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_35- PS:216902 D35_Cc12C_x_wFC (J326), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_36- PS:216903 D36_Cc12C_x_wFC (J337), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_37- PS:216904 D37_Cc12C_x_wFC (J348), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_38- PS:216905 D38_Cc12C_x_wFC (J359), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_39- PS:216906 D39_Cc12C_x_wFC (J370), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_40- PS:216907 D40_Cc12C_x_wFC (J381), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_41- PS:216908 D41_Cc12C_x_wFC (J392), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_42- PS:216909 D42_Cc12C_x_wFC (J403), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_43- PS:216910 D43_Cc12C_x_wFC (J414), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_44- PS:216911 D44_Cc12C_x_wFC (J425), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_45- PS:216912 D45_Cc12C_x_wFC (J436), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_46- PS:216913 D46_Cc12C_x_wFC (J447), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_47- PS:216914 D47_Cc12C_x_wFC (J458), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_48- PS:216915 D48_Cc12C_x_wFC (J469), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_49- PS:216916 D49_Cc12C_x_wFC (J480), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_50- PS:216917 D50_Cc12C_x_wFC (J491), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_51- PS:216918 D51_Cc12C_x_wFC (J502), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_52- PS:216919 D52_Cc12C_x_wFC (J513), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_53- PS:216920 D53_Cc12C_x_wFC (J524), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_54- PS:216921 D54_Cc12C_x_wFC (J535), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_55- PS:216922 D55_Cc12C_x_wFC (J546), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_56- PS:216923 D56_Cc12C_x_wFC (J557), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_57- PS:216924 D57_Cc12C_x_wFC (J568), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_58- PS:216925 D58_Cc12C_x_wFC (J579), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_59- PS:216926 D59_Cc12C_x_wFC (J590), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_60- PS:216927 D60_Cc12C_x_wFC (J601), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_61- PS:216928 D61_Cc12C_x_wFC (J612), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_62- PS:216929 D62_Cc12C_x_wFC (J623), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_63- PS:216930 D63_Cc12C_x_wFC (J634), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_64- PS:216931 D64_Cc12C_x_wFC (J645), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_65- PS:216932 D65_Cc12C_x_wFC (J656), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_66- PS:216933 D66_Cc12C_x_wFC (J667), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_67- PS:216934 D67_Cc12C_x_wFC (J678), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_68- PS:216935 D68_Cc12C_x_wFC (J689), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_69- PS:216936 D69_Cc12C_x_wFC (J700), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_70- PS:216937 D70_Cc12C_x_wFC (J711), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_71- PS:216938 D71_Cc12C_x_wFC (J722), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_72- PS:216939 D72_Cc12C_x_wFC (J733), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_73- PS:216940 D73_Cc12C_x_wFC (J744), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_74- PS:216941 D74_Cc12C_x_wFC (J755), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_75- PS:216942 D75_Cc12C_x_wFC (J766), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_76- PS:216943 D76_Cc12C_x_wFC (J777), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_77- PS:216944 D77_Cc12C_x_wFC (J788), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_78- PS:216945 D78_Cc12C_x_wFC (J799), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_79- PS:216946 D79_Cc12C_x_wFC (J810), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_80- PS:216947 D80_Cc12C_x_wFC (J821), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_81- PS:216948 D81_Cc12C_x_wFC (J832), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_82- PS:216949 D82_Cc12C_x_wFC (J843), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_83- PS:216950 D83_Cc12C_x_wFC (J854), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_84- PS:216951 D84_Cc12C_x_wFC (J865), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_85- PS:216952 D85_Cc12C_x_wFC (J876), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_86- PS:216953 D86_Cc12C_x_wFC (J887), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	QTFPFSBSBSG--TQFTTETIRBPFPAYVC
MA_87- PS:216954 D87_Cc12C_x_wFC (J898), trans from Pw2	BT1GQFQKQPLIATG	4012	BAS-QVBS-----S1LA	4062	WTQGFQKQPLIAT	4112	G-----ASSBAT	4162	

Sequence Listing

IPS:176879 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(J3A), frameid from Per1	VH13-73.D33.3.18RF2.JH4	4035	WTQAQDQCLBWA	4145	R1E8AT--R1E8ATTAAGVTD	4135	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4245	RDQFRRS-----1E8WAT	4235	WQQTLLTVYS	4345
IPS:176881 S 5	MA_48 D1, C1, CC1, D1C0_1, eFC_1(BAP), frameid from Per1	VH13-73.D33.3.18RF2.JH4	4036	WTQAQDQCLBWA	4146	R1E8AT--R1E8ATTAAGVTD	4136	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4246	RDQFRRS-----1E8WAT	4236	WQQTLLTVYS	4346
IPS:176879 S 3	MA_32 C1, CC1, D1C0_1, eFC_1(S4S), frameid from Per1	Geneline	4037	WTQAQDQCLBWA	4147	L1E8D---G8E8TAAAGVTD	4137	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4247	RDQFRRS-----1E8WAT	4237	WQQTLLTVYS	4347
IPS:176880 S 1	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4038	WTQAQDQCLBWA	4148	L1E8D---G8E8TAAAGVTD	4138	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4248	RDQFRRS-----1E8WAT	4238	WQQTLLTVYS	4348
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4039	WTQAQDQCLBWA	4149	L1E8D---G8E8TAAAGVTD	4139	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4249	RDQFRRS-----1E8WAT	4239	WQQTLLTVYS	4349
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4040	WTQAQDQCLBWA	4150	L1E8D---G8E8TAAAGVTD	4140	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4250	RDQFRRS-----1E8WAT	4240	WQQTLLTVYS	4350
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4041	WTQAQDQCLBWA	4151	L1E8D---G8E8TAAAGVTD	4141	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4251	RDQFRRS-----1E8WAT	4241	WQQTLLTVYS	4351
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4042	WTQAQDQCLBWA	4152	L1E8D---G8E8TAAAGVTD	4142	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4252	RDQFRRS-----1E8WAT	4242	WQQTLLTVYS	4352
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4043	WTQAQDQCLBWA	4153	L1E8D---G8E8TAAAGVTD	4143	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4253	RDQFRRS-----1E8WAT	4243	WQQTLLTVYS	4353
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4044	WTQAQDQCLBWA	4154	L1E8D---G8E8TAAAGVTD	4144	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4254	RDQFRRS-----1E8WAT	4244	WQQTLLTVYS	4354
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4045	WTQAQDQCLBWA	4155	L1E8D---G8E8TAAAGVTD	4145	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4255	RDQFRRS-----1E8WAT	4245	WQQTLLTVYS	4355
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4046	WTQAQDQCLBWA	4156	L1E8D---G8E8TAAAGVTD	4146	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4256	RDQFRRS-----1E8WAT	4246	WQQTLLTVYS	4356
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4047	WTQAQDQCLBWA	4157	L1E8D---G8E8TAAAGVTD	4147	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4257	RDQFRRS-----1E8WAT	4247	WQQTLLTVYS	4357
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4048	WTQAQDQCLBWA	4158	L1E8D---G8E8TAAAGVTD	4148	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4258	RDQFRRS-----1E8WAT	4248	WQQTLLTVYS	4358
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4049	WTQAQDQCLBWA	4159	L1E8D---G8E8TAAAGVTD	4149	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4259	RDQFRRS-----1E8WAT	4249	WQQTLLTVYS	4359
IPS:176880 S 5	MA_32 C1, CC1, D1C0_1, eFC_1(NB2), frameid from Per1	Geneline	4050	WTQAQDQCLBWA	4160	L1E8D---G8E8TAAAGVTD	4150	RFTTSIGDSRFA1LQWMLAREDAVYVTCAL-	4260	RDQFRRS-----1E8WAT	4250	WQQTLLTVYS	4360

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IPS:276879 5	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4335	K.....Y..B	4445	P.....A	4495	Y..B...Y..D..D	4545	H.....V.....	4595	Y..B..WA	4645	Y..B..WA	4695
IPS:276881 5	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4336	K.....Y..B	4446	P.....A	4496	Y..B...Y..D..D	4546	H.....V.....	4596	Y..B..WA	4646	Y..B..WA	4696
IPS:276880 1	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4337	K.....Y..B	4447	P.....A	4497	Y..B...Y..D..D	4547	H.....V.....	4597	Y..B..WA	4647	Y..B..WA	4697
IPS:276880 3	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4338	K.....Y..B	4448	P.....A	4498	Y..B...Y..D..D	4548	H.....V.....	4598	Y..B..WA	4648	Y..B..WA	4698
IPS:276880 1	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4339	K.....Y..B	4449	P.....A	4499	Y..B...Y..D..D	4549	H.....V.....	4599	Y..B..WA	4649	Y..B..WA	4699
IPS:276880 3	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4340	K.....Y..B	4450	P.....A	4500	Y..B...Y..D..D	4550	H.....V.....	4600	Y..B..WA	4650	Y..B..WA	4700
IPS:276880 5	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4341	K.....Y..B	4451	P.....A	4501	Y..B...Y..D..D	4551	H.....V.....	4601	Y..B..WA	4651	Y..B..WA	4701
IPS:276880 9	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4342	K.....Y..B	4452	P.....A	4502	Y..B...Y..D..D	4552	H.....V.....	4602	Y..B..WA	4652	Y..B..WA	4702
IPS:276880 3	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4343	K.....Y..B	4453	P.....A	4503	Y..B...Y..D..D	4553	H.....V.....	4603	Y..B..WA	4653	Y..B..WA	4703
IPS:276880 5	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4344	K.....Y..B	4454	P.....A	4504	Y..B...Y..D..D	4554	H.....V.....	4604	Y..B..WA	4654	Y..B..WA	4704
IPS:276881 3	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4405	K.....Y..B	4455	P.....A	4505	Y..B...Y..D..D	4555	H.....V.....	4605	Y..B..WA	4655	Y..B..WA	4705
IPS:276881 5	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4406	K.....Y..B	4456	P.....A	4506	Y..B...Y..D..D	4556	H.....V.....	4606	Y..B..WA	4656	Y..B..WA	4706
IPS:276881 3	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4407	K.....Y..B	4457	P.....A	4507	Y..B...Y..D..D	4557	H.....V.....	4607	Y..B..WA	4657	Y..B..WA	4707
IPS:276881 5	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4408	K.....Y..B	4458	P.....A	4508	Y..B...Y..D..D	4558	H.....V.....	4608	Y..B..WA	4658	Y..B..WA	4708
IPS:276881 3	MA_32 C2_CCs_12C0c_wFC_123A_1rand16 from Per1	4409	K.....Y..B	4459	P.....A	4509	Y..B...Y..D..D	4559	H.....V.....	4609	Y..B..WA	4659	Y..B..WA	4709
IPS:276881 5	MA_48 D12_CCs_12C0c_wFC_104P_1rand16 from Per1	4410	K.....Y..B	4460	P.....A	4510	Y..B...Y..D..D	4560	H.....V.....	4610	Y..B..WA	4660	Y..B..WA	4710

Table 46
BiTE-scFc Full Sequences

iPS#	Ab	Type	BiTE_scFc
iPS:2768797	MA_12- E12_CC_x_I2C0x_scFc_(E9U)_translation	NA	<i>No seq available</i>
		AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVKPGGSLRLSCAASG FTFTSYSMNWVRQAPGKCLEWVSSISSSSYIYADSVKGRFTISRDNK NSLYLQMNSLRDEDTAVYYCARDRIAVATYFDNWVGQGLTVTVSSGGGG SGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQ KPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQQ YANSPLTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGF TFNKYAMNWVRQAPGKGLEWVARIRSKYNNTATYYADSVKDRFTISR DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGLTVT VSSGGSGGGSGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSGTGAVTS GNYPNWVQKPGQAPRLIGGKFLAPGTPARFSGSLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELL GGPSVFLFPPKPKDTLMISRTPETVTVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVMHEAL HNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGSDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETVTVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 4711)	
		NA	<i>No seq available</i>

iPS:2768798 MA_12- E12x_I2C0x_scFC_(W1U)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVKPGGSLRLSCAASG FTFTSYSMNWVRQAPGKGLEWVSSISSSSYYIYADSVKGRFTISRDN NSLYLQMNSLRDEDTAVYYCARDRIAVATYFDNWGQGTLTVSSGGGG SGGGSGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVY YCQQYANSPLTFGGGTVEIKSGGGGSEVQLVESGGGLVQPGSLKLS CAASGF TFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGSGGGGSGGTQVVTQEPSTVSPGGTVTLTCGSSGTGAVTS GNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAL TSLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNATKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTTPVLDSDGSGGGGGSGGGGGSGGGGGSGDKT HNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNATKTPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGGGGGGGGGGGGGGG NVFSCSVMEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 4712)
		No nuc. seq. available
	NA	

iPS:2768799	MA_13- D8_CCx_I2C0x_scFc_(U7V)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSFAMSWVRQAPGKCLEWVSAISGGSGSTYYADSVKGRFTISRDN NTLYLQMNSLRAEDTAEEYCAKMVTPDYDDMDVWGQGTTVTVSSGG GGSGGGSGGGGSDIQTQSPSSLSASVGDVTVITCRASQGISNYLAWYQ QKPGKVPKLLIYAASTLQSGVPSRFSGGSGTDFLTITSSLQPEDFATYYC QQSYSTPPTFGCGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNATAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQGT VTVSSGGGGSGGGGSGTQTVVTQEPSTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTL GVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVVDG EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHE ALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGSD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 4713)
		NA	No nuc. seq. available

iPS:2768800 MA_13- D8x_I2C0x_scFc_(M7M)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSFAMSWVRQAPKGLEWVSAISGGSTYYADSVKGRFTISRDN NTLYLQMNSLRAEDTAEEYCAKMVTPDYDDMDVWGQGTIVTVSSGG GGSGGGGGGGGGDIQMTQSPSSLSASVGDRTITCRASQGISNYLAWYQ QKPGKVPKLLIYAASTLQSGVPSRFSGGSGTDFLTITSSLPQEDFATYYC QQSYSTPPTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWRQAPKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSNTAYLQMNLLKTEDAVYYCVRHGNFGNSYISYWAYWGQGT VTVSSGGGGGGGGGGGQTVVTQEPSTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAALTL GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDG EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVMHE ALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGSD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGK
	NA	(SEQ ID NO: 4714) No nuc. seq. available

iPS:2768801 MA_24- C9_CCx_I2C0x_scFc_(I2U)_translatio n	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASG YAFSKSWMNWVKQRPKCLEWIGRIYPGDGDTNNGKFKGKAALTAD KSSNTANMQLNSLTSESAVYFCARDGVFYAPLAYWGQGLTVTVSSGG GGSGGGGGGGSELVMTQSPSSLAHSVGEKITMSCKSSQSLLYSSNQKN YLAWYQQKPGQSPKLLIYWASTRESGVDPDRFTGSGGTDFTLTISSVKAE DLAVYYCQQYYSYPYTFGCGTKLELKS GGGGSEVQLVESGGGLVQP GGS LKLSCAASGFTENKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWA YWGQGLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTLTC GSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAAALTLSGVQPEDEAEYCYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDSGSFELYSKLTVDKSRWQQGNVF SCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFELYSKLT VDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 4715) No nuc. seq. available
	NA	

iPS:2768803	MA_24- C9x_I2C0x_scFc_(L9Y)_translation	AA	MDMRVPAQLLGLLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASG YAFSKSWMNWVKQRPKGLEWIGRIYPGDGDTNNGKFKGKAALTAD KSSNTANMQLNSLTSEDSAVYFCARDGVFYAPLAYWGQGLTVTVSSGG GGSGGGGGGGSELVMTQSPSSLAHSVGEKITMSCKSSQSLLYSSNQKN YLAWYQQKPGQSPKLLIYWASTRESGVDPDRFTGSGSGTDFTLTISSVKAE DLAVYYCQQYYSPYTFGGGKLELKSGGGGSEVQLVESGGGLVQPGG SLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAD SVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNGFNSYISYWA YWGQGLTVTVSSGGGGGGGGGGGSGQTVVVTQEPSLTVSPGGTIVTLTC GSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGG KAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV SCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG SGGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT VDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 4716) <i>No nuc. seq. available</i>

iPS:2768805	MA_24- G6_CCx_I2C0x_scFc_(BII)_translatio n	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASD YTFESKSWMNWVKQRPGECEWIGRVPWPGDGDTTYNEKFKGKATLTAD KSSRTAYMQLSSLTSEDSAVYFCARGNYFGSSEAYFDYWGGQTRVTVSS GGGGSGGGGGGGSELVLTQSPAIMSASPGQKVTTTCSASSNVNIHWY QQKLGSSPKLWIYDTSKLAPGVPARFSGSGSGTSYSLTISSMEAEADAASYF CHQWSSYPPTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWGGGT LVTVSSGGGGGGGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAATL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPCAP ELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSVM HEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 4717)
		NA	No nuc. seq. available

iPS:2768807	MA_24- G6x_I2C0x_scFc_(F1M)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASD YTFESKSWMNWVKQRPGEGLWIGRWVWPGDGDITTYNEKFKGKATLTAD KSSRTAYMQLSSLTSEDSAVYFCARGNYFGSSEAYFDYWGGQTRVTVSS GGGGSGGGGGGGSELVLTQSPAIMSASPGQKVTTTCSASSNVNIHWY QQKLGSSPKLWIYDTSKLAPGVPARFSGSGSGTSYSLTISSMEAEADAASYF CHQWSSYPPTFGSGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAA SGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYADSVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWAYWGGGT LVTVSSGGGGGGGGGGSGQTVVTQEPSLTVSPGGTVTLTCGSSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAAATL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPCAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALP APIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSV HEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG SDKTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED PEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCL LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMHENHNTQKSLSLSPGK
		NA	(SEQ ID NO: 4718) <i>No nuc. seq. available</i>

MA_31- iPS:2768809 H8_CCx_I2C0x_scFc_(K4E)_translati on	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASG YAFSSWMNWNVKQRPCKCLEWIGRIYPGDGTNYNGKFKDKATLTADK SSNTAYMQLSSLTSEDSAVYFCARRQLNHVFAMDYWGQGTSTVTVSSGG GGSGGGGGGGSELQMTQSPASLSASVGETVTTTCRASGNIHNYLAWY QQKQKSPQLLVYNAKTLAGGVPSRFSGSGGTQFSLKINSLOPEDFGSY YQCQHHYGTPLTFGCGTKLELKS GGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWNVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGGGGGGSGQTVVTQEPSTVSPGGTVTLTCGSSST GAVTSGNYPNWNVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGKKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCP APELLGGPSVFLFPPKPKDTLMISRTPETVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETVTCVVVDVSH EPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
	(SEQ ID NO: 4719)	No nuc. seq. available
	NA	

iPS:2768811	MA_31- H8x_I2C0x_scFc_(F9Z)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLLEQSGPELVKPGASVKISCKASG YAFSSWMNWVKQRPKGKLEWIGRIYPGDGDTNNGKFKDKATLTADK SSNTAYMQLSSLTSEDSAVYFCARRQLNHVFAMDYWGQGTSTVTVSSGG GGSGGGGGGGSELQMTQSPASLSASVGETVTITCRASGNIHNYLAWY QQKQKSPQLLVYNAKTLAGGVPSRFGSGSGTQFSLKINSLOPEDFGSY YQHHYGTPLTFGAGTKLELKS GGGGSEVQLVESGGGLVQPGGSLKLSK AASGFTFNKYAMNWNVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYVCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGGGGGGSGSQTVVTQEPSLTVSPGGTVTLTCGSST GAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCP APELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSH DPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 4720)
		NA	No nuc. seq. available

iPS:2768813	MA_32- A8_CCx_I2C0x_scFc_(A9E)_translati on	AA	MDMRVPAQLLGLLLLWLRGARCQVQLVQSGAEVKKPGASVKVSKKAS GYTFTSYDINWVRQATGQCLEWMGWMPNPSNGNTGYAQKFQGRVTMTR NTSISTAYMELSSLRSEDVAVYYCARGGGYSNGYDYGMDVWVGQGTIVT VSSGGGGSGGGGGSDIVMTQSPLSLPVSPGEPASISCRSSQSLLYSN GYNVVDWYLYQKPGQSPQLLIYLGSNRASGVPDRFSGSGGTDFTLKISKV EAEDVGYYCMQALQTPPTFGCGTRLEIKSGGGGSEVQLVESGGGLVQP GGSLKLSCAAAGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYY ADSVKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISY WAYWGQGTIVTVSSGGGGSGGGGGSQTVVTQEPSLTVSPGGTIVT LTCGSSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGSG GGGGGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLH QDWLNGKEYCKVSNKALPAPIEKTKSKAKGQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSK LTVDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 4721)
		NA	No nuc. seq. available

iPS:2768814 MA_32- A8_x_I2C0x_scFc_(G6J)_translation	AA	MDMRVPAQLLGLLLLWLRGARCQVQLVQSGAEVKKPGASVKVSKAS GYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAQKFQGRVTMT RNTSISTAYMELSSLRSEDTAVYYCARGGGYSNGDYGMADVWGQGTTV TVSSGGGGGGGGGGSDIVMTQSPSLPVSPGEPASISCRSSQSLLYS NGYNYVDWYLQKPGQSPQLLIYLGSNRASGVDRFSGSGGTDTLTKISK VEAEDVGYYCMQALQTPPTFGQGRLEIKSGGGGSEVQLVESGGGLVQ PGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATY YADSVKDRFTISRDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYIS YWAYWGQGTLVTVSSGGGGGGGGGGSGTQVTVTQEPSLTVSPGGTV TLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDK THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGG GGGGGGGGGSKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVL HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK
	(SEQ ID NO: 4722)	No nuc. seq. available
NA		

MA_48- iPS:2768815 D12_CCx_I2C0x_scFc_(M9T)_transl ation	AA	MDMRVPAQLLGLLLWLRGARCQVQLVESGGGVVQGRSLRLSCAASG FTFRSYRMHWVRQAPGKCLEWVAISYDGGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAREQWPNYYGMDVWGQGTITVTVSS GGGGGGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAV YYCQQYGSSPLTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGSLKLSLC AASGFTFNKYAMNWVRQAPGKLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSSST GAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCV MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHITCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
	(SEQ ID NO: 4723)	No nuc. seq. available
	NA	

iPS:2768816	MA_48- D12x_I2C0x_scFc_(R9D)_translation	AA	MDMRVPAQLLGLLLWLRGARCQQLVESGGGVVQGRSLRLSCAASG FTFRSYRMHWVRQAPGKGLEWVAVISYDGGNKYYADSVKGRFTISRDN SKNTLYLQMNLSRAEDTAVYYCAREQWPNYYGMDVWGQGTITVTVSS GGGGGGGGGGGGSEIVLTQSPGTLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFLTISRLEPEDFAV YYCQQYGSSPLTFGGGTLEIKSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDR FTISRDDSKNTAYLQMNLLKTEDTAVYYCVRHGNFGNSIYWAYWYWGQ GTLVTVSSGGGGGGGGGGGSGTQVVTQEPSTVSPGGTVTLTCGSST GAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGAAL TLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSHEDPEVKFNWYVD GVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCSV MHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGG GSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETCVVVDVSH EPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 4724)
		NA	No nuc. seq. available

iPS:2768817	MA_50- D9_CCx_I2C0x_scFc_(K6S)_translati on	AA	MDMRVPAQLLGLLLLWLRGARCQVQLQQSGPGLVKPSQTLTLCAISGD SVSSNSAAWNWIRQSPSRCLEWLGRTYYRSKWYNDYAVSVKSRITINPD TSKNQFSLQLNSVTPEDTAVYCVREILWFGKLNYYGMDVWGQGTTV TVSSGGGGGGGGGGSDIVLTQSPLSLPVTGDPASISCRSSQSLLHS NGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDRFSGSGGTDFTLKISR VEAEDVGYYCMQALQTPLTFGCGTKVDIKSGGGGSEVQLVESGGGLV QPGGSLKLSCAASGFENKYAMNWVRQAPKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGGGGGGGGSGGTQVVTQEPSTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LLGGKAAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGD KTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGG SGGGGGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 4725) <i>No nuc. seq. available</i>

iPS:2768818 MA_50- D9x_I2C0x_scFc_(A4U)_translation	AA	MDMRVPAQLLGLLLWLRGARCQVQLQQSGPLVKPSQTLSTCAISGD SVSSNSAAWNWIRQSPSRGLEWLGRTYYRSKWYNDYAVSVKSRITINPD TSKNQFSLQLNSVTPEDTAVYCVREILWFGKLNYYGMDVWGQGTTV TVSSGGGGGGGGGGSDIVLTQSPLSLPVTGDPASISCRSSQSLLS NGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDRFSGSGGDTFTLKISR VEAEDVGYYCMQALQTPLTFGGGTKVDIKSGGGGSEVQLVESGGGLV QPGGSLKLSAASGFENKYAMNWRQAPGKGLEWVARIRSKYNNYAT YYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGGGGGGGGGSGGQTVVTQEPSTVSPGGT VTLTCGSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGS LLGGKAAALTLGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGG SGGGGGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGIFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL YSKLTVDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 4726) <i>No nuc. seq. available</i>
	NA	

iPS:2768819 MA_78- A6_CCx_I2C0x_scFc_(D8Z)_translati on	AA	MDMRVPAQLLGLLLWLRGARCQVQLQQWAGLLKPSETLSLTCVY GGSFSGYYWNWIRQPPGKCLEWIGEINHRGSTNYPNPSLKSRVTISVDASK NQFSLKLSSTAAADTAVYYCARGGGYSDGYDYGMDVWVGQTTVTVSS GGGGGGGGGGGGSDIVLTQSPSLPVPSPGEPASISCRSSQSLLYSNGYN YVDWYLQKPGQSPQLLIYLGSRASGVPDRFSGSGGTDFTLKISKVEAE DVGVYYCMQALQTPFTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTENKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGGGGGGGGSGTQVTVTQEPSTLVSPGGTVTLTC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGG KAAATLSGVQPEDEAEYCYVWYVSNRWVFGGGTKLTVLGGGGDKTHT CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTTPVLDSDSGSFGGGGGGSGGGGGG SCSVMEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGG SGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDSGSFGFLYSKLT VDKSRWQQGNVVFSCSVMEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 4727) <i>No nuc. seq. available</i>
	NA	

iPS:2768820	MA_78- A6x_I2C0x_scFc_(K6P)_translation	AA	MDMRVPAQLLGLLLWLRGARCQVQLQWAGLLKPSETLSLTCVY GGSFSGYYWNWIRQPPGKGLEWIGEINHRGSTNYPNPSLKSRVTISVDASK NQFSLKLSVTAADTAVYYCARGGGYSDGYDYGMDVWVGQTTVTVSS GGGGGGGGGGGGDIVLTQSPLSLPVPGEPAISCRSSQSLLYSNGYN YVDWYLQKPGQSPQLLIYLGSRASGVPDRFSGSGGTDFTLKISKVEAE DVGYYCMQALQTPFTFGPGTKVEIKSGGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADS VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLLVTVSSGGGGGGGGGGGSGQTVVVTQEPSLTVSPGGTVTLTC GSSTGAVTSGNYPNWVQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGG KAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETVCVVVDVSHEDPEVKFN WYVVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKV SNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGSGGGGGGGGGGGGGGGGG SCSVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGG SGGGGSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPETVCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQD WLNKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLT VDKSRWQQGNVVFSCSVMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 4728) <i>No nuc. seq. available</i>

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iPS:2768822	MA_79- E3x_I2C0x_scFc_(N4F)_translation	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSFAMSWVRQAPGKGLEWVSAISGGSTYYADSVKGRFTISRDNK NTLYLQMNSLRAEDTAEYYCAKMTVPDYYYDMDVWGQGTITVTVSSGG GGSGGGGGGGSDIQMTQSPSSVSASVGDRTITCRASQSISSYLNWYQ QKPGKAPKSLIYAASSLQSGVPSRFSGSGGTDTFTLTSSLPEDFATYYCQ QSYRTPPTFGQGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASG FTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTA VYYCVRHGNFGNSYISYWAYWGQGTLV TVSSGGGGGGGGGGGSGTQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTS GNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPELL GGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEAL HNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGT HTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNIKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPGK	(SEQ ID NO: 4730) <i>No nuc. seq. available</i>
		NA		

MA_83- iPS:2768823 F3_CCx_I2C0x_scFc_(G5K)_translati on	AA	MDMRVPAQLLGLLLWLRGARCQVQLVQSGAEVKKPGASVKVSKAS GYSFTGYMHVVRQAPGQCLEWMGRINPNSGDTHY A QKFQGRVMTMR DTSISTAYMELSRRLRSDDTAVYYCARGLGISFFDYWGQTLVTVSSGGG GSGGGSGGGGSDIQTQSPSSLASVGDVTTTCRASQGISNYLA WYQQ KPGKVPKLLIY AASTLQSGVPSRFSGSGGTDFTLT TISSLQPEDVATYYCQ KYNSAPWTFGCGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQGT LTVSSGGGGSGGGGSGGSGTQTVVTQEPSTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDGV EVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHE ALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGSD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFCSCVMHEALHNHYTQKSLSLSPGK
	(SEQ ID NO: 4731)	No nuc. seq. available
	NA	

MA_83- F3x_12C0x_scFc_(B9A)_translation iPS:2768824	AA	MDMRVPAQLLGLLLWLRGARCQVQLVQSGAEVKKPGASVKVSKAS GYSFTGYMHVVRQAPGQGLEWMGRINPNSGDTHY A QKFQGRVTMT DTSISTAYMELSRRLRSDDTAVYYCARGLGISFFDYWGQGLVTVSSGGG GSGGGSGGGGSDIQTQSPSSLSASVGDVTTTCRASQGISNYLA WYQQ KPGKVPKLLIY AASTLQSGVPSRFSGSGGTDFTLTISLQPEDVATYYCQ KYNSAPWTFGQGTKLEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAAS GFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDS KNTAYLQMNNLKTEDAVYYCVRHGNFGNSYISYWAYWGQGL VTVSSGGGGSGGGGSGGQTVVTQEPSTVSPGGTVTLTCGSSTGAV TSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLGGKAAL TLS GVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPCPAPE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVVDGV EVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHE ALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGGGGGGGGSD KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEK TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVVFSCVMHEALHNHYTQKSLSLSPGK
(SEQ ID NO: 4732)	NA	No nuc. seq. available

MA_84- iPS:2768825	G10_CC_x_I2C0x_scFc_(H9O)_transl ation	AA	MDMRVPAQLLGLLLWLRGARCQVQLQESGGLVKPSQTLSTCTVSG DSISRDPPYWSWIRQHPGKCLEWIGYIYYSGSTYYNPSLKSRTISVDTSK NQFSLKLSSTAAADTAVYYCARDKLWFGKLNYYGMDVWVGQGTIVTV SSGGGGGGGGGGSDIVMTQTPLSLPTPGEPAISCRSSQSLLSHNSG YNYLDWYLQKPGQSPQLLIYLGSNRASGVDRFSGSGGTDTLTKISRVE AEDVGYYCMQALQTPITFGCGTRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTIVTVSSGGGGGGGGGGGSGTQVVTQEPSTVSPGGTIVTL TCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG GGGGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK	(SEQ ID NO: 4733)	No nuc. seq. available
		NA			

iPS:2768826 MA_84- G10x_I2C0x_scFc_(Y4W)_translation	AA	MDMRVPAQLLGLLLWLRGARCQVQLQESGGLVKPSQTLSTCTVSG DSISRDPPYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRTISVDTSK NQFSLKLSVTAADTAVYYCARDKLWFGKLNYYGMDVWVGQGTTVTV SSGGGGGGGGGGGGSDIVMTQTPLSLPTPGEPAISCRSSQSLLSHNSG YNYLDWYLQKPGQSPQLLIYLGSNRASGVDRFSGSGGTDFTLKISRVE AEDVGVYYCMQALQTPITFGQGRLEIKSGGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYA DSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLLVTVSSGGGGGGGGGGGSGTQVVTQEPSTVSPGGTIVTL TCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTFKFLAPGTPARFSGSLLG GKAALTLGVQPEDEAEYCVLWYSNRWVFGGGTKLTVLGGGGDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSLTVLHQDWLNGKEYKCK VSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGN VFSCVMHEALHNHYTQKSLSLSPGKGGGGGGGGGGGGGGGGGGGGGG GGGGGGGSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL TVDKSRWQQGNVVFSCVMHEALHNHYTQKSLSLSPGK
		(SEQ ID NO: 4734)

Table 47
BTE-scFc Fv#1 (MAGEB2) VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276879 7	MA_12- E12_CC_x_I2C0x_scFc_(E9U)_translat ion	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RASQSVSSSYLA (SEQ ID NO: 4735)	GASSRAT (SEQ ID NO: 4831)	QQYANSPLT (SEQ ID NO: 4927)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276879 8	MA_12- E12x_I2C0x_scFc_(W1U)_translatio n	AA	RASQSVSSSYLA (SEQ ID NO: 4736)	GASSRAT (SEQ ID NO: 4832)	QQYANSPLT (SEQ ID NO: 4928)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276879 9	MA_13- D8_CCx_I2C0x_scFc_(U7V)_translat ion	AA	RASQGISNYLA (SEQ ID NO: 4737)	AASTLQS (SEQ ID NO: 4833)	QQSYSTPPT (SEQ ID NO: 4929)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880 0	MA_13- D8x_I2C0x_scFc_(M7M)_translation	AA	RASQGISNYLA (SEQ ID NO: 4738)	AASTLQS (SEQ ID NO: 4834)	QQSYSTPPT (SEQ ID NO: 4930)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880 1	MA_24- C9_CCx_I2C0x_scFc_(I2U)_translati on	AA	KSSQSLYSSNQKNYLA (SEQ ID NO: 4739)	WASTRES (SEQ ID NO: 4835)	QQYYSYPYT (SEQ ID NO: 4931)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880 3	MA_24- C9x_I2C0x_scFc_(L9V)_translation	AA	KSSQSLYSSNQKNYLA (SEQ ID NO: 4740)	WASTRES (SEQ ID NO: 4836)	QQYYSYPYT (SEQ ID NO: 4932)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880 5	MA_24- G6_CCx_I2C0x_scFc_(B1D)_translati on	AA	SASSNVNYIH (SEQ ID NO: 4741)	DTSKLAP (SEQ ID NO: 4837)	HQWSSYPPT (SEQ ID NO: 4933)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880 7	MA_24- G6x_I2C0x_scFc_(F1M)_translation	AA	SASSNVNYIH (SEQ ID NO: 4742)	DTSKLAP (SEQ ID NO: 4838)	HQWSSYPPT (SEQ ID NO: 4934)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880 9	MA_31- H8_CCx_I2C0x_scFc_(K4E)_translat ion	AA	RASGNHNYLA (SEQ ID NO: 4743)	NAKTLAG (SEQ ID NO: 4839)	QHHYGTPLT (SEQ ID NO: 4935)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276881 1	MA_31- H8x_I2C0x_scFc_(F9Z)_translation	AA	RASGNHNYLA (SEQ ID NO: 4744)	NAKTLAG (SEQ ID NO: 4840)	QHHYGTPLT (SEQ ID NO: 4936)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276881 3	MA_32- A8_CCx_I2C0x_scFc_(A9E)_translat ion	AA	RSSQSLYSSNGYNYVD (SEQ ID NO: 4745)	LGSNRAS (SEQ ID NO: 4841)	MQALQTPPT (SEQ ID NO: 4937)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available

iPS:276881	MA_32-A8_x_I2C0x_scFc_(G6J)_translation	AA	RSSQSLLYSNGYNYVD (SEQ ID NO: 4746) <i>No nuc. seq. available</i>	LGSNRAS (SEQ ID NO: 4842) <i>No nuc. seq. available</i>		MQALQTPPT (SEQ ID NO: 4938) <i>No nuc. seq. available</i>
iPS:276881	MA_48-D12_CCx_I2C0x_scFc_(M9T)_translation	NA				
iPS:276881	MA_48-D12x_I2C0x_scFc_(R9D)_translation	AA	RASQSVSSSYLA (SEQ ID NO: 4747) <i>No nuc. seq. available</i>	GASSRAT (SEQ ID NO: 4843) <i>No nuc. seq. available</i>		QQYGSSTPLT (SEQ ID NO: 4939) <i>No nuc. seq. available</i>
iPS:276881	MA_48-D12x_I2C0x_scFc_(R9D)_translation	NA				
iPS:276881	MA_50-D9_CCx_I2C0x_scFc_(K6S)_translation	AA	RASQSVSSSYLA (SEQ ID NO: 4748) <i>No nuc. seq. available</i>	GASSRAT (SEQ ID NO: 4844) <i>No nuc. seq. available</i>		QQYGSSTPLT (SEQ ID NO: 4940) <i>No nuc. seq. available</i>
iPS:276881	MA_50-D9x_I2C0x_scFc_(K6S)_translation	NA				
iPS:276881	MA_50-D9x_I2C0x_scFc_(A4U)_translation	AA	RSSQSLHNSGNYNYLD (SEQ ID NO: 4749) <i>No nuc. seq. available</i>	LGSNRAS (SEQ ID NO: 4845) <i>No nuc. seq. available</i>		MQALQTPPT (SEQ ID NO: 4941) <i>No nuc. seq. available</i>
iPS:276881	MA_50-D9x_I2C0x_scFc_(A4U)_translation	NA				
iPS:276881	MA_78-A6_CCx_I2C0x_scFc_(D8Z)_translation	AA	RSSQSLHNSGNYNYLD (SEQ ID NO: 4750) <i>No nuc. seq. available</i>	LGSNRAS (SEQ ID NO: 4846) <i>No nuc. seq. available</i>		MQALQTPPT (SEQ ID NO: 4942) <i>No nuc. seq. available</i>
iPS:276881	MA_78-A6x_I2C0x_scFc_(D8Z)_translation	NA				
iPS:276881	MA_78-A6x_I2C0x_scFc_(K6P)_translation	AA	RSSQSLLYSNGYNYVD (SEQ ID NO: 4751) <i>No nuc. seq. available</i>	LGSNRAS (SEQ ID NO: 4847) <i>No nuc. seq. available</i>		MQALQTPPT (SEQ ID NO: 4943) <i>No nuc. seq. available</i>
iPS:276881	MA_78-A6x_I2C0x_scFc_(K6P)_translation	NA				
iPS:276881	MA_79-E3_CC_x_I2C0x_scFc_(E2Y)_translation	AA	RSSQSLLYSNGYNYVD (SEQ ID NO: 4752) <i>No nuc. seq. available</i>	LGSNRAS (SEQ ID NO: 4848) <i>No nuc. seq. available</i>		MQALQTPPT (SEQ ID NO: 4944) <i>No nuc. seq. available</i>
iPS:276881	MA_79-E3_CC_x_I2C0x_scFc_(E2Y)_translation	NA				
iPS:276881	MA_79-E3_CC_x_I2C0x_scFc_(E2Y)_translation	AA	RASQSVSSSYLA (SEQ ID NO: 4753) <i>No nuc. seq. available</i>	AASSLOS (SEQ ID NO: 4849) <i>No nuc. seq. available</i>		QQSYRTPTT (SEQ ID NO: 4945) <i>No nuc. seq. available</i>
iPS:276881	MA_79-E3x_I2C0x_scFc_(N4F)_translation	NA				
iPS:276881	MA_79-E3x_I2C0x_scFc_(N4F)_translation	AA	RASQSVSSSYLA (SEQ ID NO: 4754) <i>No nuc. seq. available</i>	AASSLOS (SEQ ID NO: 4850) <i>No nuc. seq. available</i>		QQSYRTPTT (SEQ ID NO: 4946) <i>No nuc. seq. available</i>
iPS:276881	MA_83-F3_CCx_I2C0x_scFc_(G5K)_translation	NA				
iPS:276881	MA_83-F3x_I2C0x_scFc_(G5K)_translation	AA	RASQSVSSSYLA (SEQ ID NO: 4755) <i>No nuc. seq. available</i>	AASTLOS (SEQ ID NO: 4851) <i>No nuc. seq. available</i>		QKYNAPWT (SEQ ID NO: 4947) <i>No nuc. seq. available</i>
iPS:276881	MA_83-F3x_I2C0x_scFc_(B9A)_translation	NA				
iPS:276881	MA_83-F3x_I2C0x_scFc_(B9A)_translation	AA	RASQSVSSSYLA (SEQ ID NO: 4756) <i>No nuc. seq. available</i>	AASTLOS (SEQ ID NO: 4852) <i>No nuc. seq. available</i>		QKYNAPWT (SEQ ID NO: 4948) <i>No nuc. seq. available</i>
iPS:276881	MA_84-G10_CC_x_I2C0x_scFc_(H9O)_translation	NA				
iPS:276881	MA_84-G10x_I2C0x_scFc_(H9O)_translation	AA	RSSQSLHNSGNYNYLD (SEQ ID NO: 4757) <i>No nuc. seq. available</i>	LGSNRAS (SEQ ID NO: 4853) <i>No nuc. seq. available</i>		MQALQTPPT (SEQ ID NO: 4949) <i>No nuc. seq. available</i>
iPS:276881	MA_84-G10x_I2C0x_scFc_(H9O)_translation	NA				

iPS:276882	MA_04- G10x_I2C0x_scFc_(Y4W)_translation	AA	RSSQLLHNSGNYLD (SEQ ID NO: 4758)	LGSNRAS (SEQ ID NO: 4854)	MQALQTPIT (SEQ ID NO: 4950)
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Table 48
BiTE-scFc Fv#1 (MAGEB2) VH CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276879	MA_12- E12_CC_x_I2C0x_scFc_(E9U)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	TYSMN (SEQ ID NO: 4759)	SISSSSVYVYADSVKG (SEQ ID NO: 4855)	DRIAVATYFDN (SEQ ID NO: 4951)
iPS:276879	MA_12- E12x_I2C0x_scFc_(W1U)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	TYSMN (SEQ ID NO: 4760)	SISSSSVYVYADSVKG (SEQ ID NO: 4856)	DRIAVATYFDN (SEQ ID NO: 4952)
iPS:276879	MA_13- D8_CCx_I2C0x_scFc_(U7V)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	SFAMS (SEQ ID NO: 4761)	AISGGSTYYADSVKG (SEQ ID NO: 4857)	MVTPDYVYDMV (SEQ ID NO: 4953)
iPS:276880	MA_13- D8x_I2C0x_scFc_(M7M)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	SFAMS (SEQ ID NO: 4762)	AISGGSTYYADSVKG (SEQ ID NO: 4858)	MVTPDYVYDMV (SEQ ID NO: 4954)
iPS:276880	MA_24- C9_CCx_I2C0x_scFc_(I2U)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	KSWMN (SEQ ID NO: 4763)	RIYPGDGDTNYNGKFKG (SEQ ID NO: 4859)	DGVFYAPLAY (SEQ ID NO: 4955)
iPS:276880	MA_24- C9x_I2C0x_scFc_(L9Y)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	KSWMN (SEQ ID NO: 4764)	RIYPGDGDTNYNGKFKG (SEQ ID NO: 4860)	DGVFYAPLAY (SEQ ID NO: 4956)
iPS:276880	MA_24- G6_CCx_I2C0x_scFc_(B1D)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	KSWMN (SEQ ID NO: 4765)	RVWPGDGDITTYNEKFKG (SEQ ID NO: 4861)	GNYFGSSEAYFDY (SEQ ID NO: 4957)
iPS:276880	MA_24- G6x_I2C0x_scFc_(F1M)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	KSWMN (SEQ ID NO: 4766)	RVWPGDGDITTYNEKFKG (SEQ ID NO: 4862)	GNYFGSSEAYFDY (SEQ ID NO: 4958)
iPS:276880	MA_31- H8_CCx_I2C0x_scFc_(K4E)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	SSWMN (SEQ ID NO: 4767)	RIYPGDGDTNYNGKFKD (SEQ ID NO: 4863)	RQLNHVAFMDY (SEQ ID NO: 4959)
iPS:276881	MA_31- H8x_I2C0x_scFc_(F9Z)_translation	NA	No data seq available	No data seq available	No data seq available
		AA	SSWMN (SEQ ID NO: 4768)	RIYPGDGDTNYNGKFKD (SEQ ID NO: 4864)	RQLNHVAFMDY (SEQ ID NO: 4960)
MA_33		NA	No data seq available	No data seq available	No data seq available

iPS:276881 3	MA_32- A8_CCx_I2C0x_scFe_(A9E)_translation	AA	SYDIN (SEQ ID NO: 4769) <i>No nuc. seq. available</i>	WMNPNSGNTGYAOKFQG (SEQ ID NO: 4865) <i>No nuc. seq. available</i>	GGYNSNGDYGMVDV (SEQ ID NO: 4961) <i>No nuc. seq. available</i>
iPS:276881 4	MA_32- A8_x_I2C0x_scFe_(G6J)_translation	NA			
iPS:276881 5	MA_48- D12_CCx_I2C0x_scFe_(M9T)_translation	AA	SYDIN (SEQ ID NO: 4770) <i>No nuc. seq. available</i>	WMNPNSGNTGYAOKFQG (SEQ ID NO: 4866) <i>No nuc. seq. available</i>	GGYNSNGDYGMVDV (SEQ ID NO: 4962) <i>No nuc. seq. available</i>
iPS:276881 6	MA_48- D12x_I2C0x_scFe_(R9D)_translation	AA	SYRMH (SEQ ID NO: 4771) <i>No nuc. seq. available</i>	VISYDGGNKYYADSVKVG (SEQ ID NO: 4867) <i>No nuc. seq. available</i>	EQWPNYYYGMVDV (SEQ ID NO: 4963) <i>No nuc. seq. available</i>
iPS:276881 7	MA_50- D9_CCx_I2C0x_scFe_(K6S)_translation	NA			
iPS:276881 8	MA_50- D9x_I2C0x_scFe_(A4U)_translation	AA	SYRMH (SEQ ID NO: 4772) <i>No nuc. seq. available</i>	VISYDGGNKYYADSVKVG (SEQ ID NO: 4868) <i>No nuc. seq. available</i>	EQWPNYYYGMVDV (SEQ ID NO: 4964) <i>No nuc. seq. available</i>
iPS:276881 9	MA_78- A6_CCx_I2C0x_scFe_(D8Z)_translation	NA			
iPS:276882 0	MA_78- A6x_I2C0x_scFe_(K6P)_translation	AA	SYDIN (SEQ ID NO: 4773) <i>No nuc. seq. available</i>	RTYRSKWYNDYAVSVKS (SEQ ID NO: 4869) <i>No nuc. seq. available</i>	EILWFGKLNYYYGMVDV (SEQ ID NO: 4965) <i>No nuc. seq. available</i>
iPS:276882 1	MA_79- E3_CCx_I2C0x_scFe_(E2Y)_translation	NA			
iPS:276882 2	MA_79- E3x_I2C0x_scFe_(N4F)_translation	AA	SYDIN (SEQ ID NO: 4774) <i>No nuc. seq. available</i>	RTYRSKWYNDYAVSVKS (SEQ ID NO: 4870) <i>No nuc. seq. available</i>	EILWFGKLNYYYGMVDV (SEQ ID NO: 4966) <i>No nuc. seq. available</i>
iPS:276882 3	MA_83- F3_CCx_I2C0x_scFe_(G5K)_translation	AA	GYAWN (SEQ ID NO: 4775) <i>No nuc. seq. available</i>	EINHRGSTNYPNPSLKS (SEQ ID NO: 4871) <i>No nuc. seq. available</i>	GGYSDGYDYGMVDV (SEQ ID NO: 4967) <i>No nuc. seq. available</i>
iPS:276882 4	MA_83- F3x_I2C0x_scFe_(B9A)_translation	NA			
		AA	GYAWN (SEQ ID NO: 4776) <i>No nuc. seq. available</i>	EINHRGSTNYPNPSLKS (SEQ ID NO: 4872) <i>No nuc. seq. available</i>	GGYSDGYDYGMVDV (SEQ ID NO: 4968) <i>No nuc. seq. available</i>
		NA			
		AA	SFAMS (SEQ ID NO: 4777) <i>No nuc. seq. available</i>	AISGGGTTYADSVKVG (SEQ ID NO: 4873) <i>No nuc. seq. available</i>	MVTPDYDYGMVDV (SEQ ID NO: 4969) <i>No nuc. seq. available</i>
		NA			
		AA	SFAMS (SEQ ID NO: 4778) <i>No nuc. seq. available</i>	AISGGGTTYADSVKVG (SEQ ID NO: 4874) <i>No nuc. seq. available</i>	MVTPDYDYGMVDV (SEQ ID NO: 4970) <i>No nuc. seq. available</i>
		NA			
		AA	GYAWN (SEQ ID NO: 4779) <i>No nuc. seq. available</i>	RINPSGDTHYAOKFQG (SEQ ID NO: 4875) <i>No nuc. seq. available</i>	GLGISFFDY (SEQ ID NO: 4971) <i>No nuc. seq. available</i>
		NA			
		AA	GYAWN (SEQ ID NO: 4780) <i>No nuc. seq. available</i>	RINPSGDTHYAOKFQG (SEQ ID NO: 4876) <i>No nuc. seq. available</i>	GLGISFFDY (SEQ ID NO: 4972) <i>No nuc. seq. available</i>
		NA			

iPS:276882	MA_84- G10_CC_x_I2C0x_scFc_(H9Q)_translation	AA	RDPPYWS (SEQ ID NO: 4781) <i>No nuc. seq. available</i>	YIYSGSTYNNPSLKS (SEQ ID NO: 4877) <i>No nuc. seq. available</i>	DKLWFCKLNYYYGMDV (SEQ ID NO: 4973) <i>No nuc. seq. available</i>
iPS:276882	MA_84- G10x_I2C0x_scFc_(Y4W)_translation	AA	RDPPYWS (SEQ ID NO: 4782)	YIYSGSTYNNPSLKS (SEQ ID NO: 4878)	DKLWFCKLNYYYGMDV (SEQ ID NO: 4974)

Table 49
BiTE-scFc Fv#2 (CD3) VL CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276879	MA_12- E12_CC_x_I2C0x_scFc_(E9U)_translation	NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>
iPS:276879	MA_12- E12x_I2C0x_scFc_(W1U)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4783) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4879) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4975) <i>No nuc. seq. available</i>
iPS:276879	MA_13- D8_CCx_I2C0x_scFc_(U7V)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4784) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4880) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4976) <i>No nuc. seq. available</i>
iPS:276880	MA_13- D8x_I2C0x_scFc_(M7M)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4785) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4881) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4977) <i>No nuc. seq. available</i>
iPS:276880	MA_24- C9_CCx_I2C0x_scFc_(I2U)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4786) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4882) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4978) <i>No nuc. seq. available</i>
iPS:276880	MA_24- C9x_I2C0x_scFc_(L9Y)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4787) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4883) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4979) <i>No nuc. seq. available</i>
iPS:276880	MA_24- G6_CCx_I2C0x_scFc_(B1D)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4788) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4884) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4980) <i>No nuc. seq. available</i>
iPS:276880	MA_24- G6x_I2C0x_scFc_(F1M)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4789) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4885) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4981) <i>No nuc. seq. available</i>
iPS:276880	MA_31- H8_CCx_I2C0x_scFc_(K4E)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4790) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4886) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4982) <i>No nuc. seq. available</i>
iPS:276880	MA_31- H8x_I2C0x_scFc_(K4E)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4791) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4887) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4983) <i>No nuc. seq. available</i>
		NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>

iPS:276881	MA_31-H8x_I2C0x_scFc_(F9Z)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4792) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4888) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4984) <i>No nuc. seq. available</i>
iPS:276881	MA_32-A8_CCx_I2C0x_scFc_(A9E)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4793) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4889) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4985) <i>No nuc. seq. available</i>
iPS:276881	MA_32-A8_x_I2C0x_scFc_(G6J)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4794) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4890) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4986) <i>No nuc. seq. available</i>
iPS:276881	MA_48-D12_CCx_I2C0x_scFc_(M9D)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4795) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4891) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4987) <i>No nuc. seq. available</i>
iPS:276881	MA_48-D12x_I2C0x_scFc_(R9D)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4796) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4892) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4988) <i>No nuc. seq. available</i>
iPS:276881	MA_50-D9_CCx_I2C0x_scFc_(K6S)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4797) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4893) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4989) <i>No nuc. seq. available</i>
iPS:276881	MA_50-D9x_I2C0x_scFc_(A4U)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4798) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4894) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4990) <i>No nuc. seq. available</i>
iPS:276881	MA_78-A6_CCx_I2C0x_scFc_(D8Z)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4799) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4895) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4991) <i>No nuc. seq. available</i>
iPS:276882	MA_78-A6x_I2C0x_scFc_(K6P)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4800) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4896) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4992) <i>No nuc. seq. available</i>
iPS:276882	MA_79-E3_CC_x_I2C0x_scFc_(E2Y)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4801) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4897) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4993) <i>No nuc. seq. available</i>
iPS:276882	MA_79-E3x_I2C0x_scFc_(N4F)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4802) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4898) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4994) <i>No nuc. seq. available</i>
iPS:276882	MA_83-F3_CCx_I2C0x_scFc_(G5K)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4803) <i>No nuc. seq. available</i>	GTKFLAP (SEQ ID NO: 4899) <i>No nuc. seq. available</i>	VLWYSNRWV (SEQ ID NO: 4995) <i>No nuc. seq. available</i>
		NA	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>	<i>No nuc. seq. available</i>

iPS:276882	MA_83-F3x_I2C0x_scFc_(B9A)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4804)	GTKFLAP (SEQ ID NO: 4900)	VLWYSNRWV (SEQ ID NO: 4996)
iPS:276882	MA_84-G10_CC_x_I2C0x_scFc_(H9O)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276882	MA_84-G10x_I2C0x_scFc_(Y4W)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4805)	GTKFLAP (SEQ ID NO: 4901)	VLWYSNRWV (SEQ ID NO: 4997)
iPS:276882	MA_84-G10x_I2C0x_scFc_(Y4W)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276882	MA_84-G10x_I2C0x_scFc_(Y4W)_translation	AA	GSSTGAVTSGNYPN (SEQ ID NO: 4806)	GTKFLAP (SEQ ID NO: 4902)	VLWYSNRWV (SEQ ID NO: 4998)

Table 50
BiTE-scFc Fv#2 (CD3) VH CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:276879	MA_12-E12_CC_x_I2C0x_scFc_(E9U)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276879	MA_12-E12x_I2C0x_scFc_(W1U)_translation	AA	KYAMN (SEQ ID NO: 4807)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4903)	HGNFGNSYISYWAY (SEQ ID NO: 4999)
iPS:276879	MA_12-E12x_I2C0x_scFc_(W1U)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276879	MA_13-D8_CCx_I2C0x_scFc_(U7V)_translation	AA	KYAMN (SEQ ID NO: 4808)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4904)	HGNFGNSYISYWAY (SEQ ID NO: 5000)
iPS:276879	MA_13-D8x_I2C0x_scFc_(M7M)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880	MA_13-D8x_I2C0x_scFc_(M7M)_translation	AA	KYAMN (SEQ ID NO: 4809)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4905)	HGNFGNSYISYWAY (SEQ ID NO: 5001)
iPS:276880	MA_13-D8x_I2C0x_scFc_(M7M)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880	MA_24-C9_CCx_I2C0x_scFc_(I2U)_translation	AA	KYAMN (SEQ ID NO: 4810)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4906)	HGNFGNSYISYWAY (SEQ ID NO: 5002)
iPS:276880	MA_24-C9x_I2C0x_scFc_(L9V)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880	MA_24-C9x_I2C0x_scFc_(L9V)_translation	AA	KYAMN (SEQ ID NO: 4811)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4907)	HGNFGNSYISYWAY (SEQ ID NO: 5003)
iPS:276880	MA_24-G6_CCx_I2C0x_scFc_(B1D)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880	MA_24-G6x_I2C0x_scFc_(F1M)_translation	AA	KYAMN (SEQ ID NO: 4812)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4908)	HGNFGNSYISYWAY (SEQ ID NO: 5004)
iPS:276880	MA_24-G6x_I2C0x_scFc_(F1M)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880	MA_24-G6x_I2C0x_scFc_(F1M)_translation	AA	KYAMN (SEQ ID NO: 4813)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4909)	HGNFGNSYISYWAY (SEQ ID NO: 5005)
iPS:276880	MA_24-G6x_I2C0x_scFc_(F1M)_translation	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
iPS:276880	MA_24-G6x_I2C0x_scFc_(F1M)_translation	AA	KYAMN (SEQ ID NO: 4814)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4910)	HGNFGNSYISYWAY (SEQ ID NO: 5006)
MA_24		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available

iPS:276880	MA_31- H8_CCx_I2C0x_scFc_(K4E)_translation	AA	KYAMN (SEQ ID NO: 4815) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4911) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5007) <i>No nuc. seq. available</i>
iPS:276881	MA_31- H8x_I2C0x_scFc_(F9Z)_translation	NA			
iPS:276881	MA_32- A8_CCx_I2C0x_scFc_(A9E)_translation	AA	KYAMN (SEQ ID NO: 4816) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4912) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5008) <i>No nuc. seq. available</i>
iPS:276881	MA_32- A8_CCx_I2C0x_scFc_(A9E)_translation	NA			
iPS:276881	MA_32- A8x_I2C0x_scFc_(G6J)_translation	AA	KYAMN (SEQ ID NO: 4817) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4913) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5009) <i>No nuc. seq. available</i>
iPS:276881	MA_32- A8x_I2C0x_scFc_(G6J)_translation	NA			
iPS:276881	MA_48- D12_CCx_I2C0x_scFc_(M9T)_translation	AA	KYAMN (SEQ ID NO: 4818) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4914) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5010) <i>No nuc. seq. available</i>
iPS:276881	MA_48- D12x_I2C0x_scFc_(R9D)_translation	NA			
iPS:276881	MA_48- D12x_I2C0x_scFc_(R9D)_translation	AA	KYAMN (SEQ ID NO: 4819) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4915) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5011) <i>No nuc. seq. available</i>
iPS:276881	MA_50- D9_CCx_I2C0x_scFc_(K6S)_translation	NA			
iPS:276881	MA_50- D9x_I2C0x_scFc_(A4U)_translation	AA	KYAMN (SEQ ID NO: 4820) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4916) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5012) <i>No nuc. seq. available</i>
iPS:276881	MA_50- D9x_I2C0x_scFc_(A4U)_translation	NA			
iPS:276881	MA_50- D9x_I2C0x_scFc_(A4U)_translation	AA	KYAMN (SEQ ID NO: 4821) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4917) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5013) <i>No nuc. seq. available</i>
iPS:276881	MA_78- A6_CCx_I2C0x_scFc_(D8Z)_translation	NA			
iPS:276881	MA_78- A6x_I2C0x_scFc_(K6P)_translation	AA	KYAMN (SEQ ID NO: 4822) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4918) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5014) <i>No nuc. seq. available</i>
iPS:276881	MA_78- A6x_I2C0x_scFc_(K6P)_translation	NA			
iPS:276881	MA_78- A6x_I2C0x_scFc_(K6P)_translation	AA	KYAMN (SEQ ID NO: 4823) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4919) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5015) <i>No nuc. seq. available</i>
iPS:276881	MA_79- E3_CCx_I2C0x_scFc_(E2Y)_translation	NA			
iPS:276881	MA_79- E3x_I2C0x_scFc_(N4F)_translation	AA	KYAMN (SEQ ID NO: 4824) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4920) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5016) <i>No nuc. seq. available</i>
iPS:276881	MA_79- E3x_I2C0x_scFc_(N4F)_translation	NA			
iPS:276881	MA_79- E3x_I2C0x_scFc_(N4F)_translation	AA	KYAMN (SEQ ID NO: 4825) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4921) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5017) <i>No nuc. seq. available</i>
iPS:276881	MA_79- E3x_I2C0x_scFc_(N4F)_translation	NA			
iPS:276881	MA_79- E3x_I2C0x_scFc_(N4F)_translation	AA	KYAMN (SEQ ID NO: 4826) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4922) <i>No nuc. seq. available</i>	HGFGNSYISYWAY (SEQ ID NO: 5018) <i>No nuc. seq. available</i>
iPS:276881	MA_79- E3x_I2C0x_scFc_(N4F)_translation	NA			

iPS:276882 3	MA_83- F3_CC_x_I2C0x_scFc_(G5K)_translation	AA	KYAMN (SEQ ID NO: 4827) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4923) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 5019) <i>No nuc. seq. available</i>
iPS:276882 4	MA_83- F3x_I2C0x_scFc_(B9A)_translation	AA	KYAMN (SEQ ID NO: 4828) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4924) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 5020) <i>No nuc. seq. available</i>
iPS:276882 5	MA_84- G10_CC_x_I2C0x_scFc_(H9O)_translation	AA	KYAMN (SEQ ID NO: 4829) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4925) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 5021) <i>No nuc. seq. available</i>
iPS:276882 6	MA_84- G10x_I2C0x_scFc_(Y4W)_translation	AA	KYAMN (SEQ ID NO: 4830)	RIRSKYNNYATYYADSVKD (SEQ ID NO: 4926)	HGNFGNSYISYWAY (SEQ ID NO: 5022)

Table 51
BTE-scf Variable Region Sequences

IPKs	Ab	Type	IC Region	Full (N-CDR3)	HC Region	IC Region	HC Region	IC Region	HC Region
		NA	1-255-557	1-255-557-557	1-255-557-557	1-255-557-557	1-255-557-557	1-255-557-557	1-255-557-557
IPKs:276879	MA_12- E12_C1_x_12C0x_scfE_(E9U)_trans lation	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276879	MA_12- E12_C12C0x_scfE_(N1U)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276880	MA_12- D8_C12C0x_scfE_(U7V)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276880	MA_12- D8_C12C0x_scfE_(N7M)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276880	MA_24- C3_C12C0x_scfE_(L9V)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276880	MA_24- C3_C12C0x_scfE_(F1M)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276880	MA_24- C3_C12C0x_scfE_(K4E)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276880	MA_24- C3_C12C0x_scfE_(F9Z)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276881	MA_31- H8_C12C0x_scfE_(A9E)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276881	MA_32- A8_C12C0x_scfE_(G6J)_transla tion	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557
IPKs:276881	MA_48- D12_C12C0x_scfE_(M9T)_trans lation	AA	1-255-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557	1-255-557-557-557

PS-27681	MA_48- D1X_120x_sFC_(R9D)_translation	NA	53,666,366,367,368,369,370,371,372,373,374,375,376,377,378,379,380,381,382,383,384,385,386,387,388,389,390,391,392,393,394,395,396,397,398,399,400,401,402,403,404,405,406,407,408,409,410,411,412,413,414,415,416,417,418,419,420,421,422,423,424,425,426,427,428,429,430,431,432,433,434,435,436,437,438,439,440,441,442,443,444,445,446,447,448,449,450,451,452,453,454,455,456,457,458,459,460,461,462,463,464,465,466,467,468,469,470,471,472,473,474,475,476,477,478,479,480,481,482,483,484,485,486,487,488,489,490,491,492,493,494,495,496,497,498,499,500,501,502,503,504,505,506,507,508,509,510,511,512,513,514,515,516,517,518,519,520,521,522,523,524,525,526,527,528,529,530,531,532,533,534,535,536,537,538,539,540,541,542,543,544,545,546,547,548,549,550,551,552,553,554,555,556,557,558,559,560,561,562,563,564,565,566,567,568,569,570,571,572,573,574,575,576,577,578,579,580,581,582,583,584,585,586,587,588,589,590,591,592,593,594,595,596,597,598,599,600,601,602,603,604,605,606,607,608,609,610,611,612,613,614,615,616,617,618,619,620,621,622,623,624,625,626,627,628,629,630,631,632,633,634,635,636,637,638,639,640,641,642,643,644,645,646,647,648,649,650,651,652,653,654,655,656,657,658,659,660,661,662,663,664,665,666,667,668,669,670,671,672,673,674,675,676,677,678,679,680,681,682,683,684,685,686,687,688,689,690,691,692,693,694,695,696,697,698,699,700,701,702,703,704,705,706,707,708,709,710,711,712,713,714,715,716,717,718,719,720,721,722,723,724,725,726,727,728,729,730,731,732,733,734,735,736,737,738,739,740,741,742,743,744,745,746,747,748,749,750,751,752,753,754,755,756,757,758,759,760,761,762,763,764,765,766,767,768,769,770,771,772,773,774,775,776,777,778,779,780,781,782,783,784,785,786,787,788,789,790,791,792,793,794,795,796,797,798,799,800,801,802,803,804,805,806,807,808,809,810,811,812,813,814,815,816,817,818,819,820,821,822,823,824,825,826,827,828,829,830,831,832,833,834,835,836,837,838,839,840,841,842,843,844,845,846,847,848,849,850,851,852,853,854,855,856,857,858,859,860,861,862,863,864,865,866,867,868,869,870,871,872,873,874,875,876,877,878,879,880,881,882,883,884,885,886,887,888,889,890,891,892,893,894,895,896,897,898,899,900,901,902,903,904,905,906,907,908,909,910,911,912,913,914,915,916,917,918,919,920,921,922,923,924,925,926,927,928,929,930,931,932,933,934,935,936,937,938,939,940,941,942,943,944,945,946,947,948,949,950,951,952,953,954,955,956,957,958,959,960,961,962,963,964,965,966,967,968,969,970,971,972,973,974,975,976,977,978,979,980,981,982,983,984,985,986,987,988,989,990,991,992,993,994,995,996,997,998,999,1000,1001,1002,1003,1004,1005,1006,1007,1008,1009,1010,1011,1012,1013,1014,1015,1016,1017,1018,1019,1020,1021,1022,1023,1024,1025,1026,1027,1028,1029,1030,1031,1032,1033,1034,1035,1036,1037,1038,1039,1040,1041,1042,1043,1044,1045,1046,1047,1048,1049,1050,1051,1052,1053,1054,1055,1056,1057,1058,1059,1060,1061,1062,1063,1064,1065,1066,1067,1068,1069,1070,1071,1072,1073,1074,1075,1076,1077,1078,1079,1080,1081,1082,1083,1084,1085,1086,1087,1088,1089,1090,1091,1092,1093,1094,1095,1096,1097,1098,1099,1100,1101,1102,1103,1104,1105,1106,1107,1108,1109,1110,1111,1112,1113,1114,1115,1116,1117,1118,1119,1120,1121,1122,1123,1124,1125,1126,1127,1128,1129,1130,1131,1132,1133,1134,1135,1136,1137,1138,1139,1140,1141,1142,1143,1144,1145,1146,1147,1148,1149,1150,1151,1152,1153,1154,1155,1156,1157,1158,1159,1160,1161,1162,1163,1164,1165,1166,1167,1168,1169,1170,1171,1172,1173,1174,1175,1176,1177,1178,1179,1180,1181,1182,1183,1184,1185,1186,1187,1188,1189,1190,1191,1192,1193,1194,1195,1196,1197,1198,1199,1200,1201,1202,1203,1204,1205,1206,1207,1208,1209,1210,1211,1212,1213,1214,1215,1216,1217,1218,1219,1220,1221,1222,1223,1224,1225,1226,1227,1228,1229,1230,1231,1232,1233,1234,1235,1236,1237,1238,1239,1240,1241,1242,1243,1244,1245,1246,1247,1248,1249,1250,1251,1252,1253,1254,1255,1256,1257,1258,1259,1260,1261,1262,1263,1264,1265,1266,1267,1268,1269,1270,1271,1272,1273,1274,1275,1276,1277,1278,1279,1280,1281,1282,1283,1284,1285,1286,1287,1288,1289,1290,1291,1292,1293,1294,1295,1296,1297,1298,1299,
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SADPA VARIABLE	GeneLine	K_PRI	SEQ ID NO.	K_CDR1	SEQ ID NO.	K_PRI2	SEQ ID NO.	K_CDR2	SEQ ID NO.	K_PRI3	SEQ ID NO.	K_CDR3	SEQ ID NO.	K_PRI4	SEQ ID NO.
PS-768074	YK3A27JRK4 non prev	BLVLTQVTPALGAFERBPAISG	5120	RAS - QVDS - ----G1A	5243	WTQVQFQAPRLLLT	5166	Q - ----ASBPAT	5489	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5612	QVQV - ----SGLT	5753	FOQVTVLRLA	5860
PS-768075	YK3A27JRK4	BLVLTQVTPALGAFERBPAISG	5121	RAS - QVDS - ----G1A	5244	WTQVQFQAPRLLLT	5167	Q - ----ASBPAT	5490	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5613	QVQV - ----SGLT	5754	FOQVTVLRLA	5861
PS-768076	YK3A27JRK4	BLVLTQVTPALGAFERBPAISG	5122	RAS - QVDS - ----G1A	5245	WTQVQFQAPRLLLT	5168	Q - ----ASBPAT	5491	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5614	QVQV - ----SGLT	5757	FOQVTVLRLA	5862
PS-768077	YK3A27JRK4 prev	BLVLTQVTPALGAFERBPAISG	5123	RAS - QVDS - ----G1A	5246	WTQVQFQAPRLLLT	5169	Q - ----ASBPAT	5492	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5615	QVQV - ----SGLT	5758	FOQVTVLRLA	5863
PS-768078	YK3A27JRK4 prev	BLVLTQVTPALGAFERBPAISG	5124	RAS - QVDS - ----G1A	5247	WTQVQFQAPRLLLT	5170	A - ----ASBPAT	5493	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5616	QVQV - ----SGLT	5759	FOQVTVLRLA	5864
PS-768079	YK3A20JRK1	QVLTQVTPSSLASGVQRVTTC	5125	RAS - QVDS - ----G1A	5248	WTQVQFQAPRLLLT	5171	A - ----ASBPAT	5494	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5617	QVQV - ----SGLT	5760	FOQVTVLRLA	5865
PS-768080	YK3A20JRK1 prev	QVLTQVTPSSLASGVQRVTTC	5126	RAS - QVDS - ----G1A	5249	WTQVQFQAPRLLLT	5172	A - ----ASBPAT	5495	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5618	QVQV - ----SGLT	5761	FOQVTVLRLA	5866
PS-768081	YK3A09JRK2	BLVLTQVTPALGAFERBPAISG	5127	RBS - QVLAISQVQVLA	5250	WTQVQFQAPRLLLT	5173	N - ----ASTBES	5496	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5619	QVQV - ----SGLT	5762	FOQVTVLRLA	5867
PS-768082	YK3A09JRK2	BLVLTQVTPALGAFERBPAISG	5128	RBS - QVLAISQVQVLA	5251	WTQVQFQAPRLLLT	5174	N - ----ASTBES	5497	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5620	QVQV - ----SGLT	5763	FOQVTVLRLA	5868
PS-768083	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5129	RBS - QVLAISQVQVLA	5252	WTQVQFQAPRLLLT	5175	N - ----ASTBES	5498	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5621	QVQV - ----SGLT	5764	FOQVTVLRLA	5869
PS-768084	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5130	RBS - QVLAISQVQVLA	5253	WTQVQFQAPRLLLT	5176	N - ----ASTBES	5499	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5622	QVQV - ----SGLT	5765	FOQVTVLRLA	5870
PS-768085	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5131	RBS - QVLAISQVQVLA	5254	WTQVQFQAPRLLLT	5177	N - ----ASTBES	5500	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5623	QVQV - ----SGLT	5766	FOQVTVLRLA	5871
PS-768086	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5132	RBS - QVLAISQVQVLA	5255	WTQVQFQAPRLLLT	5178	N - ----ASTBES	5501	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5624	QVQV - ----SGLT	5767	FOQVTVLRLA	5872
PS-768087	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5133	RBS - QVLAISQVQVLA	5256	WTQVQFQAPRLLLT	5179	N - ----ASTBES	5502	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5625	QVQV - ----SGLT	5768	FOQVTVLRLA	5873
PS-768088	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5134	RBS - QVLAISQVQVLA	5257	WTQVQFQAPRLLLT	5180	N - ----ASTBES	5503	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5626	QVQV - ----SGLT	5769	FOQVTVLRLA	5874
PS-768089	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5135	RBS - QVLAISQVQVLA	5258	WTQVQFQAPRLLLT	5181	N - ----ASTBES	5504	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5627	QVQV - ----SGLT	5770	FOQVTVLRLA	5875
PS-768090	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5136	RBS - QVLAISQVQVLA	5259	WTQVQFQAPRLLLT	5182	N - ----ASTBES	5505	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5628	QVQV - ----SGLT	5771	FOQVTVLRLA	5876
PS-768091	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5137	RBS - QVLAISQVQVLA	5260	WTQVQFQAPRLLLT	5183	N - ----ASTBES	5506	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5629	QVQV - ----SGLT	5772	FOQVTVLRLA	5877
PS-768092	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5138	RBS - QVLAISQVQVLA	5261	WTQVQFQAPRLLLT	5184	N - ----ASTBES	5507	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5630	QVQV - ----SGLT	5773	FOQVTVLRLA	5878
PS-768093	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5139	RBS - QVLAISQVQVLA	5262	WTQVQFQAPRLLLT	5185	Q - ----ASTBES	5508	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5631	QVQV - ----SGLT	5774	FOQVTVLRLA	5879
PS-768094	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5140	RBS - QVLAISQVQVLA	5263	WTQVQFQAPRLLLT	5186	Q - ----ASTBES	5509	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5632	QVQV - ----SGLT	5775	FOQVTVLRLA	5880
PS-768095	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5141	RBS - QVLAISQVQVLA	5264	WTQVQFQAPRLLLT	5187	L - ----GEMDAS	5510	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5633	QVQV - ----SGLT	5776	FOQVTVLRLA	5881
PS-768096	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5142	RBS - QVLAISQVQVLA	5265	WTQVQFQAPRLLLT	5188	L - ----GEMDAS	5511	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5634	QVQV - ----SGLT	5777	FOQVTVLRLA	5882
PS-768097	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5143	RBS - QVLAISQVQVLA	5266	WTQVQFQAPRLLLT	5189	L - ----GEMDAS	5512	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5635	QVQV - ----SGLT	5778	FOQVTVLRLA	5883
PS-768098	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5144	RBS - QVLAISQVQVLA	5267	WTQVQFQAPRLLLT	5190	L - ----GEMDAS	5513	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5636	QVQV - ----SGLT	5779	FOQVTVLRLA	5884
PS-768099	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5145	RBS - QVLAISQVQVLA	5268	WTQVQFQAPRLLLT	5191	L - ----GEMDAS	5514	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5637	QVQV - ----SGLT	5780	FOQVTVLRLA	5885
PS-768100	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5146	RBS - QVLAISQVQVLA	5269	WTQVQFQAPRLLLT	5192	L - ----GEMDAS	5515	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5638	QVQV - ----SGLT	5781	FOQVTVLRLA	5886
PS-768101	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5147	RBS - QVLAISQVQVLA	5270	WTQVQFQAPRLLLT	5193	L - ----GEMDAS	5516	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5639	QVQV - ----SGLT	5782	FOQVTVLRLA	5887
PS-768102	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5148	RBS - QVLAISQVQVLA	5271	WTQVQFQAPRLLLT	5194	L - ----GEMDAS	5517	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5640	QVQV - ----SGLT	5783	FOQVTVLRLA	5888
PS-768103	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5149	RBS - QVLAISQVQVLA	5272	WTQVQFQAPRLLLT	5195	A - ----ASTBES	5518	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5641	QVQV - ----SGLT	5784	FOQVTVLRLA	5889
PS-768104	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5150	RBS - QVLAISQVQVLA	5273	WTQVQFQAPRLLLT	5196	A - ----ASTBES	5519	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5642	QVQV - ----SGLT	5785	FOQVTVLRLA	5890
PS-768105	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5151	RBS - QVLAISQVQVLA	5274	WTQVQFQAPRLLLT	5197	A - ----ASTBES	5520	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5643	QVQV - ----SGLT	5786	FOQVTVLRLA	5891
PS-768106	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5152	RBS - QVLAISQVQVLA	5275	WTQVQFQAPRLLLT	5198	A - ----ASTBES	5521	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5644	QVQV - ----SGLT	5787	FOQVTVLRLA	5892
PS-768107	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5153	RBS - QVLAISQVQVLA	5276	WTQVQFQAPRLLLT	5199	A - ----ASTBES	5522	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5645	QVQV - ----SGLT	5788	FOQVTVLRLA	5893
PS-768108	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5154	RBS - QVLAISQVQVLA	5277	WTQVQFQAPRLLLT	5200	A - ----ASTBES	5523	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5646	QVQV - ----SGLT	5789	FOQVTVLRLA	5894
PS-768109	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5155	RBS - QVLAISQVQVLA	5278	WTQVQFQAPRLLLT	5201	L - ----GEMDAS	5524	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5647	QVQV - ----SGLT	5790	FOQVTVLRLA	5895
PS-768110	YK3A09JRK2 prev	BLVLTQVTPALGAFERBPAISG	5156	RBS - QVLAISQVQVLA	5279	WTQVQFQAPRLLLT	5202	L - ----GEMDAS	5525	QVQVRFSSGSD - TQPTATISLIRBPAIVYC	5648	QVQV - ----SGLT	5791	FOQVTVLRLA	5896

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GA, 34- PS:76805 Perf	GA, CC, DCN, eFC, (B0), translation on Perf	5182	5315	WYDQAPQDZLAWA	5438	ALBEXK--NB-DATYTAQSD-YGO	5561	EPT18B0SGSINTALQWMLABTGAUYVYOR	5685	HEPFBMS-----Y18NWL	5817	MOQZHTVPSSE	5932
GA, 35- PS:76807 Perf	GA, CC, DCN, eFC, (J0), translation on Perf	5183	5316	WYDQAPQDZLAWA	5439	ALBEXK--NB-DATYTAQSD-YGO	5562	EPT18B0SGSINTALQWMLABTGAUYVYOR	5686	HEPFBMS-----Y18NWL	5818	MOQZHTVPSSE	5933
GA, 36- PS:76809 Perf	GA, CC, DCN, eFC, (K0), translation on Perf	5184	5317	WYDQAPQDZLAWA	5440	ALBEXK--NB-DATYTAQSD-YGO	5563	EPT18B0SGSINTALQWMLABTGAUYVYOR	5687	HEPFBMS-----Y18NWL	5819	MOQZHTVPSSE	5934
GA, 37- PS:76811 Perf	GA, CC, DCN, eFC, (L0), translation on Perf	5185	5318	WYDQAPQDZLAWA	5441	ALBEXK--NB-DATYTAQSD-YGO	5564	EPT18B0SGSINTALQWMLABTGAUYVYOR	5688	HEPFBMS-----Y18NWL	5820	MOQZHTVPSSE	5935
GA, 38- PS:76813 Perf	GA, CC, DCN, eFC, (M0), translation on Perf	5186	5319	WYDQAPQDZLAWA	5442	ALBEXK--NB-DATYTAQSD-YGO	5565	EPT18B0SGSINTALQWMLABTGAUYVYOR	5689	HEPFBMS-----Y18NWL	5821	MOQZHTVPSSE	5936
GA, 39- PS:76815 Perf	GA, CC, DCN, eFC, (N0), translation on Perf	5187	5320	WYDQAPQDZLAWA	5443	ALBEXK--NB-DATYTAQSD-YGO	5566	EPT18B0SGSINTALQWMLABTGAUYVYOR	5690	HEPFBMS-----Y18NWL	5822	MOQZHTVPSSE	5937
GA, 40- PS:76817 Perf	GA, CC, DCN, eFC, (O0), translation on Perf	5188	5321	WYDQAPQDZLAWA	5444	ALBEXK--NB-DATYTAQSD-YGO	5567	EPT18B0SGSINTALQWMLABTGAUYVYOR	5691	HEPFBMS-----Y18NWL	5823	MOQZHTVPSSE	5938
GA, 41- PS:76819 Perf	GA, CC, DCN, eFC, (P0), translation on Perf	5189	5322	WYDQAPQDZLAWA	5445	ALBEXK--NB-DATYTAQSD-YGO	5568	EPT18B0SGSINTALQWMLABTGAUYVYOR	5692	HEPFBMS-----Y18NWL	5824	MOQZHTVPSSE	5939
GA, 42- PS:76821 Perf	GA, CC, DCN, eFC, (Q0), translation on Perf	5200	5323	WYDQAPQDZLAWA	5446	ALBEXK--NB-DATYTAQSD-YGO	5569	EPT18B0SGSINTALQWMLABTGAUYVYOR	5693	HEPFBMS-----Y18NWL	5825	MOQZHTVPSSE	5940
GA, 43- PS:76823 Perf	GA, CC, DCN, eFC, (R0), translation on Perf	5201	5324	WYDQAPQDZLAWA	5447	ALBEXK--NB-DATYTAQSD-YGO	5570	EPT18B0SGSINTALQWMLABTGAUYVYOR	5694	HEPFBMS-----Y18NWL	5826	MOQZHTVPSSE	5941
GA, 44- PS:76825 Perf	GA, CC, DCN, eFC, (S0), translation on Perf	5202	5325	WYDQAPQDZLAWA	5448	ALBEXK--NB-DATYTAQSD-YGO	5571	EPT18B0SGSINTALQWMLABTGAUYVYOR	5695	HEPFBMS-----Y18NWL	5827	MOQZHTVPSSE	5942
GA, 45- PS:76827 Perf	GA, CC, DCN, eFC, (T0), translation on Perf	5203	5326	WYDQAPQDZLAWA	5449	ALBEXK--NB-DATYTAQSD-YGO	5572	EPT18B0SGSINTALQWMLABTGAUYVYOR	5696	HEPFBMS-----Y18NWL	5828	MOQZHTVPSSE	5943
GA, 46- PS:76829 Perf	GA, CC, DCN, eFC, (U0), translation on Perf	5204	5327	WYDQAPQDZLAWA	5450	ALBEXK--NB-DATYTAQSD-YGO	5573	EPT18B0SGSINTALQWMLABTGAUYVYOR	5697	HEPFBMS-----Y18NWL	5829	MOQZHTVPSSE	5944
GA, 47- PS:76831 Perf	GA, CC, DCN, eFC, (V0), translation on Perf	5205	5328	WYDQAPQDZLAWA	5451	ALBEXK--NB-DATYTAQSD-YGO	5574	EPT18B0SGSINTALQWMLABTGAUYVYOR	5698	HEPFBMS-----Y18NWL	5830	MOQZHTVPSSE	5945
GA, 48- PS:76833 Perf	GA, CC, DCN, eFC, (W0), translation on Perf	5206	5329	WYDQAPQDZLAWA	5452	ALBEXK--NB-DATYTAQSD-YGO	5575	EPT18B0SGSINTALQWMLABTGAUYVYOR	5699	HEPFBMS-----Y18NWL	5831	MOQZHTVPSSE	5946
GA, 49- PS:76835 Perf	GA, CC, DCN, eFC, (X0), translation on Perf	5207	5330	WYDQAPQDZLAWA	5453	ALBEXK--NB-DATYTAQSD-YGO	5576	EPT18B0SGSINTALQWMLABTGAUYVYOR	5700	HEPFBMS-----Y18NWL	5832	MOQZHTVPSSE	5947
GA, 50- PS:76837 Perf	GA, CC, DCN, eFC, (Y0), translation on Perf	5208	5331	WYDQAPQDZLAWA	5454	ALBEXK--NB-DATYTAQSD-YGO	5577	EPT18B0SGSINTALQWMLABTGAUYVYOR	5701	HEPFBMS-----Y18NWL	5833	MOQZHTVPSSE	5948
GA, 51- PS:76839 Perf	GA, CC, DCN, eFC, (Z0), translation on Perf	5209	5332	WYDQAPQDZLAWA	5455	ALBEXK--NB-DATYTAQSD-YGO	5578	EPT18B0SGSINTALQWMLABTGAUYVYOR	5702	HEPFBMS-----Y18NWL	5834	MOQZHTVPSSE	5949
GA, 52- PS:76841 Perf	GA, CC, DCN, eFC, (A0), translation on Perf	5210	5333	WYDQAPQDZLAWA	5456	ALBEXK--NB-DATYTAQSD-YGO	5579	EPT18B0SGSINTALQWMLABTGAUYVYOR	5703	HEPFBMS-----Y18NWL	5835	MOQZHTVPSSE	5950
GA, 53- PS:76843 Perf	GA, CC, DCN, eFC, (B0), translation on Perf	5211	5334	WYDQAPQDZLAWA	5457	ALBEXK--NB-DATYTAQSD-YGO	5580	EPT18B0SGSINTALQWMLABTGAUYVYOR	5704	HEPFBMS-----Y18NWL	5836	MOQZHTVPSSE	5951
GA, 54- PS:76845 Perf	GA, CC, DCN, eFC, (C0), translation on Perf	5212	5335	WYDQAPQDZLAWA	5458	ALBEXK--NB-DATYTAQSD-YGO	5581	EPT18B0SGSINTALQWMLABTGAUYVYOR	5705	HEPFBMS-----Y18NWL	5837	MOQZHTVPSSE	5952
GA, 55- PS:76847 Perf	GA, CC, DCN, eFC, (D0), translation on Perf	5213	5336	WYDQAPQDZLAWA	5459	ALBEXK--NB-DATYTAQSD-YGO	5582	EPT18B0SGSINTALQWMLABTGAUYVYOR	5706	HEPFBMS-----Y18NWL	5838	MOQZHTVPSSE	5953
GA, 56- PS:76849 Perf	GA, CC, DCN, eFC, (E0), translation on Perf	5214	5337	WYDQAPQDZLAWA	5460	ALBEXK--NB-DATYTAQSD-YGO	5583	EPT18B0SGSINTALQWMLABTGAUYVYOR	5707	HEPFBMS-----Y18NWL	5839	MOQZHTVPSSE	5954
GA, 57- PS:76851 Perf	GA, CC, DCN, eFC, (F0), translation on Perf	5215	5338	WYDQAPQDZLAWA	5461	ALBEXK--NB-DATYTAQSD-YGO	5584	EPT18B0SGSINTALQWMLABTGAUYVYOR	5708	HEPFBMS-----Y18NWL	5840	MOQZHTVPSSE	5955
GA, 58- PS:76853 Perf	GA, CC, DCN, eFC, (G0), translation on Perf	5216	5339	WYDQAPQDZLAWA	5462	ALBEXK--NB-DATYTAQSD-YGO	5585	EPT18B0SGSINTALQWMLABTGAUYVYOR	5709	HEPFBMS-----Y18NWL	5841	MOQZHTVPSSE	5956
GA, 59- PS:76855 Perf	GA, CC, DCN, eFC, (H0), translation on Perf	5217	5340	WYDQAPQDZLAWA	5463	ALBEXK--NB-DATYTAQSD-YGO	5586	EPT18B0SGSINTALQWMLABTGAUYVYOR	5710	HEPFBMS-----Y18NWL	5842	MOQZHTVPSSE	5957
GA, 60- PS:76857 Perf	GA, CC, DCN, eFC, (I0), translation on Perf	5218	5341	WYDQAPQDZLAWA	5464	ALBEXK--NB-DATYTAQSD-YGO	5587	EPT18B0SGSINTALQWMLABTGAUYVYOR	5711	HEPFBMS-----Y18NWL	5843	MOQZHTVPSSE	5958
GA, 61- PS:76859 Perf	GA, CC, DCN, eFC, (J0), translation on Perf	5219	5342	WYDQAPQDZLAWA	5465	ALBEXK--NB-DATYTAQSD-YGO	5588	EPT18B0SGSINTALQWMLABTGAUYVYOR	5712	HEPFBMS-----Y18NWL	5844	MOQZHTVPSSE	5959
GA, 62- PS:76861 Perf	GA, CC, DCN, eFC, (K0), translation on Perf	5220	5343	WYDQAPQDZLAWA	5466	ALBEXK--NB-DATYTAQSD-YGO	5589	EPT18B0SGSINTALQWMLABTGAUYVYOR	5713	HEPFBMS-----Y18NWL	5845	MOQZHTVPSSE	5960
GA, 63- PS:76863 Perf	GA, CC, DCN, eFC, (L0), translation on Perf	5221	5344	WYDQAPQDZLAWA	5467	ALBEXK--NB-DATYTAQSD-YGO	5590	EPT18B0SGSINTALQWMLABTGAUYVYOR	5714	HEPFBMS-----Y18NWL	5846	MOQZHTVPSSE	5961
GA, 64- PS:76865 Perf	GA, CC, DCN, eFC, (M0), translation on Perf	5222	5345	WYDQAPQDZLAWA	5468	ALBEXK--NB-DATYTAQSD-YGO	5591	EPT18B0SGSINTALQWMLABTGAUYVYOR	5715	HEPFBMS-----Y18NWL	5847	MOQZHTVPSSE	5962
GA, 65- PS:76867 Perf	GA, CC, DCN, eFC, (N0), translation on Perf	5223	5346	WYDQAPQDZLAWA	5469	ALBEXK--NB-DATYTAQSD-YGO	5592	EPT18B0SGSINTALQWMLABTGAUYVYOR	5716	HEPFBMS-----Y18NWL	5848	MOQZHTVPSSE	5963
GA, 66- PS:76869 Perf	GA, CC, DCN, eFC, (O0), translation on Perf	5224	5347	WYDQAPQDZLAWA	5470	ALBEXK--NB-DATYTAQSD-YGO	5593	EPT18B0SGSINTALQWMLABTGAUYVYOR	5717	HEPFBMS-----Y18NWL	5849	MOQZHTVPSSE	5964
GA, 67- PS:76871 Perf	GA, CC, DCN, eFC, (P0), translation on Perf	5225	5348	WYDQAPQDZLAWA	5471	ALBEXK--NB-DATYTAQSD-YGO	5594	EPT18B0SGSINTALQWMLABTGAUYVYOR	5718	HEPFBMS-----Y18NWL	5850	MOQZHTVPSSE	5965
GA, 68- PS:76873 Perf	GA, CC, DCN, eFC, (Q0), translation on Perf	5226	5349	WYDQAPQDZLAWA	5472	ALBEXK--NB-DATYTAQSD-YGO	5595	EPT18B0SGSINTALQWMLABTGAUYVYOR	5719	HEPFBMS-----Y18NWL	5851	MOQZHTVPSSE	5966
GA, 69- PS:76875 Perf	GA, CC, DCN, eFC, (R0), translation on Perf	5227	5350	WYDQAPQDZLAWA	5473	ALBEXK--NB-DATYTAQSD-YGO	5596	EPT18B0SGSINTALQWMLABTGAUYVYOR	5720	HEPFBMS-----Y18NWL	5852	MOQZHTVPSSE	5967
GA, 70- PS:76877 Perf	GA, CC, DCN, eFC, (S0), translation on Perf	5228	5351	WYDQAPQDZLAWA	5474	ALBEXK--NB-DATYTAQSD-YGO	5597	EPT18B0SGSINTALQWMLABTGAUYVYOR	5721	HEPFBMS-----Y18NWL	5853	MOQZHTVPSSE	5968

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GeneLine		H_F1	H_CDR1	H_F2	H_CDR2	H_F3	H_CDR3	H_F4
PS-270881	MA_76	6097	6221	6343	6446	6589	6713	6837
9	Ad_CCG_12CG_eFC_10R21_transition							
PS-270882	MA_76	6098	6221	6344	6447	6590	6714	6838
8	Ad_CCG_12CG_eFC_10R21_transition							
PS-270883	MA_76	6100	6222	6346	6449	6592	6716	6840
3	Ad_CCG_12CG_eFC_10R21_transition							
PS-270884	MA_76	6101	6224	6347	6470	6593	6717	6841
4	Ad_CCG_12CG_eFC_10R21_transition							
PS-270885	MA_76	6103	6226	6349	6472	6595	6720	6843
5	Ad_CCG_12CG_eFC_10R21_transition							
PS-270886	MA_76	6104	6227	6350	6473	6596	6721	6844
6	Ad_CCG_12CG_eFC_10R21_transition							

Table 54
scFv Full Sequences

iPS#	Ab	Type	scFv
iPS:586556	17724-C9	NA	GAGGTGCAGCTGCTCGAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGG GCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTACGCATTCAAGTAAGT CCTGGATGAAGTGGGTGAAGCAGAGGCCCTGGAAGGGTCTTGAGTGGA TTGGACGGATTATCCTGGAGATGGAGATACTAACTACAATGGGAAGTT CAAGGGCAAGCCGCACTGACTGCAGACAAATCCTCCACACAGCCAA CATGCAACTCAAC
			(SEQ ID NO: 6845) EVQLLEQSGPELVKPGASVKISCKASGYAFKSWMNWVKQRPKGLEWIG RIYPGDGDTNNGKFKGKAALTADKSSNTANMQLNSLTSEDSAVYFCARD GVFYAPLAYWGQGLVTVSSGGGGGGGGGGSELVMTQSPSSLA VSV GEKITMSCKSSQSLLYSSNQKNYLAWYQQKPGQSPKLLIYWASTRESGVDP RFTGSGSGTDFTLTISSVKAEDLAVYYCQYYSYPYTFGGGTKLELK
		AA	(SEQ ID NO: 6846)

iPS:586558	17724-G6	NA	GAGGTGCAGCTGCTCGAGCAGTCTGGACCTGAGTTGGTGAAGCCTGGG GCCTCAGTGAAGATTTCCTGCAAGGCTTCTGACTACACATTCAAGTAAGT CCTGGATGAAGTGGTGAAGCAGAGGCCCTGGAGAGGCTCTTGAGTGGA TTGGACGTGTTTGGCCTGGAGATGGAGATACTACGTACAATGAGAAAGTT CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGGACAGCCTA CATGCAACTCAGC
			(SEQ ID NO: 6847)
		AA	EVQLLEQSGPELVKPGASVKISCKASDYTFKSWMNWVKQRPGEGLWIG RVWPGDGDITTYNEKFKGKATLTADKSSRTAYMQLSSLTSEDSAVYFCARG NYFGSSEAYFDYWGGQTRVTVSSGGGGGGGGGGSELVLTQSPAIMS ASPGQKVITITCSASSNVNIHWYQQKLGSPPKLWIYDTSKLAPGVPARFSG SGSGTSYSLTISSMEAEADAASYFCHQWSSYPPTFGSGTKLEIK
			(SEQ ID NO: 6848)

iPS:586574	17731-H8	NA	GAGGTGCAGCTGCTCGAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGG GCCTCAGTGAAAGATTTCCTGCAAGGCTTCTGGCTACGCATTCACTAGCT CCTGGATGAAGTGGTGAAGCAGAGGCCCTGGAAAGGCTCTTGAAGTGA TTGGACGGATTATCCTGGAGATGGAGATACTAACTACAATGGGAAGTT CAAGGACAAGGCCACACTGACTGCAGACAAATCCTCCACACACAGCCTA CATGCAACTCAGC
		AA	(SEQ ID NO: 6849) EVQLLEQSGPELVKPGASVKISCKASGYAFSSWMNWVKQRPKGLEWIG RIYPGDGDTNNGKFKDKATLTADKSSNTAYMQLSSLTSEDSAVYFCARR QLNHVFAMDYWGQGTSTVSSGGGGGGGGGGSELQMTQSPASLSA SVGETVTITCRASGNIHNYLAWYQQKQKSPQLLVYNAKTLAGGVPSRFS GSGSGTQFSLKINSIQPEDFGSYQCQHHYGTPLTFGAGTKLELK (SEQ ID NO: 6850)

iPS:586576	17732-A8	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACCAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGGCTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
		AA	(SEQ ID NO: 6851) EVQLLESGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR GGYSNGYDYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQSP LSPVSPGEPASISCRSSQSLLYSNGYNVVDWYLYQKPGQSPQLLIYLGSNRA SGVPDRFSGSGGTDFTLKISKVEAEDVGVYYCMQALQTPPTFGQGTGLEI K (SEQ ID NO: 6852)

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iPS:587871	17745-E5	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCTGAGGTGAAGAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAAACACAGGCTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
			(SEQ ID NO: 6853)
		AA	EVQLLESGAEVKKPGASVKVSKKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR GGGYSYGIDYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQSP LSPVTPGEPASISCRSSQSLLYSNGYHYLDWYLYQKPGQSPQLLIYLSIRAS GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQPLQTPPTFGPGTKLEIK
			(SEQ ID NO: 6854)

iPS:587897	17745-E8	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAAGCCTTCGGAG ACCCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTTCAGTGGTTACTA CTGGAACCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAAATCAGTCATAGTGGAAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCAGCATATCAGGAGACACGTCCTCCAAAGAACCAAGTCTCCTGAA GCTGAGCTCTGTG
		AA	(SEQ ID NO: 6855) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGEL SHSGSTNYPNPSLKSRVSIISGDTSKNQFSLKLSSTAAADTAVYYCARGGGYS HGVDYGMVDVWGQGTTVTVSSGGGGGGGGGGSELVMTQTPLSLPVI PGEPASISCRSSQSLLYSNGYNYLDWYLNKPGQSPQLLIYLGSKRASGVDPDR FSGSGGTDFTLKISRVEAEDVGYYCMQGTWPRFTFGQGTKVEIK (SEQ ID NO: 6856)

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iPS:587885	17745-G8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGATATCACATACGACGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6857)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGDITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHLR YFDWPLDYWGQGTLVTVSSGGGGGGGGGGSELTLTQSPGTLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQYGRSLFTFGPGTKVDIK
			(SEQ ID NO: 6858)

iPS:588445	17748-D12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCCGTAGCTATCG CATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGC AGTTATATCATATGATGGAGGTAATAATACTATGCAGACTCCCGTGAAG GGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 6859) EVQLLESGGVVQPGRLRLSCAASGFTFRSYRMHWVRQAPKGLEWVA VISYDGGNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARE QWPNYYYGMDVWGQGTTVTVSSGGGGGGGGGGSELVLTQSPGTL LSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFS GSGSGTDFTLTISRLEPEDFAVYYCQYQGSSPLTFGGGTKLEIK (SEQ ID NO: 6860)

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iPS:589113	17753-F4	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTTCAGTGGTTACTA CTGGAAGTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
			(SEQ ID NO: 6861)
iPS:589113	17753-F4	AA	EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGEL NHSGSTNYNPSLKSRTISVDTSKNQFSLKLSSTVTAADTA VYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSEL VMTQSPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDR FSGSGGTDFTLKISRVEAEDVGYYCYCMQALQTPFTFGPGTKVEIK
			(SEQ ID NO: 6862)

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iPS:590622	17771-D2	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCTCCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAGGGGCTGGAGTGGGTCTC AACTATTAGTGGTAGTGGTAGCACAGACTACGCAGACTCCCGTGAA GGCCCGGTTCACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 6863) EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGRGLEWVSTI SGSGGSTDYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK DGG SGWFPKLLHYGLDVWGQGT TVTSSGGGGSGGGGGSELQMTQSPS SVSASVGD RVTITCRASQGISSWLA WYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQA NSFPPTFGQGTKVEIK
			(SEQ ID NO: 6864)

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iPS:593066	17777-B4	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCTGCTGCTTCTGGATACACCTTCACCGGTTATG ATATCAACTGGGTGCGACAGGCCACTGGGCAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACCGTGGCACCCACAGGCTATGCACAGAAATTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
			(SEQ ID NO: 6865)
		AA	EVQLLESGAEVKKPGASVKVSCMASGYTFTGYDINWVRQATQGLEWMG WMNPNRGTTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR GGGYSYGYDYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQSP LSPVTPGEPASISCRSSQSLLYSNGYNLDWYLOKPGQSPQLLIYLGSNRA SGVPDRFSGSGGTDFTLKISRVEAEADVGVYYCMQALQTPLTFGGGTKVEI K
			(SEQ ID NO: 6866)

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iPS:593048	17777-C4	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGATTACACATACGACGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6867)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSDYTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHL RYSDWPLDYWGQGTLVTVSSGGGGGGGGGGSELVLTQSPGTLSLSP GERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSG SGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKLEIK
			(SEQ ID NO: 6868)

iPS:593044	17777-C5	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCCCTTCAGTGGTTACTA CTGGACCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCACAGTGGAAACCAACTACAATCCGTCCTCCCTCAAGAG TCGCGTCACCATGTCAGAAAGACACGGCCAAAGAACCAAGTTCTCCCTGAA GCTGAGCTCTGTG
		AA	(SEQ ID NO: 6869) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWTWIRQPPGKGLEWIGEI NHSGRNTYNPSLKSRVTMSEDTAKNQFSLKLSVTAADTAVYYCARGGGY SDGYDYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVLTQSPLSLPV SPGEPASISCRSSQLLYSNGYNYVDWYLQKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTWPLTFGGGGTKVDIK (SEQ ID NO: 6870)

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iPS:591971	17778-C9	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAAGCCTTCGGAG ACCCGTGTCCTCACCTGCGCTGTCTATGGTGGTCCCTCAGTGGTTACTA CTGGAACCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGATTGG GGAAATCAATCATCTGTTGGAAGCACCAACTACAACCCGTCCCTCAAGAG TCGAGTCACCATATCAGTAGACGCGTCCAAAGAACCAAGTTCTCCCTGAAG CTGAGTTCTGTG
			(SEQ ID NO: 6871)
		AA	EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGEL NHRGSTNYNPSLKSRLVTISVDASKNQSLKSSVTAADTAVYYCARGGGYS DGYDYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQTPLSLPV PGEPAISCRSSQSLLYSNGYNYVDWYLVKPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLKISKVEAEDVGYYCYCMQALQTPCSFGQGTKLEIK
			(SEQ ID NO: 6872)

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iPS:591906	17778-F1	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTTCAGTGGTACTA CTGGAAGTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGGAAAGCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
			(SEQ ID NO: 6873) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGE NHSGSTNYNPSLKSRTISVDTSKNQFSLKLSSTVAADTA VYYCARGGGYS YGYDYGMDVWQGTTTVSSGGGGGGGGGGSELVMTQSPSLPVT PGEPAISCRSSQRLLFNNGYHYLDWYLPKPGQSPQLLIYLGSNRASGVDPDR FSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPPTFGQGTKLEIK
			(SEQ ID NO: 6874)

iPS:591901	17778-H8	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGGTGTCTATGGTGGTCTTCAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATCGTGAAGCACCAACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACGCGTCCAAGAACCAGTTCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6875) EVQLLEWGAGLLKPSETLSLTGCVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHRGSTNYNPSLKSRTISVDASKNQSLKSSVTAADTAVYYCARGGGYS YGYDYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVLTQSPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDR FSGSGGTDFTLKISRVEAEDVGYYVYCMQALQTPPTFGQGQTKLEIK (SEQ ID NO: 6876)

iPS:593068	17779-D11	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGG CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTAGCAGCATACGACAGACTCCCGCGAA GGCCCGGTTCAACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTG CAATGAACAGC
		AA	(SEQ ID NO: 6877) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYGMVSRQAPGKGLEWVSA ISGSGGSTYYADSAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLV PDYYYGMDVWGQGTTVTVSSGGGGGGGGGGGSELQMTQSPSSLAS VGDRVITITCRASQSISSYLNWYQQKPGKAPKLLIYDASSLQSGVPSRFS SGTDFTLTISLQPEDFATYCYCQQSYRTPPTFGQGTKVDIK (SEQ ID NO: 6878)

iPS:593050	17779-E1	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGTGTCTATGGTGGTCTTCAAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6879) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRTISVDTSKNQFSLKLSSTAAADTA VYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSEL VLTQSPLSLPVT PGEPAISCRSSQSLLYSNGYHYLDWYLQKPGQSPQLLIFLGSNRASGVDR FSASRSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKVEIK (SEQ ID NO: 6880)

iPS:591857	17780-D12	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGGCTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
		AA	(SEQ ID NO: 6881) EVQLLESGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR GGYSNGYDYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQTP LSLPVSPGEPASISCRSSQSLLYSNGYNLDWYLQKPGQSPQLLIYLGSNRA SGVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTGLEIK (SEQ ID NO: 6882)

iPS:591851	17780-E6	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTCAGTGGTTACTA CTGGAACCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGGAAGCACACCTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGAAAGACACGTCACGGAACCAAGTCTCCCTGAAG CTGAGTTCTGTG
		AA	(SEQ ID NO: 6883) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGEI NHSGSTTYNPSLKSRTVISEDTSRNQFSLKLSSTVAADTAVYYCTRGGGYS HGYDYGMDVWGQGTTVTVSSGGGGGGGGGGSELVMTQSPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVDPDR FSGSGGTDFTLQISRVEAEDVGVYYCMQGTHTWPTFGPGTKVEIK (SEQ ID NO: 6884)

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iPS:591859	17781-B3	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGTGTCTATGGTGGTCTTCAGTGGTTTCTA CTGGAAGTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATCGTGAAGCACCAACTACAACCCGTCCCTCAAGAG TCGAGTCACCATATCAGTAGACGCGTCCAAGAACCAGTTCTCCCTGAAG CTGAGTTCTGTG
			(SEQ ID NO: 6885)
		AA	EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGFYWNWIRQPPGKGLEWIGEI NHRGSTNYNPSLKSRTISVDASKNQSLKSSVTAADTAVYYCARGGGYS DGYDYGMDVWGQGTTVTVSSGGGGGGGGGGSELVMTQSPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDR FSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPWTFGQGTKVDIK
			(SEQ ID NO: 6886)

iPS:591845	17781-H12	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTCAGTGGTTACTA CTGGAACCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAGTCATAGTGGAAGCACCAACTACAACCCGTCCTCAAGAG TCGAGTCAGCATATCAGGAGACACGTCCTCCAAAGAACCAAGTCTCCCTGAA GCTGAGCTCTGTG
		AA	(SEQ ID NO: 6887) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGEI SHSGSTNYPNPSLKSRVSIISGDTSKNQFSLKLSSTAAADTAVYYCARGGGYS HGYDYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQSPLSLPV PGEPAISICRSSLYSNGYNYVDWYVLPKPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLKISRVEAEDVGVYYCMQSIQLPWTFTGQGTKVDIK (SEQ ID NO: 6888)

iPS:593026	17783-C11	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTTCAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGGAAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACGCGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGTTCTGTG
		AA	(SEQ ID NO: 6889) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRTISVDASKNQFSLKSSVTAAATAVYYCARGGGYS DGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSELVLTQSPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPHLLIYLGSYRASGV PDR FSGSASGTDFTLKISRVEAEDVGVYYCMQGTWPLTFGGGTKLEIK (SEQ ID NO: 6890)

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iPS:593046	17783-G10	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCGTGTCTATGGTGGTCTTCAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCACTCATAGTGAAGCACCAACTACAACCCGTCCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCTGTTCTCCCTGAAG CTGAGCTCTGTG
			(SEQ ID NO: 6891)
		AA	EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI THSGSTNYNPSLKSRTVTISVDTSKNLFSKLSSVTADTA VYYCARGGGYS DGYDYGMDVWVGQGTTVTVSSGGGGGGGGGSEL VMTQTPLSLPVI PGEPAISCRSSQSLFSGNYNYLDWY LQKPGQSPQLLIYLVSKRASGV PDR FSGSGGTDFTLKISRVEAEDVGYYVCMQALQTPLTFGGGKLEIK
			(SEQ ID NO: 6892)

iPS:593062	17784-B9	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGGTAGCACATACGACAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACGCTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 6893) EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCAKVM PDYYMDMDVWGQGTTVTVSSGGGGGGGGGGGSELQMTQSPSSVSAS VGDRVITITCRASQSISSYLNWYQQKPKGKAPKLLIYAASSLQSGVPSRFS SGTDFTLTISLQPEDFAAYYCQQSYSTPPTFGQGTKVEIK (SEQ ID NO: 6894)

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iPS:593034	17784-C7	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGG CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGAAGGACTGGAGTGGTCTC AGCTATTAGTGGTAGTGGTAGCAGCATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6895)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYGMVSVVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYFCAKVMIT PDYYMDMDVWGQGTITVTVSSGGGGGGGGGGGGSELQMTQSPSSLSAS VGDRVITITCRASQGISNYLAWYQQKPGKVPKLLIYAASSLQSGVPSRFSGS GSGTDFLTITISLQPEDFATYYCQQSYSTPFTFGPGTKVEIK
			(SEQ ID NO: 6896)

iPS:593042	17784-C11	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTCAAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6897) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRTISVDTSKNQFSLKLSSTAAADTA VYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGSEL VMTQTPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDR FSGSGGTDFTLKISRVEAEDVGVYYCMQGTHTWPFTFPGTKVEIK (SEQ ID NO: 6898)

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iPS:593036	17784-G10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCCGTGATCC TTACTACTGGAGCTGGATCCGCCAGCACCCAGGAAAGGCCCTGGAGTG GATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCCC TGAAGCTGAGC
			(SEQ ID NO: 6899) EVQLLESGPGLVKPSQTLSTCTVSGDSISRDPYYWSWIRQHPGKGLEWIGY IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSVTAAADTAVYYCARDKLW FGKLNYYYGMDVWGQGTTVTVSSGGGGGGGGGGGGSELVMTQTPLSL PVTGPGEPAISCRSSQSLHNSNGYNLDWYLPKPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTREIK
		AA	(SEQ ID NO: 6900)

iPS:593018	17784-H5	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGTGTCTATGGTGGTCTTCAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATTTTCAGTTGACCCGTCACCAAGAACCCCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6901) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRTISVDPSKNQFSLKLSVTAADTAVYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSEL VLTQSPLSLPVT PGEPAISICRSSQSLFNGYYLWDWYLQKPGQSPQLLIYLGSNRASGVPR FSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPPTFGQGTKVEIK (SEQ ID NO: 6902)

iPS:593030	17785-D12	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGTGTCTATGGTGGTCTTCAAGTGGTTACTA CTGGAAGTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGGAAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6903) EVQLLEWGAGLLKPSSETLSLTCAVYGGSFSGYYWNWIRQPPGKGLEWIGEL NHSGSTNYNPSLKSRTISVDTSKNQFSLKLSSTVTAADTA VYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSEL VMTQSPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGV PDR FSGRSRGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKVDIK (SEQ ID NO: 6904)

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iPS:592136	17813-D8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCGGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTTTGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGGTAGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6905)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTSSFAMSWVRQAPGKLEWVSAI SGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTA EYYCAKMT PDYY YDM DVWGQGT TVTVSSGGGGGGGGGGSEL VMTQSPSSLSAS VGDRV TITCRASQGISNYLA WYQQKPGKVPKLLIYAAS TLQSGVPSRFSGS GSGTDFLTITISLQPEDFATYYCQQSYSTPPTFGQGTKVEIK
			(SEQ ID NO: 6906)

iPS:592170	17813-E3	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCCCTCAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCACAGTGGAAACCAACTACAATCCGTCCTCAAGAG TCGCGTCACCATGTCAGAAAGACACGGCCAAAGAACCAAGTCTCCCTGAA GCTGAGCTCTGTG
		AA	(SEQ ID NO: 6907) EVQLLEWGAGLLKPSETLSLTCAVYGGSLSGYYWSWIRQPPGKGLEWIGEI NHSGRNTYNPSLKSRTVMSEDTAKNQFSLKLSVTAADTAVYYCARGGGY SDGYDYGMDVWVGQGTTVTVSSGGGGGGGGGSELVMTQTPLSLPV TPGEPASISCRSSQLLYSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPD RFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQSLTFGGGTKLEIK (SEQ ID NO: 6908)

iPS:592166	17813-E5	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTCAAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGGAAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6909) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRTISVDTSKNQFSLKSSVTADTA VYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSEL VMTQTPLSLPVT PGEPAISCRSSQSLLYSNGYNYLDWYLQKPGQSPQLLIYLGSKRASGV PDR FSGSGGTDFTLKISRVEAEDVGYYVCMQALQTPLTFGGGKVDIK (SEQ ID NO: 6910)

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iPS:592154	17813-F1	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACCTGCGGTGTCTATGGTGGTCTTCAGTGGTTACTA CTGGAACCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATCGTGAAGCACCAACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACGCGTCCAAGAACCAGTTCTCCCTGAAG CTGAGTTCTGTG
			(SEQ ID NO: 6911) EVQLLEWGAGLLKPSETLSLTGCVYGGSFSGYYWNWIRQPPGKGLEWIGE NHRGSTNYNPSLKSRTISVDASKNQFSLKLSVTAADTAVYYCARGGGYS DGYDYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQSPLSLSVT PGEPAISICRSSRSLHNSGYNLYLDWYLQKPGQSPQLLIYLGSNRASGVADR FSGSGSIDFTLKISRVEAEDVGVYYCMQALQTPHFGGGTKVEIK
			AA (SEQ ID NO: 6912)

iPS:592150	17814-D9	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCTGAGGTGAAGAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGGCTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
		AA	(SEQ ID NO: 6913) EVQLLESGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR GGGYSYGIDYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQSP LSLSVTPGQPASISCKSSQSLLYSNGYNLDWYLPKPGQSPQLLIYLGSNRA SGVPDRFSGSGGTDFTLKISRVEAEADVGVYYCMQALQTPITFGQGTREIK
			(SEQ ID NO: 6914)

iPS:603175	18071-B1	NA	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTCAGCAGATACG GCATGGACTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG CACTTATATGGTATGATGGAAGTAATAATACTATGCAGACTCCGTGAA GGCCGATTCACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAATGAACAGC
		AA	(SEQ ID NO: 6915) EVQLLESGGTVVQPGRLRLSCAASGFTFSRYGMDWVRQAPKGLEWVA LIWYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARN YGSYSYGA YY YHGM DVWGQGT TVSSGGGGGGGGGGGGSELALTQ PPSVSGSPGQSITISCTGTSSDVGGYNVSWYQQHPGKAPKLMIEVSKRPS GVSNRFGSKSGNTASLTISGLQAEDADYYCSSYSSSTLVFGGGTKLTVL (SEQ ID NO: 6916)

iPS:603181	18071-C4	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCTGAGGTGAAGAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTACACGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGACTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
		AA	(SEQ ID NO: 6917) EVQLLESGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCVR GWGTYYYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQSPDS LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE SGVPDRFSGSGGTDFLTITISLQAEDVAVYYCQYYSTPWTFGQGTKVEI K (SEQ ID NO: 6918)

iPS:603133	18071-D4	NA	GAGGTGCAGCTGCTCGAGTCTGGGGCTGAGGTGAAGAACCCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGACTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
		AA	(SEQ ID NO: 6919) EVQLLESGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDTAVYYCAR GWGRYYSYGMDVWGQGTTVTVSSGGGGGGGGGGSELVMTQSPDS LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE SGVPDRFSGSGGTDFLTITISLQAEDVAVYYCQQYYSTPWTFGQGTKVEI K (SEQ ID NO: 6920)

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iPS:603207	18072-D6	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGATATCACATACGAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6921)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGDITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHLR YFDWPLDYWGQGTLVTVSSGGGGGGGGGGGSELTLTQSPGTLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASARATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQYGSSSLTFGGGTKVDIK
			(SEQ ID NO: 6922)

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iPS:603185	18072-G9			GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTGGCTATAG CATGAACCTGGGTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC GTCCATTAGTAGTAGTAGTACATATATACTACGCAGACTCAGTGAAG GGCCGCTTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGC AAATGAACAGC
		NA	(SEQ ID NO: 6923)	EVQLLESGGGLVKPGGSLRLSCAASGFTFSGYSMNWVRQAPGKLEWVSS ISSSSYIYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCVRSKA ARPDGMDVWGQGTTVTVSSGGGGGGGGGGGGSELVLTQPPSASGTP GQRITISCSGSSNIGSNYYVYQHLPGTAPKLLIYRNNQRPSPDRFSGS KSGTASLASGLRSEDEADYYCAAWDDSLSGVVFGGGKLTVL
		AA	(SEQ ID NO: 6924)	

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iPS:603201	18074-G12	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCTCCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGAGGGGCTGGAGTGGGTCTC AAGCATAACTATTACTGGTGTAGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAGAACACGCTGAATCTGC AAATGAACAGC
			(SEQ ID NO: 6925)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGRGLEWVSSI TITGGSTYADSVKGRFTISRDNKNTLNLMNSLRAEDTAVYYCAKDDG SGWFPKLLHYGLDVWGQGTTVTVSSGGGGGGGGGGSELVMTQSPS SLASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPS RFSGSGGTDFTFITISLQPEDFATYYCQSYSIPTFGQGQTKVEIK
			(SEQ ID NO: 6926)

iPS:601126	18078-H6	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGATATG GCATGCAGTGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG CAGTTATATCATATGATGGAAGTAATAATACTATGCAGACTCCCGTGAA GGCCGATTACCATCTCCAGAGACAAATTCCAAGAACACGCTATATCTG CAATGAACAGC
		AA	(SEQ ID NO: 6927) EVQLLESGGGVVQPGRSLRLSCAASGFTFSRYGMQWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARN YGSGSYGAYYYHGMDEVWGQTTVTSSGGGGGGGGGGSELVLTQ PPSVSKGLRQTATLTCTGNSNNVGNQGAAWLQQHQGHPPKLLSYRNNNR SGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLSAWVFGGGTKLT VL (SEQ ID NO: 6928)

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iPS:601094	18079-C8	NA	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAGCTATGG CATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAGTGGGTGGC AGTTATATCATATGATGGAAGTAATAAGTACTATGCAGACTCCCGTGAAG GGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTTCTTCTGC AAATGAACAGC
			(SEQ ID NO: 6929)
		AA	EVQLLESGGKVVPGRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNKNTLFLQMNSLRTEDTAVYYCAREQ WPNYYYGLGVWGQGTTVTVSSGGGGGGGGGGSELVLTQPSSVSKD LRQTATLTCTGNSNNVGNQGAAWLQQHQGHPPKLLSYRNNRPSGISERL SASRSGNTASLTITGLQPEDEADYYCSAWDSSLSAWVFGGGTKLTVL
			(SEQ ID NO: 6930)

iPS:601106	18079-H4	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCCAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGACTATGCACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGAAAGC
		AA	(SEQ ID NO: 6931) EVQLLESGAEVKKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYAQKFQGRVTMTTRNTSISTAYMELRSLRSEDTAVYYCAR GWGRFYSYGMDVWGQGTTVTVSSGGGGGGGGGGGGSELVMTQSPDS LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE SGVPDRFSGSGGTDFLTITISLQAEDVAVYYCQQYYSTPWTFGQGTKLEIK (SEQ ID NO: 6932)

iPS:601064	18079-H11	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAACAGTGGTAACACAGACTATACACAGAAAGTTCC AGGCAGAGTCAACCATGACCAGGAACACCTCCATAGGCACAGCCTACA TGGAGCTGAGCAGC
		AA	(SEQ ID NO: 6933) EVQLLESGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYTQKFQGRVTMTNRNTSIGTAYMELSSLRSEDTAVYYCVR GWGTYYYGMDVWGQGTTVTVSSGGGGGGGGGGGGSELVMTQSPDS LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE SGVPDRFSGSGGTDFLTITISLQAEDVAVYYCQQYYSTPWTFGQGTKLEIK
			(SEQ ID NO: 6934)

iPS:601108	18080-C5	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCATCAGCAGTGGTG ATTACTAGTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCAATGACAGTGGGAGCACCTACTATAACCCGTCCT CAAGAGTCGAGTTACCTTATCAGTAGACTCGTCTAAGAACCAGTTCTCC CTGAAGCTGAGC
		AA	(SEQ ID NO: 6935) EVQLLESGPGLVKPSQTLSTCTVSGGSISSGDYYWSWIRQHPGKGLEWIG YINDSGSTYYNPSLKSRVTLSDSSKNQFSLKLSSTAAADTAVYYCARDLL WFGKLNYYYGMDVWVGQGTTVTVSSGGGGSGGGGSELVLTQSPLS LPVTPGEPASISCRSSQSLHNSNGYNLDWYLYQKPGQSPQLLIYLGSNRASG VPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK (SEQ ID NO: 6936)

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iPS:601090	18080-H9	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGGTATTAGTGGTAGTGGTAGCACATACGACAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 6937)
		AA	EVQLLESGGGLVQPGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSG ISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKVM TPDYYYDMDVWGQGTITVTVSSGGGGGGGGGGSELTLTQSPGTLSS PGERATLSCRASQVSSGYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGS GSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGPGTKVEIK
			(SEQ ID NO: 6938)

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iPS:601096	18081-A6	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGTAGTAGTCG TTACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTG GATTGGGAGTATCTATTATAGTGGGAGCACCTACTACAACCCGTCCTC AAGAGTCGAGTCACCATATCCGTAGACACGTCCAAAGAACCAAGTCTCTCCC TGAAAGCTGAGT
			(SEQ ID NO: 6939)
		AA	EVQLLESGPGLVKPSETLSLTCTVSGDSISSRYYWGWIRQPPGKGLEWIGSI YYSGSTYYNPSLKSRTISVDTSKNQFSLKLSVTAADTA VYYCARGIFGVI TYFDYWGGQGTLVTVSSGGGGGGGGGGSEL VMTQSPDSLAVSLGER ATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVDRFS GSGSGTDFLTITISLQAEDVA VYYCQQYYSTPLTFGGGKVEIK
			(SEQ ID NO: 6940)

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iPS:601070	18081-B5	NA	GAGGTGCAGCTGCTCGAGTCAGGTCCAGGACAGGTGAAGCCCTCGCAG ACCTCTCACTCACCTGTGCCATCTCCGGGACAGTGTCTCTAGCAACA GTGCTGCTTGGAACCTGGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTG GCTGGGAAGGACATACTACAGGTCCAAGTGGTATAATGATTATGCAGT ATCTGTGAAAAGTCGAAATAACCATCAACCCAGACACATCCAAGAAACCA GTTCTCCCTGCAG
			(SEQ ID NO: 6941) EVQLLESGPGQVKPSQTLTLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLG RTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARE VLWFGKLNYYGMDVWGQTTVTVSSGGGGGGGGGGSELVLTQS PLSLPVTGEPASISCRSSQSLHHRNGYNYLDWYLLQKPGQSPQLLIYLGSR ASGVPRDRFSGSGTDFTLKISRVEAEDVGVYYCMQALQTPITFGQGTRLEI K
		AA	(SEQ ID NO: 6942)

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iPS:601078	18081-C10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCCGTGTCCTCACCTGCATTGTCTGTGGTGTCTCCATCAGCAGTAGTAG GTCCCTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTG GATTGGGAGTATCTATTATGGTGGGAGCACCTACTACAACCCGTCCCTC AAGAGTCGAGTCACCATATCCGTTGACACGTCCTCAAGAACCAAGTTCTCCC TGAAAGCTGAGC
			(SEQ ID NO: 6943)
		AA	EVQLLESGPGLVKPSETLSLTCIVSGVSISSRSYWGWIQQPGKGLEWIGSI YYGGSTYYNPSLKSRTISVDTSKNQFSLKLSSTAAADTAVYYCATTIFGV VGWFDPPWGQGNLVTVSSGGGGGGGGGGSELVMTQSPDSLAVSLGE RATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDFR SGSGSGTDFLTITISLQAEDVAVYYCQQYYSTPLTFTGGGKVEIK
			(SEQ ID NO: 6944)

iPS:601114	18081-D6	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTGCGCTGGTGAACCCACACAG ACCTCAGCGCTGACCTGACCTTCTCTGGTTTCTCATTCACCACTCATAA AATGGGTGTGGACTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTG GCTTGCACTCATTATTGGAATGATGATACGCGCTACAGCCCATCTCTG CAGAGTAGGCTCACCATCACCAGGACACCTCCAAAAAACCAAGGTGGTC CTCACAATGACC
		AA	(SEQ ID NO: 6945) EVQLLESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWND DTRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCVYRR YNWNYENWFDPPWGQGLTVSSGGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTKLEIK (SEQ ID NO: 6946)

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iPS:601098	18081-D12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCCTGGTCAAGCCTGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCATCTATGC CTTGAGCTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTAGCACATACACGACACTCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6947)
		AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSIYALSWVRQAPGKGLEWVSAI SGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGEI AARYYYGMDVWGQGTTVTVSSGGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYATSSLSQGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSTPPTFGQGTKVEIK
			(SEQ ID NO: 6948)

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iPS:601130	18082-F5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGATATG GCATGGATTGGTCCCGCAGGCTCCAGGCAAGGACTGGAGTGGGTGG CAGTTATATGGTATGATGGAAGTAATAATACTATGCAGACTCCCGTGAA GGCCGATTCAACCATCTCCAGAGACAAATTCCAAGAAATACGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 6949)
		AA	EVQLLESGGKVVPGRSLRLSCAASGFTFSRYGMDWVRQAPGKGLEWVA VIWYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARN YGSYSYGA YY YHGM DVWGQTTVTVSSGGGGGGGGGGSELALTQ PASASGSPGQSITISCTGTSSDVGGYNYSWYQQHPGKAPKLMIEYVSKRPS GVPDFRFGSKSGNTASLTVSGLQAEDEADYYCSSYAGSNVVFVGGGTKLT VL
			(SEQ ID NO: 6950)

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iPS:601068	18084-E4	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTAGTACACATACACGAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6951)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHLR YSDWPLDYWGQGTLVTVSSGGGGGGGGGGGSELTLTQSPGTLSPG ERATLSCRASQSVSSSYLA WYQQKPGQAPRLLIYGASSRATGIPARFSGSGS GTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKLEIK
			(SEQ ID NO: 6952)

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iPS:603159	18086-H4	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCTGAGGTGAAGAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAAGTTATG ATATCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAGTGGATGG GATGGATGAACCCCTAAGAGTGGTAACACAGGCTATGCACAGAAAGTTCC AGGACAGAGTCACCATGACCAGGAACACCTCCATAAGCACAGCCTACA TGGAGCTGAGCAGC
			(SEQ ID NO: 6953)
		AA	EVQLLESGAEVKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMG WMNPKSGNTGYAQKFQDRVTMTRNTSISTAYMELSSLRSDDTAVYYCVR GWGTYYYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQSPDS LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRE SGVPDRFSGSGGTDFLTITISLQAEDVAVYYCQYYSTPWTFGQGTKVDI K
			(SEQ ID NO: 6954)

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iPS:603151	18088-B10	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGATATCACATACGACGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC	(SEQ ID NO: 6955)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGDITYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHLR YFDWPLDYWGQGTLVTVSSGGGGGGGGGGSELVMTQSPGTLSPG ERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGS GTDFTLTISRLEPEDFAVYYCQQYGTSPLTFTGGGTKVDIK	(SEQ ID NO: 6956)

iPS:603189	18088-E4	NA	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCGCTGTCTATGGTGGTCTTCAAGTGGTTACTA CTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTGGATTGG GGAATCAATCATAGTGGAAAGCACCACCACTACAACCCGTCCTCAAGAG TCGAGTCACCATATCAGTAGACACGTCCAAGAACCAAGTTCTCCCTGAAG CTGAGCTCTGTG
		AA	(SEQ ID NO: 6957) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRTISVDTSKNQFSLKLSSTAAADTA VYYCARGGGYS YGYDYGMDVW/GQGTTTVSSGGGGGGGGGGSEL VMTQSPLSLPVI PGEPAISICRSSLYSNGYNLDWYLQKPGQSPQLLIYLGSKRASGV PDR FSGSGGTDFTLKISRVEAEDVGYYCMQVLTPTPTFGQGQTKLDIK (SEQ ID NO: 6958)

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iPS:603131	18089-B8	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCCGTGTCCTCACCTGCATTGTCTCTGGTGGCTCCATCAGCAGTAGTA GGTCCACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGT GGATTGGGAGTATCTATTATGGTGGGAGCACCTACTACAACCCGTCCT CAAGAAATCGAGTCACCATGTCCGTTGACACGTCCTCCAAAGAACCAAGTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 6959)
		AA	EVQLLESGPGLVKPSETLSLTCIVSGGSISSSRSYWGWIQPPGKGLEWIGSI YYGGSTYYNPCLKNRVTMSVDTSKNQFSLKLSVTAADTAVYYCATTFG VVGWFDPWGQGNLVTVSSGGGGGGGGGGSELVMTQSPDSLAVSLG ERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVDR FSGSGGTDFLTITISLQAEDVAVYYCQYYSTPLTFGGGKVDIK
			(SEQ ID NO: 6960)

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iPS:603139	18089-C8	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTGCGCTGGTGAACCCACACAG ACCTCACGCTGTCTGTTCTTCTCTGGGTTCTCACTCAGCACTAATAA AATGGCTGTGGTTGGATCCGTCAGCCCCCAGAAAGGCCCTGGAGTG GCTTGCACTCATTATTGGAATGATGATAAGCGCTACAGTCCATCTCTG AAGAGCAGGCTCACCATCACCAGGACACCTCCAAAAACCAGGTGGTC CTTACAATGACC
			(SEQ ID NO: 6961)
		AA	EVQLLESGPALVKPTQTLTLSCFSFGSLSTNKMAVGWIRQPPGKALEWLA LIYWNDKRYSPSLKSRLTITKDTSKNQVVLMTNMDPVDATYYCARRR YNWNYENWFDPPWGGILVTVSSGGGGGGGGGSELQMTQSPSSL ASVGDRVTITCRASQSISSYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIK
			(SEQ ID NO: 6962)

iPS:603169	18089-G7	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTGTGCTGGTGAACCCACACAGA CCCTCACGCTGACCTGCACCTTCTCTGGTTTCTCATTCAACCATCATAAA ATGGGTGTGGACTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTGG CTTGCACTCATTTATTGGAATGATGATAAGCGCTACAGCCCATCTCTGC AGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACAGGTGGTCC TCACAATGACC
		AA	(SEQ ID NO: 6963) EVQLLESGPVLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRR YNWNYENWFDPWGGTLTVSSGGGGGGGGGGSELQMTQSPSSLS ASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYATSSLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSIPTFTFGPGTKVEIK (SEQ ID NO: 6964)

iPS:603179	18089-G11	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGGTATTAGTGGTAGTGGTGGTAGCTCATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 6965) EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSG ISGSGSSYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKTLT PDYYDMVDVWGQGTTVTVSSGGGGGGGGGGGSELQMTQSPSSVSAS VGDRVITITCQASQDISNYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSGS GSGTDFLTITSSLPEDFATYYCQQSYSTPLTFGGGKVDIK (SEQ ID NO: 6966)

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iPS:603191	18089-H9	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGGTATTAGTGGTAGTGGTAGCACATACGACAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 6967)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTSSYAVSWVRQAPGKLEWVSGI SGSGGSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKALT PDYYYDMDVWGQGTTVTVSSGGGGGGGGGGSELQMTQSPSSLAS VGDRVITITCRASQGISNYLAWYQQKPGKVPNLLIYGASTLQLGVPSRFSGS GSGTDFLTITISLQPEDVATYYCQKYYSAPFTFGPGTKVDIK
			(SEQ ID NO: 6968)

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iPS:603205	18089-H12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAACTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTAGTACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6969)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSNYAMSWVRQAPGKLEWVSA ISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKQG GIAAAYYYDGMVDVWGQGTTVTVSSGGGGGGGGGGSELQMTQSPS SLASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPSR FSGSGGTDFLTITISLQPEDFATYYCQQSYSTPFTFGPGTKLEIK
			(SEQ ID NO: 6970)

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iPS:604972	18090-H9	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAGATATG GCATGGATTGGGTCCGCCAGGCTCCAGGCAAGGACTGGAGTGGGTGG CAGTTATATCATATGATGGAAGTAATAATACTATGCAGACTCCCGTGAA GGCCGATTACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 6971) EVQLLESGGTVVQPGRSRLSCAASGFTFSRYGMDWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARN YGSGSYGAYYYGMDVWGQTTVTVSSGGGGGGGGGGSELVLTQ LPSVSKGLRQTATLTCTGNSNNVGNQGAAWLQHQHQPPLLSYRNNNR SGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSL SAVVFGGGTKLT VL (SEQ ID NO: 6972)

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iPS:604980	18093-E2	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTACCTCCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTCATAGTGGTGGTAGCACATACGACAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 6973)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFTSYAMSWVRQAPGKGLEWVST ISHSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDG GSGWFPKLLHYGLDVWGQGTITVSSGGGGGGGGGGGGSELVMTQSP SSLASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYAASLSQSGVPS RFSGSGSGTEFTLTISSLQPEDFATYYCQQSYSTPPTFGQGTKVDIK
			(SEQ ID NO: 6974)

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iPS:604966	18093-F5		GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTGAGCATCTATGG CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTAGCACATACGACAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
	NA		(SEQ ID NO: 6975)
	AA		EVQLLESGGGLVQPGGSLRLSCAASGFTLSIYGMWVRQAPGKLEWVSAT SGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGEI SARYYYGMDVWGQGTITVSSGGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSPPTFGQGQTKVDIK
			(SEQ ID NO: 6976)

iPS:613775	18179-A3	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCCGTGTCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCTCCCGGGAAGGGCTGGAGTG GATTGGGTACATCTCTTACAGTGGGAGCACCTTCTACAACCCGTCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCCC TGAAATCTGACC
		AA	(SEQ ID NO: 6977) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQLPGKLEWIGY ISYSGSTFYNP SLKSRVTISVDTSKNQFSLNLTSTVAADTA VYYCARDRLWF GVLNYYGMDVWGLGTTTVSSGGGGSGGGSELVMTQSPLSLP VTPGEPASISCRSSQSLHNRNGYNYLDWY LQKPGQSPQLLIYLG SNRASGVF DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKVDIK (SEQ ID NO: 6978)

iPS:613783	18179-A5	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTAGTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGCTACCATATCAGTAGACACGTCTAAGGACCAAGTCTCTCC CTGAAGCTGACC
		AA	(SEQ ID NO: 6979) EVQLLESGPGLVKPSETLSLTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRAATISVDTSKDQFSLKLTSLTAADTA VYVCAREKM WFGVLNYYYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVLTQSPLS LPVTPGEPASISCRSSQSLHNSNGYNLDWYLYQKPGQSPQLLIYLGSNRASG VPDRFSGSGGTDFTLKISRVEAEDVGVYCMQALQTPFTFGPGTKVEIK (SEQ ID NO: 6980)

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iPS:613707	18179-A9	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGTTACCATATCATCAGTTGACACAGTCTAAGAACCAAGTTCTCC CTGAATCTGACC
			(SEQ ID NO: 6981) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRTISVDTSKNQFSLNLTSTVTAADTAVYYCARDRL WFGVLNYYYGMDVWVGQTTVTVSSGGGGSGGGGGSELVMTQSPL SLPVTGPEPASISCRSSQSLHNSNGYNVDWYLVKPGQSPQLLIYLGSNRAS GVPDRFSGSGGADFTLKISRVEAEDVGVYYCMQALQTPPLTFGGGGTKVEIK
			(SEQ ID NO: 6982)

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iPS:613697	18179-A10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTAGTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGCTACCATATCAGTAGACACGTCTAAGGACCAAGTTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 6983) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRAATISVDTSKDQFSLKLSVTAADTA VYYCARDQL WFGVLNYYYGMDVWVGQTTVTVSSGGGGGGGGGGSELVLTQSPG TSLSPGERATLSCRSSQSLHRNGYNLDWYLYQKPGQSPQLLIYLGSNRAS GVPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK
		AA	(SEQ ID NO: 6984)

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iPS:613685	18179-B7	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTTAGACTCTCTGTGTGAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 6985)
iPS:613685	18179-B7	AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNSGSYYNYFSVMDVWGQGTTVTVSSGGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCQARQDISDYLNWFQKPGRAPKLLIFAASSLQGGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQQYSPMPFTFGPGTKVDIK
			(SEQ ID NO: 6986)

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iPS:613711	18179-B8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 6987)
iPS:613711	18179-B8	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNSGSYYNYFSVMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQS PSSLASVGDVRVTITCRTSQSINSYLNWFQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTITISLQPEDFATYYCQQSYSTPFTFGPGTKVDIK
			(SEQ ID NO: 6988)

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iPS:613765	18179-C4	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTAGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGCTACCATATCAGTAGACACGTCTAAGGACCAGTTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 6989) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRA TISVDTSKDQFSLKLSVTAADTA VYYCARDRL WFGVLNYYYGMDVWVGPGTTVTVSSGGGGGGGGGGSELVMTQSPL SLPVTPGEPASISCRSSQSLHSTGYNLDWYLYQKPGQSPQLLIYLGSRAS GVPDRFSGSGTDFTLKISRVEAGDVGFYYCMQALQTPRTFGQGTKLEIK
		AA	(SEQ ID NO: 6990)

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iPS:613777	18179-C6	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTAGTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGCTACCATATCAGTAGACACGCTCTAAGGACCAGTTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 6991) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRAATISVDTSKDQFSLKLSVTAADTA VYYCARDQL WFGVLNYYYGMDVWVGQTTVTVSSGGGGGGGGGGSELVMTQTPL SLPVTGPEPASISCRSSQSLHNRNGYNYLDWYHLKPGQSPQLLIYLGSNRAS GVPDRFIGSGSGTDFTLKISKVEAEDVGIYYCMQALQTPRTFGQGTKVEIK
			(SEQ ID NO: 6992)

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iPS:613687	18179-C7	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCO TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTG GATTGGGTACATCTCTCACAGTGGGAGCACTTATTACAATCCGTCCTC AAGAGTCGAGTAACCATATCATGACACAGTCTAAGAAATCAGTTCTCCO TGAATCTGACC
			(SEQ ID NO: 6993) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIGY ISHSGSTYYNP SLKSRVTISVDTSKNQFSLNLTSTVTAADTAVYYCAREKMW FGVLNYYYGMDVWGLGTTTVTVSSGGGGGGGGGSELVLTQSPLSLP VTPGEPASISCRSSQSLLHRNGYHYLDWY LQKPGQSPQLLIYLGSNRASGV DRFIGSGGTDFTLEISRVEAEDVGYYCMQALQTPSFQGQTKLEIK
		AA	(SEQ ID NO: 6994)

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iPS:613787	18179-C10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAGCCTTCACAG ACCCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCO TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTG GATTGGGTACATCTCTCACAGTGGGAGCACTTATTACAATCCGTCCTC AAGAGTCGAGTAACCATATCATAGACACGTCTAAGAAATCAGTTCTCCC TGAAGCTGACC
			(SEQ ID NO: 6995) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIGY ISHSGSTYYNP SLKSRVTISVDTSKNQFSLKLTSTVTAADTAVYYCARDRLWH GVLNYYYGMDVWGLGTTVTVSSGGGGGGGGGGSELVLTQSPLSLP VTPGEPASISCRSSQSLHHRNGYNYLDWY LQKPGQSPQLLIYLGSNRASGVVP DRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPFTFGPGTKVEIK
		AA	(SEQ ID NO: 6996)

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iPS:613675	18179-D8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTTAGACTCTCTGTGTGACGCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAATG
			(SEQ ID NO: 6997)
iPS:613675	18179-D8	AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNSGSYYNYFSVMDVWVGQGTTVTVSSGGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSMPTFTFGPGTKVDIK
			(SEQ ID NO: 6998)

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iPS:613753	18179-D9	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTTAGACTCTCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 6999)
iPS:613753	18179-D9	AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFVSMDVWQGTTTVSSGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCRTSQSINSYLNWFQKPGKAPKLLIFAASSLQSGVPS RFSGSGSGTDFTLTISSLQREDFATYQCQSYSTPFTFGPGTKVDIK
			(SEQ ID NO: 7000)

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iPS:613689	18179-E6	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7001)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNSGSYYNYFSVMDVWVGQGTTVTVSSGGGGGGGGGGGSELQMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTITSSLPEDFATYYCQQTYSMPTFTFGPGTKLEIK
			(SEQ ID NO: 7002)

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iPS:613679	18179-F3	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCTGACCCCTCACCTGCACCTGTCTCTGGTGGCTCCATCAGTAGTTACTA CTGGAGCTGGATCCGGCAGCCCGCCGGGAAGGACTGGAGTGGATTGG GCATATCTATACCAAGTGGGAGCACCAACTACAACCCCTCCCTCAAAGAGT CGAGTCACCATGTCAGTGGGACTCGTCCAGAACCAAGATTCTCCCTGAAGC TGACCTCTCTG
			(SEQ ID NO: 7003)
		AA	EVQLLESGPGLVKPSETLTLTCTVSGGSISSYYWSWIRQPAGKGLEWIGHIY TSGSTNYPNPSLKS RVMTMSVDSSKNQFSLKLTSLTAADTAVYYCAREKMMWF GVLNYYYGMDVWVGQTTVTVSSGGGGGGGGGGSELVLTQSPLSLP VTPGEPASISCRSSQSLHNRNGYNLDWYLVKPGQSPQLLIYLGSNRASGVP DRFIGSGTDFTLTLEISRVEAEDVGVIYCMQALQTPSFGQGTKEIK
			(SEQ ID NO: 7004)

iPS:613701	18179-F4	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCTCCCCGGGAAGGCCCTGGAGTG GATTGGGTACATCTCTTACAGTGGGAGCACCTTCTACAACCCGTCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCCC TGAATCTGACC
			(SEQ ID NO: 7005) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQLPGKLEWIGY ISYSGSTFYNP SLKSRVTISVDTSKNQFSLNLTSTVAADTA VYYCARDRLWF GVLNYYGMDVWGLGTTVTVSSGGGGGGGGGGSELVLTQSPLSLP VTPGEPASISCRSSQSLHHRNGYHYLDWY LQKPGQSPQLLIYLGSNRASGV DRFSGSGGTDFTLKISRVEAEDVGYYCMQALQTPFTFGPGTKVEIK
iPS:613701	18179-F4	AA	(SEQ ID NO: 7006) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQLPGKLEWIGY ISYSGSTFYNP SLKSRVTISVDTSKNQFSLNLTSTVAADTA VYYCARDRLWF GVLNYYGMDVWGLGTTVTVSSGGGGGGGGGGSELVLTQSPLSLP VTPGEPASISCRSSQSLHHRNGYHYLDWY LQKPGQSPQLLIYLGSNRASGV DRFSGSGGTDFTLKISRVEAEDVGYYCMQALQTPFTFGPGTKVEIK
			(SEQ ID NO: 7006)

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iPS:613715	18179-F6	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTAGTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTC CAAGAGTCGAGCTACCATATCAGTAGACACGTCTAAGGACCAGTTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 7007) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRAATISVDTSKDQFSLKLSVTAADTA VYYCARDQL WFGVLNYYYGMDVWVGQTTVTVSSGGGGGGGGGGSELVMTQSPL SLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLYQKPGQSPQLLIYLGSNRAS GVPDRFSGSGGTDFTLKISRVEAEDVGFYYCMQALQTPRTFGQGTKVEIK
			(SEQ ID NO: 7008)

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iPS:613731	18179-F10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTACGGAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTGATTCTT CTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGACTGGAGTGGATTGG ATATATCTATTACAGAGGGAGCACCAACTACCACCCCTCCCTCAAGAGT CGAGTCACCATGTTCAGTGGACACGTCCAAGAACCAAGTTCTCCCTGAAGC TGACCTCTCTG
			(SEQ ID NO: 7009) EVQLLESGPGLVKPTETLSLTCTVSGGSISDFFWSWIRQPPGKGLEWIGYIYY RGSTNYHPSLKSRLVMSVDTSKNQFSCLK.TSLTAADTAVYYCAREKMWFG VLNYYYGMDVWVGQTTVTVSSGGGGGGGGGGSELVMTQTPLSLPV TPGEPASISCRSSQSLHSGNYNYLDWYLNKPGQSPQLLIYLGSNRASGVDP RFSGSGSGTDFTLKISRVEAEDVGFYYCMQALQTPRTFGQGTKVEIK
		AA	(SEQ ID NO: 7010)

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iPS:613681	18179-G8	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGTGGCGCCATCAGCAGTGGTG ATTACTGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGCTACCATATCAGTAGACACGTCTAAGGACCAGTTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 7011) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRAATISVDTSKDQFSLKLSVTAADTA VYYCARDQL WFGVLNYYYGMDVWVGQTTVTVSSGGGGGGGGGGSELVMTQSPL SLPVTPGEPASISCRSSQSLHNRNGYNYLDWYHLKPGQSPQLLIYLGSNRAS GVPDRFSGSGTDFTLKISRVEAEDVGVYYCMQALQTPRTFGQGTKVEIK
		AA	(SEQ ID NO: 7012)

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iPS:613789	18179-G9	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCACCCAGGATGGGCCTGGAGTG GATTGGGTACATCTATTACAGTGGGAGCACCTCTACAACCCGTCCTC AAGAGTCGAGTCACCATGTCACTGGACTCGTCCAAAGAACCAAGTCTCTCCC TGAAAGCTGACC
			(SEQ ID NO: 7013)
		AA	EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGMGLEWIG YIYYSGSTSYNPSLKSRVTMSVDSSKNQSLKLTSTVTAADTAVYYCARDLL WFGKLNYYYGLDVWGQGTTVTVSSGGGGGGGGGGSELVMTQTPLS LPVTPGEPASISCRSSQSLHRNGYNLDWYLQKPGQSPQLLIYLGSNRASG VPDRFIGSGSGTDFTLKISRVEAEDVGVYYCMQALQTPSFQGQTKVEIK
			(SEQ ID NO: 7014)

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iPS:613709	18179-H6	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCGCCATCAGCAGTGGTG ATTACTGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAACCCGTCCTT CAAGAGTCGAGCTACCATATCAGTAGACACGTCTAAGAAACCAGTTCTCC CTGAAGCTGAGC
			(SEQ ID NO: 7015) EVQLLESGPGLVKPSQTLSTCTVSGGAISSGDYYWSWIRQHPGKGLEWIG YIDKSGSTYYNPSLKSRA TISVDTSKNQFSLKLSVTAADTA VYYCARDLL WFGKLNYYYGLDVWGQGT TVTSSGGGGGGGGGGSELVMTQTPLS LPVTPGEPASISCRSSQSLLHRNGYNYLDWY LQKPGQSPQLLIYLGSNRASG VPDRFSGSGGTDFTLKISRVEAEDAGVYYCMQSLHLPPTFGGGTKLEIK
			(SEQ ID NO: 7016)

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iPS:613779	18179-H9	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGCCCTGGAGTG GATTGGGTACATCTCTCACAGTGGGAGCACTTATTACAATCCGTCCTC AAGAGTCGAGTAACCATATCATGACACACGTCTAAGAAACCAGTTCTCCO TGAATCTGACC
			(SEQ ID NO: 7017) EVQLLESGPGLVKPSQTLSTCTVSGGSISSNPYYWSWIRQHPGKGLEWIGY ISHSGSTYYNPSLKSRVTISVDTSKNQFSLNLTSTVTAADTAVYYCAREKMW FGVLNYYYGMDVWGQGTTVTVSSGGGGGGGGGGSELVLTQSPLSL PVTPGEPASISCRSSQLLHRNGYHYLDWYLYLQKPGQSPQLLIYLGSNRASGV PSRFGSGSGTDFTLKISRVEAEDVGIYYCMQALQTPFTFGPGTKVEIK
		AA	(SEQ ID NO: 7018)

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iPS:615270	18181-A11	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCO TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTG GATTGGGTACATCTCTTACAGTGGGAGCACCTACTACAACCCGTCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACACGTTCTCCC TGAATCTGACC
			(SEQ ID NO: 7019) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIGY ISYSGSTYYNP SLKSRVTISVDTSKNQFSLNLTSTAAADTAVYYCARDRLWH GVLNYYYGMDVWGP GTTVTVSSGGGGSGGGGSELVMTQSPLSLP VTPGEPASISCRSSQSL LHRNGYN YLDWY LQKPGQSPQLLIYLG SNRASGVP DRFSGSGGTDFTLKISRVEAEDVGIYYCMQALQTPFTFGPGTKVEIK
		AA	(SEQ ID NO: 7020)

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iPS:615224	18181-C6	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGCCCTGGAGTG GATTGGGTACATCTTACAGTGGGAGCACCTACTACAACCCGTCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACACGTTCTCCC TGAATCTGACC
			(SEQ ID NO: 7021) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIGY ISYSGSTYYNPSLKSRVTISVDTSKNQFSLNLTSTAAADTAVYYCARDRLWH GVLNYYYGMDVWGP GTTVTVSSGGGGSGGGGSELVMTQSPLSLP VTPGEPASISCRSSQSLHSTGYNYLDWY LQKPGQSPQLLIYLGSNRASGVP DRFSGSGGTDFTLKISRVEAEDVGFYYCMQGLQTPRTFGQGTKLEIK
		AA	(SEQ ID NO: 7022)

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iPS:615238	18181-G7	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTTAGACTCTCTGTGTGCA GCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAAGAGATGATTCAAAAAAACAGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7023)
		AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNGGSYYNYFSVMDVWQGTTVTVSSGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSPMPFTFGPGTKVEIK
			(SEQ ID NO: 7024)

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iPS:615268	18181-H10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAATTACTA CTGGAGCTGGGTCCGGCAGCCCGCCGGGAAGGACTGGAGTGGATTGG TCATATCTATACCAAGTGGGAGCACCAACTTCAACCCCTCCCTCAAGAGT CGAGTCACCATGTCAAGTGGACACGTCCAAGAACCAAGTTCTCCCTGAAGC TGACCTCTCTG
			(SEQ ID NO: 7025) EVQLLESGPGLVKPSETLSLTCTVSGGSISNYYSWVRQPAKGLEWIGHI YTSGSTNFPNPSLKSRVTMSVDTSKNQFSLKLTSLTAADTAVYYCAREKMW FGVLNYYYGMDVWGQGTTVTVSSGGGGGGGGGGSELVMTQSPLSL PVTGPGEASISCRSSQSLHSHNGYNLDWYLPKPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLKISRVEAEDVGIYYCMQALQTPRTFGQGTKVDIK
		AA	(SEQ ID NO: 7026)

iPS:613561	18182-A3	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGTAGCACATACACGAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 7027) EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFGN TATLIISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL (SEQ ID NO: 7028)

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iPS:613655	18182-A5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACTTACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7029)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLNFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVQWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADFCYQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7030)

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iPS:613591	18182-A6	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGAAGTGGTGGGCACATACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7031)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLVTVSSGGGGGGGGGGGGSELVVTQEPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7032)

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iPS:613619	18182-A7	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7033)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQLPSVSVAPG QTARITCGGNNIGSKSVHWHQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYHCQVWVDSSDHSVVFGGGTKLTVL
			(SEQ ID NO: 7034)

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iPS:613573	18182-A8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7035)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQSSSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADFCYQVWDSDDHVVFGGGTKLTVL
			(SEQ ID NO: 7036)

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iPS:613513	18182-A11	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7037)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPPSVSVTPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLTISRVEAGDEADYYCQVWDSDDHVVFGGGTKLTVL
			(SEQ ID NO: 7038)

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iPS:613639	18182-B1	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGGCACATACAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7039)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQLPSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNF GNTATLIISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7040)

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iPS:613603	18182-B4	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTAGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GCCCAGTTCAACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7041)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKARFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGGSELMLTQPPSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWVDSSDHDVVFGGGTKLTVL
			(SEQ ID NO: 7042)

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iPS:613617	18182-B6	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGTAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7043)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGGSELMLTQPHSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNF GNTATLTISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7044)

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iPS:613635	18182-B7		GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC	(SEQ ID NO: 7045)	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGQGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDHWGQGTLVTVSSGGGGGGGGGGGSELMLTQPHSVSVAPG QTARITCGGNNIGSKSVQWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADFCYQVWDSSSDHVVFGGGTKLTVL
		NA			(SEQ ID NO: 7046)
		AA			

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iPS:613543	18182-B10	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAAC TGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACTTACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAA TTCCAA GAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7047)
iPS:613543	18182-B10	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMNWWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLNFDYWGQGTLVTVSSGGGGGGGGGGGSELMLTQPHSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWVDSSDHDVVFGGGTKLTVL
			(SEQ ID NO: 7048)

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iPS:613643	18182-C2	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7049)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVQWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADFYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7050)

iPS:613607	18182-C3	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
		AA	(SEQ ID NO: 7051) EVQLLESGGDLVQPGGSLRLSCAASGFTTSSHAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQ TARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVVDSSSDHAFVFGGGTKLTVL (SEQ ID NO: 7052)

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iPS:613571	18182-C4	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACGACGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7053)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGGSELMLTQPHSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWVDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7054)

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iPS:613661	18182-C5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7055)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSTI SGSGGGTYAYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLNFDYWGGTGLVTVSSGGGGGGGGGGSELVLTQPASVSVAPGQ TARITCGGNIGIKSVHWYQKPGQAPVLVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDSDDHVVFGGGTKLTVL
			(SEQ ID NO: 7056)

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iPS:613621	18182-C10	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATCCAAAGAACACGGCTGTATCTG CAAATGAACAGC
(SEQ ID NO: 7057)			EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGGGSELVLTQSSSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFGN TATLIISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL
AA			(SEQ ID NO: 7058)

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iPS:613629	18182-C12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGAAATCACTTTAGCAGCTATG CCATGAGCTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCT CAGCTATTAGTGGTAGTGGTGGGCACATACACGAGACTCCCGGA AGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT GCAATGAACAGC	(SEQ ID NO: 7059)
		AA	EVQLLESGGDLVQPGGSLRLSCAASGITFSSYAMSWVRQAPGKGLEWVSAI SGSGGGTYADSGKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLVTSSGGGGGGGGGGGGSELMLTQPHSVSVAPGQ TARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLIISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL	(SEQ ID NO: 7060)

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iPS:613549	18182-D4	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7061)
		AA	EVQLLESGGDLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAPGKG VHLNFDYWGGTLLVTVSSGGGGGGGGGGSELALTQPASASVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7062)

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iPS:613645	18182-D8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7063)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQLSSVSVAPG QTARITCGGNNIGSKSVQWYQQKPGQSPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYHCQVVDSSDHDHVFGGTKLTVL
			(SEQ ID NO: 7064)

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iPS:613537	18182-D9	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGGTAGTGGTGGCACATACGACACTCCCGTGAAG GGCCGGTTCACCATCTCCAGGGACAAATTCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7065) EVQLLESGGDLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLNFDYWGGQTLVTVSSGGGGGGGGGGGGSELVVTQEPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNF GNTATLIISRVEAGDEADYYCQVWDSNSDHDVVFGGGTKLTVL
		AA	(SEQ ID NO: 7066)

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iPS:613541	18182-D11	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAAC TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACTTACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAA TTCCAA GAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7067)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMNWWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGK GVHLNFDYWGGQTLVTVSSGGGGGGGGGGGSELMLTQPPSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVVDSSDHDHVFGGTKLTVL
			(SEQ ID NO: 7068)

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iPS:613657	18182-E2	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTGGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
(SEQ ID NO: 7069)			EVQLLESGGDLVQPGGSLRLSCAASGFTFGSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNNIGSKSVHWYQQKPGQAPVMMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYHCQVVDSSSDHVVFGGGTKLTVL
AA			(SEQ ID NO: 7070)

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iPS:613519	18182-E3	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGTAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7071)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVQWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGTKLTVL
			(SEQ ID NO: 7072)

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iPS:613595	18182-E8	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAATGAGCAGC
			(SEQ ID NO: 7073)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYLQMSSLRAEDTAVYYCATGKG VHLGFDYWGGTLVTVSSGGGGGGGGGGSELVLTQPASVSVAPGQ TARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGTKLTVL
			(SEQ ID NO: 7074)

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iPS:613667	18182-E11	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GCCCAGTTCAACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7075)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKARFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGGSELMLTQPHSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWVDSSDHDVVFGGGTKLTVL
			(SEQ ID NO: 7076)

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iPS:613529	18182-F1	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7077)
		AA	EVQLLESGGDLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCATGK GVHLNFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQSPSVVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGTKLTVL
			(SEQ ID NO: 7078)

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iPS:613531	18182-F6	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGATTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7079)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLNFDYWGGQTLVTVSSGGGGGGGGGGSELALTQPPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDSSSDHVMFGGGTKLTVL
			(SEQ ID NO: 7080)

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iPS:613623	18182-F8	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCCGGATTACCTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7081)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVST SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7082)

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iPS:613641	18182-G3	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGACTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGCACTGGGTCCGCCAGGCTCCGGGGCAGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7083)
		AA	EVQLLESGGDLVQPGGSLRLSCAASGFTTFSSYAMHWVRQAPGQGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQ TARITCGGNIGSKSVHWHQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGTKLTVL
			(SEQ ID NO: 7084)

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iPS:613527	18182-G4	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGGCACTTACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAGCAGC
			(SEQ ID NO: 7085)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMTWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFGN TATLIISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7086)

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iPS:613651	18182-G5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGGCACATACAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7087)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPASVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN FGNTATLIISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7088)

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iPS:613625	18182-G9		GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACGACGAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC	(SEQ ID NO: 7089)
		NA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELALTQPASASVAPG QTARISCGGNNIGSKGVQWYQQKPGQAPVLYVDNDRPSGIPERFSGSNF GNTATLIISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL	(SEQ ID NO: 7090)
		AA		

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iPS:613589	18182-G11	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTAGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GCCCAGTTCAACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7091)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTTYADSVKARFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVQWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGGTKLTVL
			(SEQ ID NO: 7092)

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iPS:613587	18182-H5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGGCACATACAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7093)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVVTQEPSVSVAPG QTARITCGGNNIGSKSVHWHQKPGQAPVLVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADFYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7094)

iPS:603153	18089-D12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTACCTATGG CATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAATGGGTGGC AGTTATATCATATGATGGAAGTAATAAATACTATGCAGACTCCCGTGAAG GGCCGATTCACCATCTCCAGAGACGATTCCAAAGAACACGCTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 7095) EVQLLESGGTVVQPGRLRLSCAASGFTFTSTYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARG QLLTGYWGQGTLLTVSSGGGGGGGGGGSELVMTQSPSSLSASVGDR VTITCRASQGISNYLAWYQQKPKVPKLLIYAASLTQSGVPSRFSGSGGT FTLTISLQPEDVATYYCQKYNAPFTFGPGTKVEIK
			(SEQ ID NO: 7096)

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iPS:613717	18179-G12	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAGGTCTCCTGCAAGGCTTCTGTTACACCTTTACCAGGAATG GTCTCAGCTGGGTGCGACAGGCCCTTGACAAAGGCTTGAAGTGGATGG GATGGATCAGCGGTTACAATGGTGACACAAACTATGCACAGAAAGCTCC AGGCAGAGGCACCATGACCACAGACACATCCACGAGCACAGCCTACA TGGAGCTGAGGAGC
			(SEQ ID NO: 7097)
		AA	EVQLLESGAEVKKPGASVKVCKASGYTFTRNGLSWVRQAPGQGLEWMG WISGYNGDTNYAQKLQGRGTMTTDTSTAYMELRSLRSDDTAVYYCAR GRATFDYWGGTLVTVSSGGGGGGGGGGSELVMTQSPSSLSASVGD RVTITCRASQGISNYLAWYQQKPKVPKLLISAASTLQSGVPSRFSGSGGT DFTLTISLQPEDVATYYCQKYNAPFTFGPGTKLEIK
			(SEQ ID NO: 7098)

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iPS:613759	18179-C1	NA	GAGGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGGCC TCAGTGAAAGGTCTCCTGCAAGGCTTCTGTTACACCTTTACCAGGAATG GTCTCAGCTGGGTGCGACAGGCCCTTGACAAAGGCTTGAAGTGGATGG GATGGATCAGCGGTTACAATGGTGACACAAACTATGCACAGAAAGCTCC AGGCAGAGGCACCATGACCACAGACACATCCACGAGCACAGCCTACA TGGAGCTGAGGAGC
			(SEQ ID NO: 7099)
		AA	EVQLLESGAEVKKPGASVKVCKASGYTFTRNGLSWVRQAPGQGLEWMG WISGYNGDTNYAQKLQGRGTMTTDTSTAYMELRSLRSDDTAVYYCAR GRATFDYWGGTLVTVSSGGGGGGGGGGSELVMTQSPSSLSASVGD RVTITCRASQGISNYLAWYQQKPKVPKLLISAASLTQSGVPSRFSGSGGT DFTLTISLQPEDVATYYCQKYNAPFTFGPGTKVDIK
			(SEQ ID NO: 7100)

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iPS:604976	18093-B11	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTGACTACTA CATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTC ATACATTAGTAAAGTGGTAGTACCATATATACTACGCAGACTCTGTGAAG GGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7101)
		AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSDYMSWIRQAPGKGLEWVSYI SKSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYNY GHFDYWGGQGLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQTAR ITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPSGIPERFSGSNSGNTA TLTISRVEAGDEADYYCQVVDSSDHHVVFVGGGTKLTVL
			(SEQ ID NO: 7102)

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iPS:613599	18182-B5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7103)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGTKLTVL
			(SEQ ID NO: 7104)

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iPS:613567	18182-H9	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGTGAAG GCCCAGTTCAACCATCTCCAGAGACAATTCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7105)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKARFTISRDN SKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNNIGSKSVHWHQKPGQAPVLVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADFCYQVWDSDDHVVFGGGTKLTVL
			(SEQ ID NO: 7106)

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iPS:613583	18182-E6	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCCGGATTACCTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7107)
		AA	EVQLLESGGGLVQPGLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCATGK GVHLNFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPSSVSAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRV AAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7108)

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iPS:613565	18182-G6	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGCCACATACACGACACTCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7109)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQ TARITCGGNIGSKSVHWHQKPGQSPVLVIYDDNDRPSGIPERFSGFNSGN TATLTISRVEAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7110)

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iPS:613647	18182-G2	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGCCACATACAAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7111)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVVDSSSDHVFGGTKLTVL
			(SEQ ID NO: 7112)

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iPS:613517	18182-H12	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATCCAAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7113)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLVTVSSGGGGSGGGGGGSELMLTQPHSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDSSDHHVVFGGTKLTVL
			(SEQ ID NO: 7114)

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iPS:613523	18182-G8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAAC TGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGGCACATACTACGCAGACTCCCGGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTG CAATGAACAGC	(SEQ ID NO: 7115)
		AA	EVQLLESGGGLVKPGGSLRLSCAASGFTTFSSYAMNWWVRQAPKGLEWVSA ISGSGGGTYADSGKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGK GVHLNFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL	(SEQ ID NO: 7116)

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iPS:613521	18182-E10	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTC GTCTATTAGTGTAGCGGTGGTGGCACATACTACGCAGCCTCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7117)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGQGLEWVSSI SGSGGGTYAAASVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLNFDYWGGTLVTVSSGGGGSGGGGGGSELALTQPASASVAPGQ TARITCGGNIGSKSVHWHQKPGQAPVLVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADFCYQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7118)

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iPS:613627	18182-B12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAGCAGC
			(SEQ ID NO: 7119)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNKNTLYLQMSSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWHQKPGQAPLVVYDDNDRPSGIPERFSGNSGN TATLTISRVEAGDEADYYCQVWDYSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7120)

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iPS:613525	18182-E5	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGAAGTGGTGGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
			(SEQ ID NO: 7121)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWHQKPGQAPLVVYDDNDRPSGIPERFSGNSGN TATLTISRVEAGDEADYYCQVWDYSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7122)

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iPS:613555	18182-A4	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGG TCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACTTTAGCAGCTATGC CATGACCTGGGTCCGCCAGGCTCCAGGCGAGGGCTGGAGTGGGTCTC GTCTATTAGTGGTAGTGGTGGTGGCACATACGCAGCCTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7123)
		AA	EVQLLESGGTVVQPGRLRLSCAASGFTFSYAMTWVRQAPGQGLEWVSS ISGSGGGTYAAASVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPVLVYDDNDRPSGIPERFSGSNFG NTATLIISRV AAGDEADYYCQVWDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7124)

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iPS:613545	18182-E1	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGGCACATACAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAAATGAACAGC
			(SEQ ID NO: 7125)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVVDSSSDHVVFGGGTKLTVL
			(SEQ ID NO: 7126)

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iPS:601102	18081-B9	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCTGTCCCTCACCCTGCACTGTCTCTGGTGACTCCATCAGTAGTACG TTACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTG GATTGGGAGTATCTATTATAGTGGGAGCACCTACTACAACCCGTCCCTC AAGAGTCGAGTCACCATATCCGTAGACACGTCCTCCAAAGAACCAAGTCTCTCCC TGAAAGCTGAGC
			(SEQ ID NO: 7127) EVQLLESGPGLVKPSETLSLTCTVSGDSISSRYYWGWIRQPPGKGLEWIGSI YYSGSTYYNPSLKSRLVTISVDTSKNQFSLKLSVTAADTA VYYCARGIFGVI TYFDYWGGQGLVTVSSGGGGSGGGGGGSELVMTQSPDSLAVSLGER ATINCKSSQSVLYSSNNKNYLA WYQQKPGQPPKLLIYWASTRESGVDRFS GSGSGTDFLTITISLQAEDEVAVYYCQQFYSTPITFGQGRLEIK
		AA	(SEQ ID NO: 7128)

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iPS:601120	18081-E7	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGTAGTAGTCG TTACTACTGGGGCTGGATCCGCCAGCCCCCAGGGAAGGGGCTGGAGTG GATTGGGAGTATCTATTATAGTGGGAGCACCTACTACAACCCGTCCTC AAGAGTCGAGTCACCATATCCGTAGACACGTCCTCCAAAGAACCACTTCTCCC TGAAGCTGAGC
			(SEQ ID NO: 7129) EVQLLESGPGLVKPSETLSLTCTVSGDSISSRYYWGWIRQPPGKGLEWIGSI YYSGSTYYNPSLKSRLVTISVDTSKNQFSLKLSVTAADTA VYYCARGIFGVI TYFDYWGGQGLVTVSSGGGGSGGGGGSELVMTQTPDSLAVSLGER ATINCKSSQSVLYSSNNKNYLA WYQQKPGQPPKLLIYWASTRESGVDRFS GSGSGTDFLTITISLQAEDVA VYYCQQYYSTPLTFGGGKVEIK
			(SEQ ID NO: 7130)

iPS:603137	18089-D11	NA	GAGGTGACGTGCTCGAGTCTGGTCTCTGTGCTGGTGAAACCCACACAGAACCTCACGCTGACCTGCACCTTCTCTGGTTCTCTATTCACCACTCATAAATGGGTGAGGACTGGATCCGTACGCCCCAGGAAAGGCCCTGGAGTGGCTTGCACTCATTTATTGGAATGATGATAAGCGCTACAACCCATCTCTGCAGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCCAGGTGGTCCTCACAATGACC
			(SEQ ID NO: 7131) EVQLLESGPVLVKPTQTLTLCTFSGFSTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYNPQLQSLTITKDTSKNQVLTMTNMDPVDATYYCAYRR YNWNYENWFDPPWGQGLVTVSSGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQISINYNWYQQKPKAPKLLIYAASLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYITPFTFGGGTKLEIK
iPS:603137	18089-D11	AA	(SEQ ID NO: 7132) EVQLLESGPVLVKPTQTLTLCTFSGFSTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYNPQLQSLTITKDTSKNQVLTMTNMDPVDATYYCAYRR YNWNYENWFDPPWGQGLVTVSSGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQISINYNWYQQKPKAPKLLIYAASLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYITPFTFGGGTKLEIK
			(SEQ ID NO: 7132) EVQLLESGPVLVKPTQTLTLCTFSGFSTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYNPQLQSLTITKDTSKNQVLTMTNMDPVDATYYCAYRR YNWNYENWFDPPWGQGLVTVSSGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQISINYNWYQQKPKAPKLLIYAASLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYITPFTFGGGTKLEIK

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iPS:603187	18089-C9	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTACGCTGGTGAACCCACACAG ACCTCAGCGTGACCTGCACCTTCTCTGGTTTCTCATTCACCACTCATAA AATGGGTGTGGACTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTG GCTTGCACTCATTTATTGGAATGATGATAAGCGCTACAGCCCATCTCTG CAGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCAAGGTGGTC CTCACAATGACC
			(SEQ ID NO: 7133) EVQLLESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAYRR YNWNYENWFDPPWGQGTLVTVSSGGGGGGGGGGSELQMTQSPSSLS ASVGDRTITCRASQFISSYLNWYQQKPGKAPKLLIYAASLQSGVPSRFSG RSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGPGTKVEIK
			(SEQ ID NO: 7134)

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iPS:603165	18089-D8	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTATGCTGGTGAACCCACACAGA CCCTCACGCTGACCTGCACCTTCTCTGGTTTCTCATTCAACCATCATAAA ATGGGTGTGGACTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTGG CTTGCACTCATTTATTGGAATGATGATAAGCGCTACAGCCCATCTCTGC AGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCAAGGTGGTCC TCACAATGACC
			(SEQ ID NO: 7135)
		AA	EVQLLESGPMLVKPTQTLTLCTFSGFSTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRR YNWNYENWFDPWGGTLTVSSGGGGGGGGGGSELVMTQSPDLS ASVGDRTITCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPSRFSG SGSGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQGTREIK
			(SEQ ID NO: 7136)

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iPS:601080	18081-F9	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTATGCTGGTGAACCCACACAGACCTCACGCTGACCTGCACCTTCTCTGGTTTCTCATTCAACCACTCATAAATGGGTGTGGACTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTGGCTTGCACTCATTTATTGGAATGATGATAAGCGCTACAGCCCCTCTCTGCAGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCAAGGTGGTCCTCACAATGACC
			(SEQ ID NO: 7137)
		AA	EVQLLESGPMLVKPTQTLTLCTFSGFSTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRR YNWN YENWFDPWGGTLTVSSGGGGGGGGGGGGSELQMTQSPSSLS ASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKVEIK
			(SEQ ID NO: 7138)

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iPS:601116	18081-H11	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTCGGCTGGTGAACCCACACAG ACCTCAGCGTGACCTGCACCTTCTCTGGTTTCTCATTCACCACTCATAA AATGGGTGTGGACTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTG GCTTGCACTCATTTATTGGAATGATGATAAGCGCTACAGCCCATCTCTG CAGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCAAGGTGGTC CTCACAATGACC
			(SEQ ID NO: 7139) EVQLLESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDDDKRYSPSLQSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAYRR YNWNYENWFDPPWGQGLTVTVSSGGGGGGGGGGSELQMTQSPSSL ASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYAASLQSGVPSRFS GSGGTDFTLTISSLQPEDFATYYCQQSYTTPFTFGPGTKVEIK
		AA	(SEQ ID NO: 7140)

iPS:601086	18081-B6	NA	GAGGTGACGCTGCTCGAGTCTGGTCTCTATGCTGGTGAAACCCACACAGAACCTCACGCTGACCTGCACCTTCTCTGGTTCTCATTCACCACTCATAAAATGGGTGTGGACTGGATCCGTACGCCCCAGGAAAGGCCCTGGAGTGGCTTGCACTCATTTATTGGAATGATGATAAGCGCTACAGCCCATCTCTGCAGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCCAGGTGGTCCTCACAATGACC
			(SEQ ID NO: 7141) EVQLLESGPMLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDDDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRR YNWNYENWFDPPWGQGLVTVSSGGGGGGGGGSELVMTQSPSSLS ASVGDRTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPSRFSG SGSGTDFTLTISSLQPEDFAATYYCQQSYSTPFTFGPGTKLEIK
iPS:601086	18081-B6	AA	(SEQ ID NO: 7142)

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iPS:603195	18089-B2	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCTCCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAGGGGCTGGAGTGGGTCTC AACTATTAGTATTAGTGGGTAGCACAAACTACGCAGACTCCCGTGAAG GGCCGGTTCACCATCTCCAGAGACAAATCCAAAGAACACGCTGTATCTGC AAATGAACAGC
			(SEQ ID NO: 7143)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGRGLEWVSTI SISGGSTNYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDGGS GWFPKLLHYGLDVWGQGTTVTVSSGGGGGGGGGGSELQMTQSPSS LSASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYAASLSQSGVPSRF SGSGSGTDFTLTISSLQPEDFATYYCQQSYSIPLTFGGGTKEIK
			(SEQ ID NO: 7144)

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iPS:613743	18179-E1	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACAAACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTATCTGCAAATG
			(SEQ ID NO: 7145) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCT TPSYSGSYNYFSVMDVWGQGTTVTVSSGGGGGGGGGGGSELVMTQ SPSSLASVGDVTVITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVP SRFSGSGSGTDFTLTISLQPEDFATYYCQQTYSMPFTFGPGTKVDIK
			(SEQ ID NO: 7146)

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iPS:613691	18179-H7	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTTAGACTCTCCTGTGCA GCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG CCGTATTAAAGCAAAACTTATGGTGGGACAACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTATCTGCAAATG
			(SEQ ID NO: 7147) EVQLLESGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYFSVMDVWVGQTTVTVSSGGGGGGGGGGGGSELQMTQS PSSLASVGDRTITCRTSQSISSYLNWFQQKPGKAPKLLIFAASSLQSGVPS RFSGSGSGTDFLTITSSLPEDFATYYCQQSYSSPFTFGPGTKVEIK
		AA	(SEQ ID NO: 7148)

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iPS:613785	18179-B12	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTTAGACTCTCCTGTGCAAGCCTCTGGATTCACTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7149)
iPS:613785	18179-B12	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNSGSYYNYFSVMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQS PSSLASVGDVTVITCRTSQSISSYLNWFQQKPGKAPKLLIFAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSMPTFTFGPGTKVEIK
			(SEQ ID NO: 7150)

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iPS:613733	18179-D11	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTTAGACTCTCTGTGTGACGCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7151)
iPS:613733	18179-D11	AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFSVMDVWQGTTTVTVSSGGGGGGGGGGGGSELQMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTITISLQPEDFATYYCQQTYSPMPFTFGPGTKVDIK
			(SEQ ID NO: 7152)

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iPS:613723	18179-D7	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACAACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7153) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFSVMDVWQGTTVTVSSGGGGGGGGGGSELVMTQS PSSLASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSMPFTFGPGTKVDIK
			(SEQ ID NO: 7154)

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iPS:613769	18179-A7	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTTAGACTCTCTGTGCAAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7155)
		AA	EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFSVMDVWGQGTITVSSGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSMPTFTFGPGTKVDIK
			(SEQ ID NO: 7156)

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iPS:615240	18181-H7	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCO TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGCCCTGGAGTG GATTGGGTACATCTCTTACAGTGGGATCACCAACTACAACCCCTCCCTC AAGAGTCGAGTCACCATGTCAGTGGACACGTCCCAAGAACCAAGTTCTCCO TGAAAGCTGACC
			(SEQ ID NO: 7157) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIGY ISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTSLTAADTAVYYCAREKMW FGVLNYYYGMDVWGQGTITVTVSSGGGGGGGGGGSELVMTQTPLSL PVTGPGEPAISCRSSQSLHNRNGYNLDWYLYQKPGQSPQLLIYLGSNRASGV PDRFSGSGGTDFTLKISRVEAGDVGVYYCMQALQTPWTFGGQGTKVEIK
		AA	(SEQ ID NO: 7158)

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iPS:615266	18181-G10	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCCGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCTCCCCGGGAAGGGCCTGGAGTG GATTGGGTACATCTCTTACAGTGGGAGCACCTTCTACAACCCGTCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCCC TGAATCTGACC
			(SEQ ID NO: 7159) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQLPGKLEWIGY ISYSGSTFYNPSLKS RVTVTISVDTSKNQFSLNLTSTVAADTAVYYCARDRLWF GVLNYYYGMDVWGLGTTVTVSSGGGGGGGGGSELVMTQSPLSLP VTPGEPASISCRSSQSLHSTGYNYVDWY LQKPGQSPQLLIYLGSNRASGVP DRFSGSGGTDFTLKISRVEAEDVGFYYCMQALQTPRTFGQGTKVEIK
		AA	(SEQ ID NO: 7160)

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iPS:615250	18181-G8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAATG
			(SEQ ID NO: 7161)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSNSGSYYNYFSVMDVWQGTTTVTVSSGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPKGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTITSSLPEDFATYYCQQTYSMPTFTFGGGTKVEIK
			(SEQ ID NO: 7162)

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iPS:615194	18181-F3	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGG TCCCTTAGACTCTCCTGTGCA GCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG CCGTATTAAAGGCAACACTTATGGTGGGACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAAGAGATGATTCAAAAAAACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7163)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPKGLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFVSMDVWQGTTTVTSSGGGGGGGGGGGSELVMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSSPFTFGPGTKVEIK
			(SEQ ID NO: 7164)

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iPS:615180	18181-F1	NA	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGG TCCCTTAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACAAACAGACTACGCTGCACC CGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACACGCT GTTTCTGCAAAATG
			(SEQ ID NO: 7165) EVQLLESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFSVMDVWQGTTTVTVSSGGGGGGGGGGSELVMTQS PSSLASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQTYSPPFTFGPGTKLEIK
		AA	(SEQ ID NO: 7166)

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iPS:615184	18181-E2	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCCAGGACTGGTGAAGCCTTCACAG ACCCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCO TTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGCCCTGGAGTG GATTGGGTACATCTCTCACAGTGGGAGCACTTATTACAATCCGTCCTC AAGAGTCGAGTAACCATATCATGATAGACACGTCTAAGAAATCAGTTCTCCC TGAATCTGACC
			(SEQ ID NO: 7167) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIGY ISHSGSTYYNPCLKSRVTISVDTSKNQFSLNLTSTAAADTAVYYCARDRLWH GVLNYYYGMDVWGLGTTVTVSSGGGGGGGGGSELVMTQSPLSLP VTPGEPASISCRSSQSLHSSGYNLDWYLQKPGQSPQLLIYLGSNRASGVP DRFSGSGGTDFTLKISKVEAEDVGYYCMQALQTPRTFGQGTKVDIK
		AA	(SEQ ID NO: 7168)

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iPS:615252	18181-C9	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCAGGACTGGTGAAAGCCTTCACAG ACCCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATCC TTACTACTGGAGCTGGATCCGCCAGCTCCCCGGGAAGGGCCTGGAGTG GATTGGGTACATCTCTTACAGTGGGAGCACCTTCTACAACCCGTCCTC AAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCAAGTTCTCCC TGAATCTGACC
			(SEQ ID NO: 7169) EVQLLESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQLPGKLEWIGY ISYSGSTFYNPSLKS RV TISVDTSKNQFSLNLT SVT AADTA VYYCARDRLWF GVLNYYYGMDVWGLGTTVTVSSGGGGGGGGGGSELVLTQSPLSLP VTPGEPASISCRSSQSLLHRNGYN YLDWY LQKPGQSPQLLIYLGSNRASGVVP DRFSGSGGTDFTLKISRVEAEDVGVYYCMQGLQTPFTFGPGTKVEIK
		AA	(SEQ ID NO: 7170)

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iPS:615242	18181-B8	NA	GAGGTGCAGCTGCTCGAGTCGGGGCCCAGGACTGGTGAAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGGTTCCATCAGCAGTGGTG GTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGT GGATTGGGTACATCTCTCACAGTGGGAGCACTTATTACAATCCGTCCT CAAGAGTCGAGTAACCATATCAGTAGACACGCTCTAAGAAATCAGTTCTCC CTGAATCTGACC
			(SEQ ID NO: 7171) EVQLLESGPGLVKPSQTLSTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YISHSGSTYYNPSLKSRVTISVDTSKNQFSLNLTSTVAADTA VYFCAREKM WFGVLNYYYGMDVWVGQGTTVTVSSGGGGGGGGGGSELVMTQTPL SLPVTPGEPASISCRSSQSLHNRNGYNLDWYLYLQKPGQSPQLLIYLGSNRAS GVPDRFIGSGSGTDFLTLEISRVEAEDVGVYYCMQALQTPSFQGQTKVEIK
		AA	(SEQ ID NO: 7172)

iPS:615222	18181-A6	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGTCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGTATTAAAGGCAACACTTATGGTGGGACACACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTATCTGCAATG (SEQ ID NO: 7173)
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSVVRQAPGKLEWVG RIKGNTYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCT TPSYSGSYNYFSVMDVWGQGTITVTVSSGGGGGGGGGGGGSELVMTQ SPSSLSASVGDRTITCRASQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVP SRFSGSGSGTDFTLTISSLQPEDFATYYCQQQYTSMPFTFGPGTKLEIK (SEQ ID NO: 7174)
iPS:1855072	18403-F12-AS	NA	No info. seq available
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSA ISGSGGGTYAAASVKGRFTISRDNKNTLYLQMSSLRAEDTAVYYCVTKG VHLGFDYWGGTLLTVTVSSGGGGGGGGGGGGSSVLTQPPSVSVAPGQT ARITCGGNNIGSKSVHWYQQKPGAPVMVVDNDRPSGIPERFSGSNFG NTATLIISRVAAAGDEADYYCQVWDYRYLSQVFGGGTKLTVL

iPS:1855074	18403-G10-AS	NA	(SEQ ID NO: 7175) <i>No nuc. seq. available</i>
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYAAASVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGQGLTVTVSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDYSGRQVFGGGTKLTVL
iPS:1855054	02-C1-86-A4-N-F5_final	NA	(SEQ ID NO: 7176) <i>No nuc. seq. available</i>
		AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVA VISYDAETVKYAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARG QLLTGYWGGQGLTVTVSSGGGGGGGGSSDIQMTQSPSSLSASVGD VTITCRASQGISNYLAWYQQKPKVPLIYAASLTQSGVPSRFSGSGSGTD FTLTISLQPEDVATYYCQKYNAPFTFGPGTKVEIK
iPS:1855068	03-F3-88-B3-F9_final	NA	(SEQ ID NO: 7177) <i>No nuc. seq. available</i>
		AA	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVS ISKSSYTVTYADAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATYN YGHFDYWGGQGLTVTVSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNNIGSKSVHWYQQKPGQAPVLYVYDDADRPSGIPERFSGSNSG TATLTISRVEAGDEADYYCQVWDASAGYGVVFGGGTKLTVL
iPS:1855106	81-H7-SG-F28_final	NA	(SEQ ID NO: 7178) <i>No nuc. seq. available</i>

		AA	QVQLQESGPGLVKPSQTLSTCTVSGDSISSNPYYWSWIRQHPGKGLEWIG YISYSGITNYPNPSLKSRVTMSVDTSKNQFSLKLTSLTAADTAVYYCAREKM WFGVLNYYYGMDVWGQGTITVTVSSGGGGGGGGGGSDIVMTQTPL SLPVTPGEPASISCRSSQSLHRSYNYLDWYLOKPGQSPQLLIYLGSRAS GVPDFRFGSGSGTDFTLKISRVEAGDVGVYCMQALQTPWTFGQGTKEIK
iPS:1891845	18081-B9_final	NA	(SEQ ID NO: 7179) <i>No nuc. seq. available</i>
		AA	QVQLQESGPGLVKPSETLSLTCTVSGDSISSRYYWGWIQPPGKGLEWIGS IYYSGSTYYPNPSLKSRVTISVDTSKNQFSLKLTSSVTAADTAVYYCARGIFGV TYFDYWGGQGLVTVSSGGGGGGGGGGSDIVMTQSPDSLAVSLGERA TINCKSSQSVLYSSNNKNYLAWYQQKPGQPKLLIYWASTRESGVPDFRFG SGSGTDFTLTISLSLQAEDVAVYYCQFYSTPTITFGQGTLEIK
iPS:1891847	18398-C7_final	NA	(SEQ ID NO: 7180) <i>No nuc. seq. available</i>
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSSI SGSGGGTYAASVKGRFTISRDNSKNTLYQMNSLRAEDTAVYYCATGKG VHLGFDYWGGQGLVTVSSGGGGGGGGGGSSYVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDYSPLRHVFGGGTKLTVL
iPS:1891849	18403-D8_final	NA	(SEQ ID NO: 7181) <i>No nuc. seq. available</i>
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSTI SGSGGGTYAASVKGRFTISRDNSKNTLYQMNSLRAEDTAVYYCATGKG VHLGFDYWGGQGLVTVSSGGGGGGGGGGSSYVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFG NTATLTISRVEAGDEADYYCQVWDYRTLDWVFGGGTKLTVL

iPS:1855064	18403-D8_AS_final	NA	(SEQ ID NO: 7182) <i>No nuc. seq. available</i>
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKGLEWVSTI SGSGGGTYAASVKGRFTISRDNSKNTLYQMNSLRAEDTAVYYCATGKG VHLGFDYWGGQTLVTSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDYRTLDWVFGGGTKLTVL
iPS:1855066	18403-E11_AS_final	NA	(SEQ ID NO: 7183) <i>No nuc. seq. available</i>
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNAASVKGRFTISRDNSKNTLYQMNSLRAEDTAAYYCVTGK GVHLGFDYWGGQTLVTSSGGGGGGGGSSYYVLTQPPSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVL
iPS:1891851	18403-F12_final	NA	(SEQ ID NO: 7184) <i>No nuc. seq. available</i>
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDNSKNTLYQMSSLRAEDTAVYYCVTGK VHLGFDYWGGQTLVTSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFG NTATLIISRAAGDEADYYCQVWDYRYSQVFGGGTKLTVL
iPS:1855072	18403-F12-AS_final	NA	(SEQ ID NO: 7185) <i>No nuc. seq. available</i>

		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCVTGKG VHLGFDYWGGTTLVTVSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFG NTATLIISRVAAAGDEADYYCQVWDYRYLSQVFGGGTKLTVL (SEQ ID NO: 7186) <i>No nuc. seq. available</i>
iPS:1891853	18403-G10_final	NA	
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYAASVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCATGKG VHLGFDYWGGTTLVTVSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVL (SEQ ID NO: 7187) <i>No nuc. seq. available</i>
iPS:1855074	18403-G10-AS_final	NA	
		AA	EVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMSSLRAEDTAVYYCATGKG VHLGFDYWGGTTLVTVSSGGGGGGGGSSYYVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDYSGQRQVFGGGTKLTVL (SEQ ID NO: 7188) <i>No nuc. seq. available</i>
iPS:1891855	18409-E2_final	NA	
		AA	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIKSKTYGGTTDYAAPVKGRFTISRDNSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYFVSVMIDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQSYSSPFTFGPGTKVEIK

iPS:1891857	18409-F12_final		NA	(SEQ ID NO: 7189) <i>No nuc. seq. available</i>
		AA		QITLKESGPALVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPGKALEWLAL IYWNDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRRY NWNENWFDPPWGQGTLVTVSSGGGGGGGGGGSDIQMTQSPSSLAS SVGDRV/TITCQASQDISNYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSG RSGTDFTLTISSLPEDFATYYCQSYYPYPTLFGPGTKVEIK
iPS:1891859	18409-G10_final	NA		(SEQ ID NO: 7190) <i>No nuc. seq. available</i>
		AA		QITLKESGPALVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPGKALEWLAL IHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRRY WNYENWFDPPWGQGTLVTVSSGGGGGGGGGGSDIQMTQSPSSLAS VGDRV/TITCQASQDISNYFNWYQKPGKAPKLLIYAASSLQSGVPSRFSG GSGTDFTLTISSLPEDFATYYCQSYITPFTFGPGTKVEIK
iPS:1891861	18409-H7_final	NA		(SEQ ID NO: 7191) <i>No nuc. seq. available</i>
		AA		QITLKESGPALVKPTQTLTLTCTFSGFSFTTHKMGVDWIRQPPGKALEWLAL IYWNDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRRY NWNENWFDPPWGQGTLVTVSSGGGGGGGGGGSDIQMTQSPSSLAS SVGDRV/TITCQASQDISNYLNWYQKPGKAPKLLIYAASSLQSGVPSRFSG GSGTDFTLTISSLPEDFATYYCQSYFPVVEFGPGTKVEIK
iPS:1891863	18409-H10_final	NA		(SEQ ID NO: 7192) <i>No nuc. seq. available</i>

		AA	QITLKESGPTLVKPTQTLTCTFSGFSFTTHKMGVDWIRQPPGKALEWLAIIYWNDDKRYSPSLQSRLTITKDTSKNQVVL TMTNMDPVDATATYYCAYRRY NWNENWFDPWGQGTLVTVSSGGGGGGGGGGSDIQMTQSPSSL SVGDRVTITCQASQDISNYLNWYQKPGKAPKLLIYAASSLQSGVPSRFS RGSGTDFTLTISSLQPEDFATYYCQSYTPPTTFGPGTKVEIK
		NA	(SEQ ID NO: 7193) <i>No nuc. seq. available</i>
		AA	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIRSRSYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFVSMVDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSMPFTFGGGTKVEIK
		NA	(SEQ ID NO: 7194) <i>No nuc. seq. available</i>
		AA	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYFVSMVDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCIQAYTSPFTFGPGTKLEIK
		NA	(SEQ ID NO: 7195) <i>No nuc. seq. available</i>
		AA	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFVSMVDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQS PSSLSASVGDRTITCRTSQSISSYLNWYQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQTYSMPFTFGPGTKVDIK

iPS:1891871	18410-D6_final		NA	(SEQ ID NO: 7196) <i>No nuc. seq. available</i>
		AA		EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RILNNA YGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCT TPSYSGSYNYFSVMDVWGQGTITVTVSSGGGGGGGGGGSDIQMTQ SPSSLSASVGDRTITCRTSQSISSYLNWYQQKPGRAPKLLIFAASSLQGGVP SRFSGSGGTDFTLTISSLQPEDFATYYCQQTYSMPTFTGPGTKVDIK
iPS:1891873	18410-G10_final		NA	(SEQ ID NO: 7197) <i>No nuc. seq. available</i>
		AA		EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGQGTLVTVSSGGGGGGGGGGSSYYLTQPPSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWDYVAPRHVFGGGTKLTVL
iPS:1855092	18410-G10_AS_final		NA	(SEQ ID NO: 7198) <i>No nuc. seq. available</i>
		AA		EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNAAASVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGQGTLVTVSSGGGGGGGGGGSSYYLTQPPSVSVAPG QTARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSN SGNTATLTISRVEAGDEADYYCQVWDYVAPRHVFGGGTKLTVL
iPS:1891875	18410-H1_final		NA	(SEQ ID NO: 7199) <i>No nuc. seq. available</i>

		AA	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RITSGIYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYFVMDVWVGQGTTVTVSSGGSGGGGGSDIQMTQS PSSLASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQSGVPS RFSGSGGTDFTLTISSLQPEDFATYYCQQTYSMPFTFGPGTKVDIK (SEQ ID NO: 7200)
iPS:1891877	18410-H3_final	NA	<i>No nuc. seq. available</i>
		AA	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIRSRPYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYFVMDVWVGQGTTVTVSSGGSGGGGGSDIQMTQS PSSLASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQSGVPS RFSGSGGTDFTLTISSLQPEDFATYYCQQTYSMPFTFGPGTKLEIK (SEQ ID NO: 7201)
iPS:1891879	18486-A4_final	NA	<i>No nuc. seq. available</i>
		AA	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSTYGMHWVRQAPGKLEWVA VISYDASNKYYAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARG QLLTGYWVGQGTLVTVSSGGSGGGGGSDIQMTQSPSSLASVGDRT VTITCRASQGISNYLAWYQQKPKVPKLLIYAASLTQSGVPSRFSGSGGT FTLTISSLQPEDFATYYCQKYNAPFTFGPGTKVEIK (SEQ ID NO: 7202)

Table 55
scFv VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:586556	17724-C9	NA	AAGTCAGTCAGAGCCTTTATATAGTAC AATCAAAAGAACTACTTGGCC	TGGGCATCCACTAGGAATCT	CAGCAATATTATAGCTATCCGTACAG
			(SEQ ID NO: 7203)	(SEQ ID NO: 7919)	(SEQ ID NO: 8635)
		AA	KSSQSLYSNQKNYLA	WASTRES	QQYYSYPYT
IPS:586558	17724-G6		(SEQ ID NO: 7204)	(SEQ ID NO: 7920)	(SEQ ID NO: 8636)
		NA	AGTGCAGCTCAAATGTAAATTACATACAC	GACACATCCAAACTGGCTCCT	CATCAGTGGAGTAGTATACCCACCTACG
			(SEQ ID NO: 7205)	(SEQ ID NO: 7921)	(SEQ ID NO: 8637)
IPS:586574	17731-H8	AA	SASSNVNYIH	DTSKLAP	HQWSSYPPT
			(SEQ ID NO: 7206)	(SEQ ID NO: 7922)	(SEQ ID NO: 8638)
		NA	CGAGCAAGTGGGAATATTCACAAATTATTTA GCT	AATGCAAAACCTTAGCAGGA	CAACATCATTAATGGTACTCCGCTCAGC
IPS:586576	17732-A8	AA	RASGNHNYLA	(SEQ ID NO: 7207)	(SEQ ID NO: 8639)
			(SEQ ID NO: 7208)	NAKTLAG	QHHYGTPLT
		NA	AGGTCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATGTGGAT	TTGGGTCTTAATCGGGCCTCC	ATGCAAGCTCTACAAACTCTCTCCACC
IPS:587871	17745-E5	AA	RSSQSLYSNGYNYVD	(SEQ ID NO: 7209)	(SEQ ID NO: 8641)
			(SEQ ID NO: 7210)	LGSNRAS	MQALQTPPT
		NA	AGGTCTAGTCAGAGCCTCTGTATAGTAAT GGATACCACTATTTGGAT	TTGGGTCTTATCCGGGCCTCC	ATGCAACCTCTACAAACTCTCTCCACT
IPS:587897	17745-E8	AA	RSSQSLYSNGYHYLD	(SEQ ID NO: 7211)	(SEQ ID NO: 8643)
			(SEQ ID NO: 7212)	LGSIRAS	MQPLQTPPT
		NA	AGGTCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTTGGAT	TTGGGTCTTAAAGCGGCCTCC	ATGCAAGGTACACACTGGCCTCGGACG
IPS:587885	17745-G8	AA	RSSQSLYSNGYNYLD	(SEQ ID NO: 7213)	(SEQ ID NO: 8645)
			(SEQ ID NO: 7214)	LGSKRAS	MQGTHWPRT
		NA	AGGCCAGTCAGAGTGTAGCAGCAGCTA CTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGGTCACTATTCACT
IPS:588445	17748-D12	AA	RASQSVSSSYLA	(SEQ ID NO: 7215)	(SEQ ID NO: 8647)
			(SEQ ID NO: 7216)	GASSRAT	QQYGRSLFT
		NA	AGGCCAGTCAGAGTGTAGCAGCAGCTA CTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGGTCACTACCGCTCACT
IPS:589113	17753-F4	AA	RASQSVSSSYLA	(SEQ ID NO: 7217)	(SEQ ID NO: 8649)
			(SEQ ID NO: 7218)	GASSRAT	QQYGRSLFT
		NA	AGGTCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTTGGAT	TTGGGTCTTAAATCGGGCCTCC	ATGCAAGCTCTACAAACTCCCATTTCACT
IPS:590622	17771-D2	AA	RSSQSLYSNGYNYLD	(SEQ ID NO: 7219)	(SEQ ID NO: 8651)
			(SEQ ID NO: 7220)	LGSNRAS	MQALQTPPT
		NA	CGGGCAGTCAGGGTATTAGCAGCTGGTTA GCC	GCTGCATCCAGTTTGCAAAAGT	CAACAGGCTAACAGTTTCCCTCCGACG
			(SEQ ID NO: 7221)	(SEQ ID NO: 7937)	(SEQ ID NO: 8653)

iPS:593066	17777-B4	AA	RASQISSWLA (SEQ ID NO: 7222)	AASLIQS (SEQ ID NO: 7938)	QQANSFPPT (SEQ ID NO: 8654)
		NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7223)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7939)	ATGCAAGCTCTACAAACTCCTCTCACT (SEQ ID NO: 8655)
		AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 7224)	LGSNRAS (SEQ ID NO: 7940)	MQALQTPPT (SEQ ID NO: 8656)
iPS:593048	17777-C4	NA	AGGGCAGTCAGAGTGTAGCAGCAGCTA CTTAGCC (SEQ ID NO: 7225)	GGTGCAATCCAGCAGGCCACT (SEQ ID NO: 7941)	CAGCAGTATGGTAGTCAACCGCTCACT (SEQ ID NO: 8657)
		AA	RASQVSSSYLA (SEQ ID NO: 7226)	GASSRAT (SEQ ID NO: 7942)	QQYSSPLT (SEQ ID NO: 8658)
iPS:593044	17777-C5	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7227)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7943)	ATGCAAGGTACACACTGGCCGCTCACT (SEQ ID NO: 8659)
		AA	RSSQSLLYSNGYNYVD (SEQ ID NO: 7228)	LGSNRAS (SEQ ID NO: 7944)	MQGTHWPLT (SEQ ID NO: 8660)
iPS:591971	17778-C9	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7229)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7945)	ATGCAAGCTCTACAAACTCCTCCGACG (SEQ ID NO: 8661)
		AA	RSSQSLLYSNGYNYVD (SEQ ID NO: 7230)	LGSNRAS (SEQ ID NO: 7946)	MQALQTPCS (SEQ ID NO: 8662)
iPS:591906	17778-F1	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACCACTATTGGAT (SEQ ID NO: 7231)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7947)	ATGCAAGCTCTACAAACTCCTCCGACG (SEQ ID NO: 8663)
		AA	RSSQRLFSNGYHYLD (SEQ ID NO: 7232)	LGSNRAS (SEQ ID NO: 7948)	MQALQTPPT (SEQ ID NO: 8664)
iPS:591901	17778-H8	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7233)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7949)	ATGCAAGCTCTACAAACTCCTCCGACG (SEQ ID NO: 8665)
		AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 7234)	LGSNRAS (SEQ ID NO: 7950)	MQALQTPPT (SEQ ID NO: 8666)
iPS:593068	17779-D11	NA	CGGCAAGTCAGAGCATTAGCAGCTATTTA AAT (SEQ ID NO: 7235)	GATGCAATCCAGTTTGCAAAAGT (SEQ ID NO: 7951)	CAACAGAGTTACAGAACCCCTCCGACG (SEQ ID NO: 8667)
		AA	RASQISSYLN (SEQ ID NO: 7236)	DASSLOS (SEQ ID NO: 7952)	QQSYRTPPT (SEQ ID NO: 8668)
iPS:593050	17779-E1	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACCACTATTGGAT (SEQ ID NO: 7237)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7953)	ATGCAAGCTCTACAAACTCCTCAATCACT (SEQ ID NO: 8669)
		AA	RSSQSLLYSNGYHYLD (SEQ ID NO: 7238)	LGSNRAS (SEQ ID NO: 7954)	MQALQTPPT (SEQ ID NO: 8670)
iPS:591857	17780-D12	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7239)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7955)	ATGCAAGCTCTACAAACTCCTCGATCACC (SEQ ID NO: 8671)
		AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 7240)	LGSNRAS (SEQ ID NO: 7956)	MQALQTPPT (SEQ ID NO: 8672)
iPS:591851	17780-E6	NA	AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7241)	TGGGTTCTAATCGGGCCCTCC (SEQ ID NO: 7957)	ATGCAAGGTACACACTGGCCATTCACCT (SEQ ID NO: 8673)
		AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 7241)	LGSNRAS (SEQ ID NO: 7957)	MQGTHWPTT (SEQ ID NO: 8673)

PS:591859	17781-B3	NA	(SEQ ID NO: 7242) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7958) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8674) ATGCAAGCTCTACAAACTCCGTGGACG
		AA	(SEQ ID NO: 7243) RSSQSLLYSNGYNYLD	(SEQ ID NO: 7959) LGSNRAS	(SEQ ID NO: 8675) MQALQTPWT
		NA	(SEQ ID NO: 7244) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7960) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8676) ATGCAAGCTATACAGCTTCCTGTGGACG
PS:591845	17781-H12	AA	(SEQ ID NO: 7245) RSSQSLLYSNGYNYVD	(SEQ ID NO: 7961) LGSNRAS	(SEQ ID NO: 8677) MQSIQLPWT
		NA	(SEQ ID NO: 7246) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7962) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8678) ATGCAAGGTACACACTGGCCCTCTCACT
		AA	(SEQ ID NO: 7247) RSSQSLLYSNGYNYLD	(SEQ ID NO: 7963) LGSYRAS	(SEQ ID NO: 8679) MQGTHWPILT
PS:593026	17783-C11	AA	(SEQ ID NO: 7248) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7964) TTGGTCTCTAAGCGGGCCTCC	(SEQ ID NO: 8680) ATGCAAGCTCTACAAACTCCGCTCACT
		AA	(SEQ ID NO: 7249) RSSQSLLFSNGYNYLD	(SEQ ID NO: 7965) LVSKRAS	(SEQ ID NO: 8681) MQALQTPILT
		NA	(SEQ ID NO: 7250) CGGGAAGTCAGAGCATTAGCAGCTATTTA AAT	(SEQ ID NO: 7966) GCTGCATCCAGTTTGCAAAGT	(SEQ ID NO: 8682) CAACAGAGTTACAGTACCCCTCCGACG
PS:593062	17784-B9	AA	(SEQ ID NO: 7251) RASQSISSVLN	(SEQ ID NO: 7967) AASSLQS	(SEQ ID NO: 8683) QQSYSTPPT
		NA	(SEQ ID NO: 7252) CGGGCGAGTCAGGGCAATTAGCAATTATTTA GCC	(SEQ ID NO: 7968) GCTGCATCCAGTTTGCAAAGT	(SEQ ID NO: 8684) CAACAGAGTTACAGTACCCCAATTCAC
		AA	(SEQ ID NO: 7253) RASQGISNYLA	(SEQ ID NO: 7969) AASSLQS	(SEQ ID NO: 8685) QQSYSTPPT
PS:593034	17784-C7	AA	(SEQ ID NO: 7254) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7970) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8686) ATGCAAGGTACACACTGGCCAATTCAC
		AA	(SEQ ID NO: 7255) RSSQSLLYSNGYNYLD	(SEQ ID NO: 7971) LGSNRAS	(SEQ ID NO: 8687) MQGTHWPPT
		NA	(SEQ ID NO: 7256) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7972) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8688) ATGCAAGCTCTACAAACTCCGATCACC
PS:593042	17784-C11	AA	(SEQ ID NO: 7257) RSSQSLLHSNGYNYLD	(SEQ ID NO: 7973) LGSNRAS	(SEQ ID NO: 8689) MQALQTPILT
		NA	(SEQ ID NO: 7258) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7974) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8690) ATGCAAGCTCTACAAACTCTCCGACG
		AA	(SEQ ID NO: 7259) RSSQSLLFSNGYNYLD	(SEQ ID NO: 7975) LGSNRAS	(SEQ ID NO: 8691) MQALQTPPT
PS:593036	17784-G10	AA	(SEQ ID NO: 7260) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7976) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8692) ATGCAAGCTCTACAAACTCCATTCAC
		NA	(SEQ ID NO: 7261) AGGCTAGTCAGAGCCTCTGTATAGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7977) TTGGGTTCCTAAATCGGGCCTCC	(SEQ ID NO: 8693) ATGCAAGCTCTACAAACTCCATTCAC
		AA	(SEQ ID NO: 7262) RSSQSLLYSNGYNYLD	(SEQ ID NO: 7978) LGSNRAS	(SEQ ID NO: 8694) MQALQTPPT

IPS:592136	17813-D8	NA	CGGCGAGTCAGGGCAATTAGCAATTTA GCC	GCTGCATCCACTTTTGCAATCA	CAACAGAGTTACAGTACCCCCTCCGACG
		AA	RASQGISNYLA (SEQ ID NO: 7263)	AASTLQS (SEQ ID NO: 7979)	(SEQ ID NO: 8695) QQSYSTPPT (SEQ ID NO: 8696)
IPS:592170	17813-E3	NA	AGGTCTAGTCAGAGCCTCTCTGTATAGTAAT GGATACAACATAITTTGGAT	TGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAATCTCTCACT
		AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 7265)	LGSNRAS (SEQ ID NO: 7981)	(SEQ ID NO: 8697) MQALQSLT (SEQ ID NO: 8698)
IPS:592166	17813-E5	NA	AGGTCTAGTCAGAGCCTCTCTGTATAGTAAT GGATACAACATAITTTGGAT	TGGGTTCTAAGCGGGCCTCC	ATGCAGGCTCTACAAAATCCGCTCACT
		AA	RSSQSLLYSNGYNYLD (SEQ ID NO: 7268)	LGSKRAS (SEQ ID NO: 7983)	(SEQ ID NO: 8699) MQALQIPLT (SEQ ID NO: 8700)
IPS:592154	17813-F1	NA	AGGTCTAGTCGGAGCCTCTCTGCATAGTAAT GGATACAACATAITTTGGAT	TGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAAATCCTCAT
		AA	RSSRSLHNSGYNYLD (SEQ ID NO: 7269)	LGSNRAS (SEQ ID NO: 7985)	(SEQ ID NO: 8701) MQALQIPH (SEQ ID NO: 8702)
IPS:592150	17814-D9	NA	AAGTCTAGTCAGAGCCTCTCTGTATAGTAAT GGATACAACATAITTTGGAT	TGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAAATCCGATCAC
		AA	KSSQSLLYSNGYNYLD (SEQ ID NO: 7271)	LGSNRAS (SEQ ID NO: 7987)	(SEQ ID NO: 8703) MQALQIPT (SEQ ID NO: 8704)
IPS:603175	18071-B1	NA	ACTGGAACCAGCAGTGACGTTGGTGGTTAT AACTATGTCCTC	GAGGTCAGTAAGCGGCCCTCA	AGCTCATATACAGCAGCAGCACTCTGGTA
		AA	TGTSDDVGGYNYVS (SEQ ID NO: 7273)	EVSKRPS (SEQ ID NO: 7989)	(SEQ ID NO: 8705) SSYTSSSTLV (SEQ ID NO: 8706)
IPS:603181	18071-C4	NA	AAGTCCAGCCAGAGTGTTTTATACAGCTCC AACAAATAAGAACTACTTAGCT	TGGGCATCTACCCGGGAATCC	CAGCAATATTATAGTACTCCGTGGACG
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7276)	WASTRES (SEQ ID NO: 7991)	(SEQ ID NO: 8707) QQYYSTPWT (SEQ ID NO: 8708)
IPS:603133	18071-D4	NA	AAGTCCAGCCAGAGTGTTTTATACAGCTCC AACAAATAAGAACTACTTAGCT	TGGGCATCTACCCGGGAATCC	CAGCAATATTATAGTACTCCGTGGACG
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7277)	WASTRES (SEQ ID NO: 7993)	(SEQ ID NO: 8709) QQYYSTPWT (SEQ ID NO: 8710)
IPS:603207	18072-D6	NA	AGGCGAGTCAGAGTGTTAGCAGCAGCTA CTTAGCC	GGTGCATCCCGCAGGGCCACT	CAGCAGTATGGTAGCTCGCTCACT
		AA	RASQSVSSSYLA (SEQ ID NO: 7279)	GASARAT (SEQ ID NO: 7995)	(SEQ ID NO: 8711) QQYGSSLT (SEQ ID NO: 8712)
IPS:603185	18072-G9	NA	TCTGGCAGCAGCTCCAACATCGGAAGTAAT TATGTATAC	AGGAAATAATCAGCGGCCCTCA	GCAGCATGGGATGACAGCCTGAGTGGTGT GGTA
		AA	SGSSSNGSNYYV (SEQ ID NO: 7281)	RNNQRPS (SEQ ID NO: 7997)	(SEQ ID NO: 8713) AAWDDSLSGVV (SEQ ID NO: 8714)

iPS:603201	18074-G12	NA	CAGGCGAGTCAGGACATTAGCAACTATTTA AAT (SEQ ID NO: 7283)	GATGCATCCAATTGGAAACA (SEQ ID NO: 7999)	CAACAGAGTTACAGTATCCCTCCGACG (SEQ ID NO: 8715)
		AA	QASQDISNYLN (SEQ ID NO: 7284)	DASNLET (SEQ ID NO: 8000)	QOSYSIPPT (SEQ ID NO: 8716)
iPS:601126	18078-H6	NA	ACTGGGAACAGCAACAATGTTGGCAACCA AGGAGCAGCT (SEQ ID NO: 7285)	AGGAATAACAACCGGCCCTCA (SEQ ID NO: 8001)	TCAGCATGGGACAGCAGCCTCAGTGTCTGG GTG (SEQ ID NO: 8717)
		AA	TGNSNNVGNQGA (SEQ ID NO: 7286)	RNNRPS (SEQ ID NO: 8002)	SAWDSSLSAWV (SEQ ID NO: 8718)
iPS:601094	18079-C8	NA	ACTGGGAACAGCAACAATGTTGGCAACCA AGGAGCAGCT (SEQ ID NO: 7287)	AGGAATAACAACCGGCCCTCA (SEQ ID NO: 8003)	TCAGCATGGGACAGCAGCCTCAGTGTCTGG GTG (SEQ ID NO: 8719)
		AA	TGNSNNVGNQGA (SEQ ID NO: 7288)	RNNRPS (SEQ ID NO: 8004)	SAWDSSLSAWV (SEQ ID NO: 8720)
iPS:601106	18079-H4	NA	AAGTCAGCCAGAGTGTTTATACAGCTCC AACAAATAAGAACTACTTAGCT (SEQ ID NO: 7289)	TGGGCATCTACCCGGGAATCC (SEQ ID NO: 8005)	CAGCAATATTATAGTACTCCGTGGACG (SEQ ID NO: 8721)
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7290)	WASTRES (SEQ ID NO: 8006)	QQYYSIPWT (SEQ ID NO: 8722)
iPS:601064	18079-H11	NA	AAGTCAGCCAGAGTGTTTATACAGCTCC AACAAATAAGAACTACTTAGCT (SEQ ID NO: 7291)	TGGGCATCTACCCGGGAATCC (SEQ ID NO: 8007)	CAGCAATATTATAGTACTCCGTGGACG (SEQ ID NO: 8723)
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7292)	WASTRES (SEQ ID NO: 8008)	QQYYSIPWT (SEQ ID NO: 8724)
iPS:601108	18080-C5	NA	AGGTCTAGTCAGAGCCTCTGTCATAGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7293)	TGGGTCTTAATCGGGCCTCC (SEQ ID NO: 8009)	ATGCAAGCTCTACAACTCCTCGGACG (SEQ ID NO: 8725)
		AA	RSSQSLHNSNGNYLD (SEQ ID NO: 7294)	LGNSRAS (SEQ ID NO: 8010)	MQALQTPRT (SEQ ID NO: 8726)
iPS:601090	18080-H9	NA	AGGCCAGTCAGAGTGTTAGCAGCGGCTA CTTAGCC (SEQ ID NO: 7295)	GGTGCATCCAGCAGGGCCACT (SEQ ID NO: 8011)	CAGCAGTATGGTAGCTCACCATTCACT (SEQ ID NO: 8727)
		AA	RASQSVSSGYLA (SEQ ID NO: 7296)	CASSRAT (SEQ ID NO: 8012)	QQYGSPPFT (SEQ ID NO: 8728)
iPS:601096	18081-A6	NA	AAGTCAGCCAGAGTGTTTATACAGCTCC AACAAATAAGAACTACTTAGCT (SEQ ID NO: 7297)	TGGGCATCTACCCGGGAATCC (SEQ ID NO: 8013)	CAGCAATATTATAGTACTCCGCTCACT (SEQ ID NO: 8729)
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7298)	WASTRES (SEQ ID NO: 8014)	QQYYSIPLT (SEQ ID NO: 8730)
iPS:601070	18081-B5	NA	AGGTCTAGTCAGAGCCTCTGTCATCGTAAT GGATACAACTATTGGAT (SEQ ID NO: 7299)	TGGGTCTTAATCGGGCCTCC (SEQ ID NO: 8015)	ATGCAAGCTCTACAACTCCGATCACC (SEQ ID NO: 8731)
		AA	RSSQSLHNSNGNYLD (SEQ ID NO: 7300)	LGNSRAS (SEQ ID NO: 8016)	MQALQTPRT (SEQ ID NO: 8732)
iPS:601078	18081-C10	NA	AAGTCAGCCAGAGTGTTTATACAGCTCC AACAAATAAGAACTACTTAGCT (SEQ ID NO: 7301)	TGGGCATCTACCCGGGAATCC (SEQ ID NO: 8017)	CAGCAATATTATAGTACTCCGCTCACT (SEQ ID NO: 8733)
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7302)	WASTRES (SEQ ID NO: 8018)	QQYYSIPLT (SEQ ID NO: 8734)

PS:601114	18081-D6	NA	CGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	GCTGCATCCAGATTTGCAAAGT	CAACAGAGTTACAGTACCCCAATTCCT
		AA	RASQSISSYLN (SEQ ID NO: 7303)	(SEQ ID NO: 8019)	(SEQ ID NO: 8735)
		AA	RASQSISSYLN (SEQ ID NO: 7304)	AASLQS (SEQ ID NO: 8020)	QQSYSTPPT (SEQ ID NO: 8736)
PS:601098	18081-D12	NA	CGGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	GCTACATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCCTCCGACG
		AA	(SEQ ID NO: 7305)	(SEQ ID NO: 8021)	(SEQ ID NO: 8737)
		AA	RASQSISSYLN (SEQ ID NO: 7306)	ATSSLQS (SEQ ID NO: 8022)	QQSYSTPPT (SEQ ID NO: 8738)
PS:601130	18082-F5	NA	ACTGGAACCGACGAGTGACGTTGGTGGTTAT AACTATGTCCTC	GAGGTCAGTAAGCGGCCCTCA	AGCTCATATGCAAGGCAGCAACAATGTGGTA
		AA	(SEQ ID NO: 7307)	(SEQ ID NO: 8023)	(SEQ ID NO: 8739)
		AA	TGTSDDVGGYNYVS (SEQ ID NO: 7308)	EVSKRPS (SEQ ID NO: 8024)	SSYAGSNNVV (SEQ ID NO: 8740)
PS:601068	18084-E4	NA	AGGCCAGTCAGAGTGTTAGCAGCAGCTA CTTAGCC	GGTGCAATCCAGACGGGCCACT	CAGCAGTATGGAAGCTACCCGCTCACT
		AA	(SEQ ID NO: 7309)	(SEQ ID NO: 8025)	(SEQ ID NO: 8741)
		AA	RASQSVSSSYLA (SEQ ID NO: 7310)	GASSRAT (SEQ ID NO: 8026)	QQYGSSPLT (SEQ ID NO: 8742)
PS:603159	18086-H4	NA	AAGTCAGCCAGAGTGTTTATACAGCTCC AACAAATAAGAACTACTTAGCT	TGGGCATCTACCCGGGAATCC	CAGCAATATTATAGTACTCCGTGGACG
		AA	(SEQ ID NO: 7311)	(SEQ ID NO: 8027)	(SEQ ID NO: 8743)
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7312)	WASTRES (SEQ ID NO: 8028)	QQYYSTPWT (SEQ ID NO: 8744)
PS:603151	18088-B10	NA	AGGCCAGTCAGAGTGTTAGCAGCAGCTA CTTAGCC	GGTGCAATCCAGACGGGCCACT	CAGCAGTATGGTACCTCACCCGCTCACT
		AA	(SEQ ID NO: 7313)	(SEQ ID NO: 8029)	(SEQ ID NO: 8745)
		AA	RASQSVSSSYLA (SEQ ID NO: 7314)	GASTRAT (SEQ ID NO: 8030)	QQYGTSPLT (SEQ ID NO: 8746)
PS:603189	18088-E4	NA	AGGTCTAGTCAGAGCCTCCTGTATAGTAAT GGATACAACATAITTTGGAT	TTGGGTTCTAAGCGGGCCTCC	ATGCAAGTTCTACAAACCCCTCCGACG
		AA	(SEQ ID NO: 7315)	(SEQ ID NO: 8031)	(SEQ ID NO: 8747)
		AA	RSSQSLYSNGYNYLD (SEQ ID NO: 7316)	LGSKRAS (SEQ ID NO: 8032)	MQVLQTPPT (SEQ ID NO: 8748)
PS:603131	18089-B8	NA	AAGTCAGCCAGAGTGTTTATACAGCTCC AACAAATAAGAACTACTTAGCT	TGGGCATCTACCCGGGAATCC	CAGCAATATTATAGTACTCCGCTCACT
		AA	(SEQ ID NO: 7317)	(SEQ ID NO: 8033)	(SEQ ID NO: 8749)
		AA	KSSQSVLYSSNNKNYLA (SEQ ID NO: 7318)	WASTRES (SEQ ID NO: 8034)	QQYYSTPLT (SEQ ID NO: 8750)
PS:603139	18089-C8	NA	CGGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCCGCTCACT
		AA	(SEQ ID NO: 7319)	(SEQ ID NO: 8035)	(SEQ ID NO: 8751)
		AA	RASQSISSYLN (SEQ ID NO: 7320)	AASLQS (SEQ ID NO: 8036)	QQSYSTPLT (SEQ ID NO: 8752)
PS:603169	18089-G7	NA	CGGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	GCTACATCCAGTTTGCAAAGT	CAACAGAGTTACAGTATCCCAATTCCT
		AA	(SEQ ID NO: 7321)	(SEQ ID NO: 8037)	(SEQ ID NO: 8753)
		AA	RASQSISSYLN (SEQ ID NO: 7322)	ATSSLQS (SEQ ID NO: 8038)	QQSYSTPPT (SEQ ID NO: 8754)

PS:603179	18089-G11	NA	CAGCGAGTCAGGACATTAGCAACTATTTA AAT	GCTGCATCCAGTTTGCAAAGT	CAACAGAGTTACAGTACCCCGCTCACT
		AA	QASQDISNYLN (SEQ ID NO: 7323)	AASSLQS (SEQ ID NO: 8039)	QQSYSTPLT (SEQ ID NO: 8755)
		NA	CGGCGAGTCAGGCGATTAGCAATTATTG GCA	GGTGCAATCCACTTTGCAAATTA (SEQ ID NO: 7324)	CAAAAGATTACAGTATGCCCAATTCAC
PS:603191	18089-H9	AA	RASQDISNYLA (SEQ ID NO: 7325)	GASTLQL (SEQ ID NO: 8041)	QKYSAPPT (SEQ ID NO: 8757)
		NA	CGGCAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGCAAAGT (SEQ ID NO: 7326)	CAACAGAGTTACAGTACCCCAATTCAC
		AA	RASQISSYLN (SEQ ID NO: 7328)	AASSLQS (SEQ ID NO: 8042)	QKYSAPPT (SEQ ID NO: 8758)
PS:603205	18089-H12	AA	RASQISSYLN (SEQ ID NO: 7327)	AASSLQS (SEQ ID NO: 8043)	QKYSAPPT (SEQ ID NO: 8759)
		AA	RASQISSYLN (SEQ ID NO: 7328)	AASSLQS (SEQ ID NO: 8044)	QKYSAPPT (SEQ ID NO: 8760)
		NA	ACTGGGAACAGCAACAATGTTGGCAACCA AGGAGCAGCT	AGGAATAACAACCGGCCCTCA (SEQ ID NO: 7329)	TCAGCATGGGACAGCAGCCTCAGTGTCTGTGTA
PS:604972	18090-H9	AA	TGNSNNVGNQGA (SEQ ID NO: 7330)	RNNRPS (SEQ ID NO: 8045)	SAWDSLSAVV (SEQ ID NO: 8762)
		NA	CAGCGAGTCAGGACATTAGCAACTATTTA AAT	GCTGCATCCAGTTTGCAAAGT (SEQ ID NO: 7331)	CAACAGAGTTACAGTACCCCTCCGACG
		AA	QASQDISNYLN (SEQ ID NO: 7332)	AASSLQS (SEQ ID NO: 8046)	QKYSAPPT (SEQ ID NO: 8763)
PS:604980	18093-E2	AA	TGNSNNVGNQGA (SEQ ID NO: 7333)	RNNRPS (SEQ ID NO: 8047)	SAWDSLSAVV (SEQ ID NO: 8764)
		NA	CAGCGAGTCAGGACATTAGCAACTATTTA AAT	GCTGCATCCAGTTTGCAAAGT (SEQ ID NO: 7334)	CAACAGAGTTACAGTATGCCCTCCGACG
		AA	RASQISSYLN (SEQ ID NO: 7335)	AASSLQS (SEQ ID NO: 8051)	QKYSAPPT (SEQ ID NO: 8766)
PS:613775	18179-A3	NA	AGGTCATGTCAGAGCCTCTGCACAGAAAT GGATACAACTATTGGAT	TTGGGTTCTAATCGGGCCTCC (SEQ ID NO: 7336)	ATGCAAGCTCTACAAAATCCCAATTCAC
		AA	RSSQSLHRNGNYLD (SEQ ID NO: 7337)	LGSNRAS (SEQ ID NO: 8052)	MQALQTPPT (SEQ ID NO: 8767)
		NA	AGGTCATGTCAGAGCCTCTGCATAGTAAT GGATACAACTATTGGAT	TTGGGTTCTAATCGGGCCTCC (SEQ ID NO: 7338)	ATGCAAGCTCTACAAAATCCCAATTCAC
PS:613783	18179-A5	AA	RSSQSLHRNGNYLD (SEQ ID NO: 7339)	LGSNRAS (SEQ ID NO: 8053)	MQALQTPPT (SEQ ID NO: 8768)
		NA	AGGTCATGTCAGAGCCTCTGCATAGTAAT GGATACAACTATTGGAT	TTGGGTTCTAATCGGGCCTCC (SEQ ID NO: 7340)	ATGCAAGCTCTACAAAATCCCAATTCAC
		AA	RSSQSLHRNGNYLD (SEQ ID NO: 7341)	LGSNRAS (SEQ ID NO: 8054)	MQALQTPPT (SEQ ID NO: 8770)
PS:613707	18179-A9	NA	AGGTCATGTCAGAGCCTCTGCATAGTAAT GGATACAACTATTGGAT	TTGGGTTCTAATCGGGCCTCC (SEQ ID NO: 7342)	ATGCAAGCTCTACAAAATCCCAATTCAC
		AA	RSSQSLHRNGNYLD (SEQ ID NO: 7343)	LGSNRAS (SEQ ID NO: 8055)	MQALQTPPT (SEQ ID NO: 8771)
		NA	AGGTCATGTCAGAGCCTCTGCATAGTAAT GGATACAACTATTGGAT	TTGGGTTCTAATCGGGCCTCC (SEQ ID NO: 7344)	ATGCAAGCTCTACAAAATCCCAATTCAC
PS:613697	18179-A10	AA	RSSQSLHRNGNYLD (SEQ ID NO: 7345)	LGSNRAS (SEQ ID NO: 8056)	MQALQTPPT (SEQ ID NO: 8772)
		NA	AGGTCATGTCAGAGCCTCTGCATAGTAAT GGATACAACTATTGGAT	TTGGGTTCTAATCGGGCCTCC (SEQ ID NO: 7346)	ATGCAAGCTCTACAAAATCCCAATTCAC
		AA	RSSQSLHRNGNYLD (SEQ ID NO: 7347)	LGSNRAS (SEQ ID NO: 8057)	MQALQTPPT (SEQ ID NO: 8773)

IPS:613685	18179-B7	NA	CAGCGAGGCAAGGACATTAGCGACTATTTA AAT	(SEQ ID NO: 7343)	GCTGCATCCAGTTTTCGAAAGGT	CAACAGACTTACAGTATGCCATTCACT
		AA	QARQDIDYLN	AASLQG	(SEQ ID NO: 8059)	(SEQ ID NO: 8775)
			(SEQ ID NO: 7344)	(SEQ ID NO: 8060)	QQTYSMPFT	
IPS:613711	18179-B8	NA	CGGCAAGTCAGAGCAATTAACAGCTATTTA AAT	(SEQ ID NO: 7345)	GCTGCATCCAGTTTTCGAAAGT	CAACAGAGTTACAGTACCCCATTCACT
		AA	RTSQSINSYLN	AASLQS	(SEQ ID NO: 8061)	(SEQ ID NO: 8777)
			(SEQ ID NO: 7346)	(SEQ ID NO: 8062)	QQSYSIPFT	
IPS:613765	18179-C4	NA	AGGTCTAGTCAGAGCCCTCTGCATAGTACT GGATACAACTAATTGGAT	(SEQ ID NO: 7347)	TTGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAACTCTCTCGGACG
		AA	RSSQSLHSTGYNYLD	LGSNRAS	(SEQ ID NO: 8063)	(SEQ ID NO: 8779)
			(SEQ ID NO: 7348)	(SEQ ID NO: 8064)	MQALQIPRT	
IPS:613777	18179-C6	NA	AGGTCTAGTCAGAGCCCTCTGCATAGAAAT GGATACAAATATTGGAT	(SEQ ID NO: 7349)	TTGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAACTCTCTCGGAGG
		AA	RSSQSLHHRNGYNYLD	LGSNRAS	(SEQ ID NO: 8065)	(SEQ ID NO: 8781)
			(SEQ ID NO: 7350)	(SEQ ID NO: 8066)	MQALQIPRT	
IPS:613687	18179-C7	NA	AGGTCTAGTCAGAGCCCTCTGCATCGTAAT GGATACCCTAATTGGAT	(SEQ ID NO: 7351)	TTGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAACTCCAGT
		AA	RSSQSLHHRNGYHYLD	LGSNRAS	(SEQ ID NO: 8067)	(SEQ ID NO: 8783)
			(SEQ ID NO: 7352)	(SEQ ID NO: 8068)	MQALQIPS	
IPS:613787	18179-C10	NA	AGGTCTAGTCAGAGCCCTCTGCATAGAAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7353)	TTGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAACTCCAATTCACT
		AA	RSSQSLHHRNGYNYLD	LGSNRAS	(SEQ ID NO: 8069)	(SEQ ID NO: 8785)
			(SEQ ID NO: 7354)	(SEQ ID NO: 8070)	MQALQIPFT	
IPS:613675	18179-D8	NA	CGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	(SEQ ID NO: 7355)	GCTGCATCCAGTTTTCGAAAGGT	CAACAGACTTACAGTATGCCATTCACT
		AA	RTSQSISSYLN	AASLQG	(SEQ ID NO: 8071)	(SEQ ID NO: 8787)
			(SEQ ID NO: 7356)	(SEQ ID NO: 8072)	QQTYSMPFT	
IPS:613753	18179-D9	NA	CGGCAAGTCAGAGCAATTAACAGCTATTTA AAT	(SEQ ID NO: 7357)	GCTGCATCCAGTTTTCGAAAGT	CAACAGAGTTACAGTACCCCATTCACT
		AA	RTSQSINSYLN	AASLQS	(SEQ ID NO: 8073)	(SEQ ID NO: 8789)
			(SEQ ID NO: 7358)	(SEQ ID NO: 8074)	QQSYSIPFT	
IPS:613689	18179-E6	NA	CGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	(SEQ ID NO: 7359)	GCTGCATCCAGTTTTCGAAAGT	CAACAGACTTACAGTATGCCATTCACT
		AA	RTSQSISSYLN	AASLQG	(SEQ ID NO: 8075)	(SEQ ID NO: 8791)
			(SEQ ID NO: 7360)	(SEQ ID NO: 8076)	QQTYSMPFT	
IPS:613679	18179-F3	NA	AGGTCTAGTCAGAGCCCTCTGCATCGTAAT GGATACAACTAATTGGAT	(SEQ ID NO: 7361)	TTGGGTTCTAATCGGGCCTCC	ATGCAAGCTCTACAAACTCCAGT
		AA	RSSQSLHHRNGYNYLD	LGSNRAS	(SEQ ID NO: 8077)	(SEQ ID NO: 8793)
			(SEQ ID NO: 7362)	(SEQ ID NO: 8078)	MQALQIPS	

iPS:613701	18179-F4	NA	AGGTCTAGTCAGAGCCTCTGTCATCGTAAT (SEQ ID NO: 7363)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8079)	ATGCAAGCTCTCCAAACTCCATTCACT (SEQ ID NO: 8795)
		AA	RSSQSLHRNGYHYLD (SEQ ID NO: 7364)	LGSNRAS (SEQ ID NO: 8080)	MQALQTPPT (SEQ ID NO: 8796)
iPS:613715	18179-F6	NA	AGGTCTAGTCAGAGCCTCTGTCATAGTAAT (SEQ ID NO: 7365)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8081)	ATGCAAGCTCTACAAACTCTCTCGGACG (SEQ ID NO: 8797)
		AA	RSSQSLHNSNGYNYLD (SEQ ID NO: 7366)	LGSNRAS (SEQ ID NO: 8082)	MQALQTPPT (SEQ ID NO: 8798)
iPS:613731	18179-F10	NA	AGGTCTAGTCAGAGCCTCTGTCATAGTAAT (SEQ ID NO: 7367)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8083)	ATGCAAGCTCTACAAACTCTCTCGGACG (SEQ ID NO: 8799)
		AA	RSSQSLHNSNGYNYLD (SEQ ID NO: 7368)	LGSNRAS (SEQ ID NO: 8084)	MQALQTPPT (SEQ ID NO: 8800)
iPS:613681	18179-G8	NA	AGGTCTAGTCAGAGCCTCTGTCATAGAAAT (SEQ ID NO: 7369)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8085)	ATGCAAGCTCTACAAACTCTCTCGGACG (SEQ ID NO: 8801)
		AA	RSSQSLHRNGYNYLD (SEQ ID NO: 7370)	LGSNRAS (SEQ ID NO: 8086)	MQALQTPPT (SEQ ID NO: 8802)
iPS:613789	18179-G9	NA	AGGTCTAGTCAGAGCCTCTGTCATAGAAAT (SEQ ID NO: 7371)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8087)	ATGCAAGCTCTACAAACTCTCCAGT (SEQ ID NO: 8803)
		AA	RSSQSLHRNGYNYLD (SEQ ID NO: 7372)	LGSNRAS (SEQ ID NO: 8088)	MQALQTPS (SEQ ID NO: 8804)
iPS:613709	18179-H6	NA	AGGTCTAGTCAGAGCCTCTGTCATAGAAAT (SEQ ID NO: 7373)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8089)	ATGCAAGCTCTACATCTCTCTCCCACT (SEQ ID NO: 8805)
		AA	RSSQSLHRNGYNYLD (SEQ ID NO: 7374)	LGSNRAS (SEQ ID NO: 8090)	MQSLHLPPT (SEQ ID NO: 8806)
iPS:613779	18179-H9	NA	AGGTCTAGTCAGAGCCTCTGTCATCGTAAT (SEQ ID NO: 7375)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8091)	ATGCAAGCTCTACAAACTCCATTCACT (SEQ ID NO: 8807)
		AA	RSSQSLHRNGYHYLD (SEQ ID NO: 7376)	LGSNRAS (SEQ ID NO: 8092)	MQALQTPPT (SEQ ID NO: 8808)
iPS:615270	18181-A11	NA	AGGTCTAGTCAGAGCCTCTGTCATAGAAAT (SEQ ID NO: 7377)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8093)	ATGCAAGCTCTCCAAACTCCATTCACT (SEQ ID NO: 8809)
		AA	RSSQSLHRNGYNYLD (SEQ ID NO: 7378)	LGSNRAS (SEQ ID NO: 8094)	MQALQTPPT (SEQ ID NO: 8810)
iPS:615224	18181-C6	NA	AGGTCTAGTCAGAGCCTCTGTCATAGTACT (SEQ ID NO: 7379)	TTGGGTTCTAAATCGGGCCTCC (SEQ ID NO: 8095)	ATGCAAGCTCTACAAACTCTCTCGGACG (SEQ ID NO: 8811)
		AA	RSSQSLHSTGYNYLD (SEQ ID NO: 7380)	LGSNRAS (SEQ ID NO: 8096)	MQGLQTPPT (SEQ ID NO: 8812)
iPS:615238	18181-G7	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA (SEQ ID NO: 7381)	GCTGCATCCAGTTTGCAAGGT (SEQ ID NO: 8097)	CAACAGACTTACAGTATGCCATTCACT (SEQ ID NO: 8813)
		AA	RTSOSISSYLN (SEQ ID NO: 7382)	AASSLQ (SEQ ID NO: 8098)	QQTYSMPPT (SEQ ID NO: 8814)

IPS:613635	18182-B7	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAG	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVQ (SEQ ID NO: 7403)	DDNDRPS (SEQ ID NO: 8119)	QVWDSSDHVV (SEQ ID NO: 8835)
IPS:613543	18182-B10	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7405)	DDNDRPS (SEQ ID NO: 8121)	QVWDSSDHVV (SEQ ID NO: 8837)
IPS:613643	18182-C2	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAG	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7406)	DDNDRPS (SEQ ID NO: 8122)	QVWDSSDHVV (SEQ ID NO: 8838)
IPS:613607	18182-C3	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7407)	DDNDRPS (SEQ ID NO: 8123)	QVWDSSDHVV (SEQ ID NO: 8839)
IPS:613571	18182-C4	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7408)	DDNDRPS (SEQ ID NO: 8124)	QVWDSSDHVV (SEQ ID NO: 8840)
IPS:613661	18182-C5	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7410)	DDNDRPS (SEQ ID NO: 8126)	QVWDSSDHVV (SEQ ID NO: 8842)
IPS:613621	18182-C10	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7411)	DDNDRPS (SEQ ID NO: 8127)	QVWDSSDHVV (SEQ ID NO: 8843)
IPS:613629	18182-C12	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7412)	DDNDRPS (SEQ ID NO: 8128)	QVWDSSDHVV (SEQ ID NO: 8844)
IPS:613549	18182-D4	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7413)	DDNDRPS (SEQ ID NO: 8129)	QVWDSSDHVV (SEQ ID NO: 8845)
IPS:613645	18182-D8	NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7414)	DDNDRPS (SEQ ID NO: 8130)	QVWDSSDHVV (SEQ ID NO: 8846)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7415)	DDNDRPS (SEQ ID NO: 8131)	QVWDSSDHVV (SEQ ID NO: 8847)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7416)	DDNDRPS (SEQ ID NO: 8132)	QVWDSSDHVV (SEQ ID NO: 8848)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7417)	DDNDRPS (SEQ ID NO: 8133)	QVWDSSDHVV (SEQ ID NO: 8849)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7418)	DDNDRPS (SEQ ID NO: 8134)	QVWDSSDHVV (SEQ ID NO: 8850)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7419)	DDNDRPS (SEQ ID NO: 8135)	QVWDSSDHVV (SEQ ID NO: 8851)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7420)	DDNDRPS (SEQ ID NO: 8136)	QVWDSSDHVV (SEQ ID NO: 8852)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7421)	DDNDRPS (SEQ ID NO: 8137)	QVWDSSDHVV (SEQ ID NO: 8853)
		NA	GGGGAACAAACATTGGAAGTAAAAAGTGT GCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA
		AA	GGNIGKSVH (SEQ ID NO: 7422)	DDNDRPS (SEQ ID NO: 8138)	QVWDSSDHVV (SEQ ID NO: 8854)

IPS:613537	18182-D9	NA	GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAATAGTGATCATGTG GTA
		AA	(SEQ ID NO: 7423) GGNIGSKSVH	(SEQ ID NO: 8139) DDNDRPS	(SEQ ID NO: 8855) QVWDSNSDHVV
			(SEQ ID NO: 7424) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8140) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8856) CAGGTGTGGGATAGTAGTAGTGATCATGTG ATA
IPS:613541	18182-D11	NA	(SEQ ID NO: 7425) GGNIGSKSVH	(SEQ ID NO: 8141) DDNDRPS	(SEQ ID NO: 8857) QVWDSNSDHVI
		AA	(SEQ ID NO: 7426) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8142) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8858) CAGGTGTGGGATAGTAGTAGTGATCATGTG GTA
			(SEQ ID NO: 7427) GGNIGSKSVH	(SEQ ID NO: 8143) DDNDRPS	(SEQ ID NO: 8859) QVWDSNSDHVV
IPS:613657	18182-E2	NA	(SEQ ID NO: 7428) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8144) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8860) CAGGTGTGGGATAGTAGTAGTGATCATGTG GTA
		AA	(SEQ ID NO: 7429) GGNIGSKSVQ	(SEQ ID NO: 8145) DDNDRPS	(SEQ ID NO: 8861) QVWDSNSDHVV
			(SEQ ID NO: 7430) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8146) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8862) CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA
IPS:613595	18182-E8	NA	(SEQ ID NO: 7431) GGNIGSKSVH	(SEQ ID NO: 8147) DDNDRPS	(SEQ ID NO: 8863) QVWDSNSDHVV
		AA	(SEQ ID NO: 7432) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8148) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8864) CAGGTGTGGGATAGTAGTAGTGATCATGTG GTA
			(SEQ ID NO: 7433) GGNIGSKSVH	(SEQ ID NO: 8149) DDNDRPS	(SEQ ID NO: 8865) QVWDSNSDHVV
IPS:613667	18182-E11	NA	(SEQ ID NO: 7434) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8150) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8866) CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA
		AA	(SEQ ID NO: 7435) GGNIGSKSVH	(SEQ ID NO: 8151) DDNDRPS	(SEQ ID NO: 8867) QVWDSNSDHVV
			(SEQ ID NO: 7436) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8152) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8868) CAGGTGTGGGATAGTAGTAGTGATCATGTG ATG
IPS:613529	18182-F1	NA	(SEQ ID NO: 7437) GGNIGSKSVH	(SEQ ID NO: 8153) DDNDRPS	(SEQ ID NO: 8869) QVWDSNSDHVM
		AA	(SEQ ID NO: 7438) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8154) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8870) CAGGTGTGGGATAGTAGTAGTGATCATGTG GTA
			(SEQ ID NO: 7439) GGNIGSKSVH	(SEQ ID NO: 8155) DDNDRPS	(SEQ ID NO: 8871) QVWDSNSDHVV
IPS:613531	18182-F6	NA	(SEQ ID NO: 7440) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8156) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8872) CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA
		AA	(SEQ ID NO: 7441) GGNIGSKSVH	(SEQ ID NO: 8157) DDNDRPS	(SEQ ID NO: 8873) QVWDSNSDHVV
			(SEQ ID NO: 7442) GGNIGSKSVH	(SEQ ID NO: 8158) DDNDRPS	(SEQ ID NO: 8874) QVWDSNSDHVV
IPS:613641	18182-G3	NA	(SEQ ID NO: 7443) GGGGAAACAACATTGGGAAGTAAAAGTGTGCAC	(SEQ ID NO: 8159) GATGATAACGACCGGCCCTCA	(SEQ ID NO: 8875) CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA
		AA	(SEQ ID NO: 7444) GGNIGSKSVH	(SEQ ID NO: 8160) DDNDRPS	(SEQ ID NO: 8876) QVWDSNSDHVV
			(SEQ ID NO: 7445) GGNIGSKSVH	(SEQ ID NO: 8161) DDNDRPS	(SEQ ID NO: 8877) QVWDSNSDHVV

IPS:613527	18182-G4	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7443)	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA (SEQ ID NO: 8875)
		AA	GGNIGSKSVH (SEQ ID NO: 7444)	DDNDPRS	QVWDSSSDHVV (SEQ ID NO: 8876)
IPS:613651	18182-G5	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7445)	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA (SEQ ID NO: 8877)
		AA	GGNIGSKSVH (SEQ ID NO: 7446)	DDNDPRS	QVWDSSSDHVV (SEQ ID NO: 8878)
IPS:613625	18182-G9	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7447)	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA (SEQ ID NO: 8879)
		AA	GGNIGSKGVQ (SEQ ID NO: 7448)	DDNDPRS	QVWDSSSDHVV (SEQ ID NO: 8880)
IPS:613589	18182-G11	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7449)	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTG GTA (SEQ ID NO: 8881)
		AA	GGNIGSKSVQ (SEQ ID NO: 7450)	DDNDPRS	QVWDSSSDHVV (SEQ ID NO: 8882)
IPS:613587	18182-H5	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7451)	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA (SEQ ID NO: 8883)
		AA	GGNIGSKSVH (SEQ ID NO: 7452)	DDNDPRS	QVWDSSSDHVV (SEQ ID NO: 8884)
IPS:603153	18089-D12	NA	CGGCGAGTCAGGGCATTAGCAATTATTTA GCC (SEQ ID NO: 7453)	GCTGCATCCACTTTGCAATCA	CAAAAGTATAACAGTGCCCAATTCAC (SEQ ID NO: 8885)
		AA	RASQGISNYLA (SEQ ID NO: 7454)	AASITLOS	QKYNAPPT (SEQ ID NO: 8886)
IPS:613717	18179-G12	NA	CGGCGAGTCAGGGCATTAGCAATTATTTA GCC (SEQ ID NO: 7455)	GCTGCATCCACTTTGCAATCA	CAAAAGTATAACAGTGCCCAATTCAC (SEQ ID NO: 8887)
		AA	RASQGISNYLA (SEQ ID NO: 7456)	AASITLOS	QKYNAPPT (SEQ ID NO: 8888)
IPS:613759	18179-C1	NA	CGGCGAGTCAGGGCATTAGCAATTATTTA GCC (SEQ ID NO: 7457)	GCTGCATCCACTTTGCAATCA	CAAAAGTATAACAGTGCCCAATTCAC (SEQ ID NO: 8889)
		AA	RASQGISNYLA (SEQ ID NO: 7458)	AASITLOS	QKYNAPPT (SEQ ID NO: 8890)
IPS:604976	18093-B11	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7459)	GATGATAGCGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATCAT GTGGTA (SEQ ID NO: 8891)
		AA	GGNIGSKSVH (SEQ ID NO: 7460)	DDSDPRS	QVWDSSSDHVV (SEQ ID NO: 8892)
IPS:613599	18182-B5	NA	GGGGAACAACATTGGAAGTAAAAAGTGT GCAC (SEQ ID NO: 7461)	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTGATCATGTG GTA (SEQ ID NO: 8893)
		AA	GGNIGSKSVH (SEQ ID NO: 7462)	DDNDPRS	QVWDSSSDHVV (SEQ ID NO: 8894)

PS:613567	18182-H9	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7463)	DDNDRPS (SEQ ID NO: 8179)	QVWDSSSDHVV (SEQ ID NO: 8895)
PS:613583	18182-E6	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7465)	DDNDRPS (SEQ ID NO: 8181)	QVWDSSSDHVV (SEQ ID NO: 8897)
PS:613565	18182-G6	NA	GGGGAAATAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7466)	DDNDRPS (SEQ ID NO: 8182)	QVWDSSSDHVV (SEQ ID NO: 8898)
PS:613647	18182-C2	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7468)	DDNDRPS (SEQ ID NO: 8184)	QVWDSSSDHVV (SEQ ID NO: 8900)
PS:613517	18182-H12	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7470)	DDNDRPS (SEQ ID NO: 8186)	QVWDSSSDHVI (SEQ ID NO: 8902)
PS:613523	18182-C8	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7472)	DDNDRPS (SEQ ID NO: 8188)	QVWDSSSDHVV (SEQ ID NO: 8904)
PS:613521	18182-E10	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7474)	DDNDRPS (SEQ ID NO: 8190)	QVWDSSSDHVV (SEQ ID NO: 8906)
PS:613627	18182-B12	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATTATAGTAGTGATCATGTGTG
		AA	GGNIGSKSVH (SEQ ID NO: 7476)	DDNDRPS (SEQ ID NO: 8192)	QVWDSSSDHVV (SEQ ID NO: 8908)
PS:613525	18182-E5	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTG
		AA	GGNIGSKSVH (SEQ ID NO: 7478)	DDNDRPS (SEQ ID NO: 8194)	QVWDSSSDHVV (SEQ ID NO: 8910)
PS:613555	18182-A4	NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGCAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7480)	DDNDRPS (SEQ ID NO: 8196)	QVWDSSSDHVV (SEQ ID NO: 8912)
		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTGCAC	GATGATAACGACCGGCCCTCA	CAGGTGTGGGATAGTAGTAGTGATCATGTGTGA
		AA	GGNIGSKSVH (SEQ ID NO: 7482)	DDNDRPS (SEQ ID NO: 8198)	QVWDSSSDHVV (SEQ ID NO: 8914)

IPS:613743	18179-E1	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8935) QQTYSMPFT (SEQ ID NO: 8936)
		AA	RTSQSISSYLN (SEQ ID NO: 7503) AASSLQ (SEQ ID NO: 8219) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8937) QQSYSSPFT (SEQ ID NO: 8938)
IPS:613691	18179-H7	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8939) QQTYSMPFT (SEQ ID NO: 8940)
		AA	RTSQSISSYLN (SEQ ID NO: 7504) AASSLQ (SEQ ID NO: 8220) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8941) QQTYSMPFT (SEQ ID NO: 8942)
IPS:613785	18179-B12	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8943) QQTYSMPFT (SEQ ID NO: 8944)
		AA	RTSQSISSYLN (SEQ ID NO: 7505) AASSLQ (SEQ ID NO: 8221) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8945) QQTYSMPFT (SEQ ID NO: 8946)
IPS:613733	18179-D11	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8947) QQTYSMPFT (SEQ ID NO: 8948)
		AA	RTSQSISSYLN (SEQ ID NO: 7506) AASSLQ (SEQ ID NO: 8222) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8949) QQTYSMPFT (SEQ ID NO: 8950)
IPS:613723	18179-D7	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8951) QQTYSMPFT (SEQ ID NO: 8952)
		AA	RTSQSISSYLN (SEQ ID NO: 7507) AASSLQ (SEQ ID NO: 8223) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8953) QQSYSSPFT (SEQ ID NO: 8954)
IPS:613769	18179-A7	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8955) QQTYSMPFT (SEQ ID NO: 8956)
		AA	RTSQSISSYLN (SEQ ID NO: 7508) AASSLQ (SEQ ID NO: 8224) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8957) QQTYSMPFT (SEQ ID NO: 8958)
IPS:615240	18181-H7	NA	AGGTCTAGTCAGAGCCTCTCTGATAGAAAT GGATACAACTATTGGAT	TTGGGTCTTAATCGGGCCCTCC	ATGCAAGCTCTACAAACTCCCTCGGACG (SEQ ID NO: 8947) MQALQTPWT (SEQ ID NO: 8948)
		AA	SSQSLHNRNGYNYLD (SEQ ID NO: 7513) AASSLQ (SEQ ID NO: 8229) AGGTCTAGTCAGAGCCTCTCTGATAGAAAT GGATACAACTATTGGAT		ATGCAAGCTCTACAAACTCCCTCGGACG (SEQ ID NO: 8949) MQALQTPWT (SEQ ID NO: 8950)
IPS:615266	18181-G10	NA	AGGTCTAGTCAGAGCCTCTCTGATAGAAAT GGATACAACTATTGGAT	TTGGGTCTTAATCGGGCCCTCC	ATGCAAGCTCTACAAACTCCCTCGGACG (SEQ ID NO: 8951) MQALQTPWT (SEQ ID NO: 8952)
		AA	SSQSLHNRNGYNYLD (SEQ ID NO: 7514) AASSLQ (SEQ ID NO: 8230) AGGTCTAGTCAGAGCCTCTCTGATAGAAAT GGATACAACTATTGGAT		ATGCAAGCTCTACAAACTCCCTCGGACG (SEQ ID NO: 8953) MQALQTPWT (SEQ ID NO: 8954)
IPS:615250	18181-G8	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8955) QQTYSMPFT (SEQ ID NO: 8956)
		AA	RTSQSISSYLN (SEQ ID NO: 7515) AASSLQ (SEQ ID NO: 8231) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8957) QQTYSMPFT (SEQ ID NO: 8958)
IPS:615194	18181-F3	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8959) QQTYSMPFT (SEQ ID NO: 8960)
		AA	RTSQSISSYLN (SEQ ID NO: 7516) AASSLQ (SEQ ID NO: 8232) CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT		CAACAGAGCTTACAGTATGCCATTCACT (SEQ ID NO: 8961) QQTYSMPFT (SEQ ID NO: 8962)

IPS:615180	18181-F1	NA	CGGACAAAGTCAGAGCAATTAGCAGCTATTTA AAT (SEQ ID NO: 7523)	GCTGCATCCAGTTTGGCAAGGT	CAACAGACTTACAGTAGTCCATTCACT
IPS:615184	18181-E2	AA	RTSQSISSYLN (SEQ ID NO: 7524)	AASLQG (SEQ ID NO: 8240)	QQTYSPPFT (SEQ ID NO: 8956)
		NA	AGGTCTAGTCAGAGCCTCCTGCATAGTAGT GGATACAACTAATTGGAT	TTGGGTTCTAATCGGGCCTCC	ATGCAGGCTCTACAAACTCCTCGGAGG
		AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7525)	LGSNRAS (SEQ ID NO: 8241)	MOALQTPRT (SEQ ID NO: 8957)
		NA	AGGTCTAGTCAGAGCCTCCTGCACAGAAAT GGATACAACTAATTGGAT	TTGGGTTCTAATCGGGCCTCC	ATGCAGGCTCTACAAACTCCTCAATCACT
IPS:615252	18181-C9	AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7526)	LGSNRAS (SEQ ID NO: 8242)	MOALQTPRT (SEQ ID NO: 8958)
		NA	AGGTCTAGTCAGAGCCTCCTGCACAGAAAT GGATACAACTAATTGGAT	TTGGGTTCTAATCGGGCCTCC	ATGCAGGCTCTACAAACTCCTCAATCACT
		AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7527)	LGSNRAS (SEQ ID NO: 8243)	MOALQTPRT (SEQ ID NO: 8959)
		NA	AGGTCTAGTCAGAGCCTCCTGCATAGAAAT GGATACAACTAATTGGAT	TTGGGTTCTAATCGGGCCTCC	ATGCAGGCTCTACAAACTCCTCAATCACT
IPS:615242	18181-B8	AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7528)	LGSNRAS (SEQ ID NO: 8244)	MOALQTPRT (SEQ ID NO: 8960)
		NA	AGGTCTAGTCAGAGCCTCCTGCATAGAAAT GGATACAACTAATTGGAT	TTGGGTTCTAATCGGGCCTCC	ATGCAGGCTCTACAAACTCCTCAATCACT
		AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7529)	LGSNRAS (SEQ ID NO: 8245)	MOALQTPRT (SEQ ID NO: 8961)
		NA	AGGTCTAGTCAGAGCCTCCTGCATAGAAAT GGATACAACTAATTGGAT	TTGGGTTCTAATCGGGCCTCC	ATGCAGGCTCTACAAACTCCTCAATCACT
IPS:615222	18181-A6	AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7530)	LGSNRAS (SEQ ID NO: 8246)	MOALQTPRT (SEQ ID NO: 8962)
		NA	CGGCAAGTCAGAGCAATTAGCAGCTATTTA AAT	GCTGCATCCAGTTTGGCAAGGT	CAACAGACTTACAGTAGTCCATTCACT
		AA	RASQSISSYLN (SEQ ID NO: 7531)	AASLQG (SEQ ID NO: 8247)	QQTYSMPFT (SEQ ID NO: 8963)
		NA	RASQSISSYLN (SEQ ID NO: 7532)	AASLQG (SEQ ID NO: 8248)	QQTYSMPFT (SEQ ID NO: 8964)
IPS:1855072	18403-F12-AS	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GGNIGSKSVH (SEQ ID NO: 7533)	DDNDRPS (SEQ ID NO: 8249)	QVWDYRYLSQV (SEQ ID NO: 8965)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GGNIGSKSVH (SEQ ID NO: 7534)	DDNDRPS (SEQ ID NO: 8250)	QVWDYSGQRQV (SEQ ID NO: 8966)
IPS:1855054	02-C1-86-A4-N-F5_final	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RASQGISNYLA (SEQ ID NO: 7535)	AASLQS (SEQ ID NO: 8251)	QKYNAPFT (SEQ ID NO: 8967)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GGNIGSKSVH (SEQ ID NO: 7536)	DDADRPS (SEQ ID NO: 8252)	QVWDASAGYGVV (SEQ ID NO: 8968)
IPS:1855106	81-H7-SG-F78_final	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RSSQSLHSSGYNLYD (SEQ ID NO: 7537)	LGSNRAS (SEQ ID NO: 8253)	MOALQTPWT (SEQ ID NO: 8969)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KSSQSVLYSSNKNYLA (SEQ ID NO: 7538)	WASTRES (SEQ ID NO: 8254)	QQFYSTPIT (SEQ ID NO: 8970)
IPS:1891845	18081-B9_final	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KSSQSVLYSSNKNYLA (SEQ ID NO: 7538)	WASTRES (SEQ ID NO: 8254)	QQFYSTPIT (SEQ ID NO: 8970)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KSSQSVLYSSNKNYLA (SEQ ID NO: 7538)	WASTRES (SEQ ID NO: 8254)	QQFYSTPIT (SEQ ID NO: 8970)
IPS:1891847	18398-C7_final	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KSSQSVLYSSNKNYLA (SEQ ID NO: 7538)	WASTRES (SEQ ID NO: 8254)	QQFYSTPIT (SEQ ID NO: 8970)
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KSSQSVLYSSNKNYLA (SEQ ID NO: 7538)	WASTRES (SEQ ID NO: 8254)	QQFYSTPIT (SEQ ID NO: 8970)

		AA	GGNIGSKSVH (SEQ ID NO: 7539) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8255) <i>No int. seq. available</i>	QVWDYSPLRHV (SEQ ID NO: 8971) <i>No int. seq. available</i>
iPS:1891849	18403-D8_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7540) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8256) <i>No int. seq. available</i>	QVWDYRTILDWV (SEQ ID NO: 8972) <i>No int. seq. available</i>
iPS:185064	18403-D8_AS_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7541) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8257) <i>No int. seq. available</i>	QVWDYRTILDWV (SEQ ID NO: 8973) <i>No int. seq. available</i>
iPS:185066	18403-E11_AS_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7542) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8258) <i>No int. seq. available</i>	QVWDYYSNRAV (SEQ ID NO: 8974) <i>No int. seq. available</i>
iPS:1891851	18403-F12_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7543) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8259) <i>No int. seq. available</i>	QVWDYRYSQV (SEQ ID NO: 8975) <i>No int. seq. available</i>
iPS:185072	18403-F12-AS_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7544) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8260) <i>No int. seq. available</i>	QVWDYRYSQV (SEQ ID NO: 8976) <i>No int. seq. available</i>
iPS:1891853	18403-G10_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7545) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8261) <i>No int. seq. available</i>	QVWDYSGQRQV (SEQ ID NO: 8977) <i>No int. seq. available</i>
iPS:185074	18403-G10-AS_final	NA			
		AA	GGNIGSKSVH (SEQ ID NO: 7546) <i>No int. seq. available</i>	DDNDPS (SEQ ID NO: 8262) <i>No int. seq. available</i>	QVWDYSGQRQV (SEQ ID NO: 8978) <i>No int. seq. available</i>
iPS:1891855	18409-E2_final	NA			
		AA	RTSQSSSYLN (SEQ ID NO: 7547) <i>No int. seq. available</i>	AASSLQ (SEQ ID NO: 8263) <i>No int. seq. available</i>	QOSYSSPFT (SEQ ID NO: 8979) <i>No int. seq. available</i>
iPS:1891857	18409-F12_final	NA			
		AA	QASQDISNYLN (SEQ ID NO: 7548) <i>No int. seq. available</i>	AASSLQ (SEQ ID NO: 8264) <i>No int. seq. available</i>	QOSYYPTL (SEQ ID NO: 8980) <i>No int. seq. available</i>
iPS:1891859	18409-G10_final	NA			
		AA	QASQDISNYFN (SEQ ID NO: 7549) <i>No int. seq. available</i>	AASSLQ (SEQ ID NO: 8265) <i>No int. seq. available</i>	QOSYTPPT (SEQ ID NO: 8981) <i>No int. seq. available</i>
iPS:1891861	18409-H7_final	NA			
		AA	QASQDISNYLN (SEQ ID NO: 7550) <i>No int. seq. available</i>	AASSLQ (SEQ ID NO: 8266) <i>No int. seq. available</i>	QOSYFPVVE (SEQ ID NO: 8982) <i>No int. seq. available</i>
iPS:1891863	18409-H10_final	NA			
		AA	QASQDISNYLN (SEQ ID NO: 7551) <i>No int. seq. available</i>	AASSLQ (SEQ ID NO: 8267) <i>No int. seq. available</i>	QOSYTPPTT (SEQ ID NO: 8983) <i>No int. seq. available</i>
iPS:1891865	18410-B5_final	NA			

		AA	RTSOSISSYLN (SEQ ID NO: 7552)	AASSLQ (SEQ ID NO: 8268)	QQYTSMPFT (SEQ ID NO: 8984)
iPS:1891867	18410-B6_final	NA	No time seq available	No time seq available	No time seq available
		AA	RTSOSISSYLN (SEQ ID NO: 7553)	AASSLQ (SEQ ID NO: 8269)	IQAYTSPFT (SEQ ID NO: 8985)
iPS:1891869	18410-D3_final	NA	No time seq available	No time seq available	No time seq available
		AA	RTSOSISSYLN (SEQ ID NO: 7554)	AASSLQ (SEQ ID NO: 8270)	QQYTSMPFT (SEQ ID NO: 8986)
iPS:1891871	18410-D6_final	NA	No time seq available	No time seq available	No time seq available
		AA	RTSOSISSYLN (SEQ ID NO: 7555)	AASSLQ (SEQ ID NO: 8271)	QQYTSMPFT (SEQ ID NO: 8987)
iPS:1891873	18410-G10_final	NA	No time seq available	No time seq available	No time seq available
		AA	GGNIGSKSVH (SEQ ID NO: 7556)	DDNDPS (SEQ ID NO: 8272)	QVWDYVAPRHV (SEQ ID NO: 8988)
iPS:1855092	18410-G10_AS_final	NA	No time seq available	No time seq available	No time seq available
		AA	GGNIGSKSVH (SEQ ID NO: 7557)	DDNDPS (SEQ ID NO: 8273)	QVWDYVAPRHV (SEQ ID NO: 8989)
iPS:1891875	18410-H1_final	NA	No time seq available	No time seq available	No time seq available
		AA	RTSOSISSYLN (SEQ ID NO: 7558)	AASSLQ (SEQ ID NO: 8274)	QQYTSMPFT (SEQ ID NO: 8990)
iPS:1891877	18410-H3_final	NA	No time seq available	No time seq available	No time seq available
		AA	RTSOSISSYLN (SEQ ID NO: 7559)	AASSLQ (SEQ ID NO: 8275)	QQYTSMPFT (SEQ ID NO: 8991)
iPS:1891879	18486-A4_final	NA	No time seq available	No time seq available	No time seq available
		AA	RASQISNYLA (SEQ ID NO: 7560)	AASTLQ (SEQ ID NO: 8276)	QKYNAPFT (SEQ ID NO: 8992)

Table 56

scFv VH CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:586556	17724-C9	NA	AAGTCCTGGATGAAC	CGGATTATCTGGAGATGGAGATACTAAC TACAATGGGAAGTTCAAGGCC	GATGGAGTCTTCTATGCCCTCTTGCTTAC
		AA	(SEQ ID NO: 7561)	(SEQ ID NO: 8277)	(SEQ ID NO: 8993)
		AA	KSWMN	RIVPGDGDINYNKFKG	DGVFYAPLAY
			(SEQ ID NO: 7562)	(SEQ ID NO: 8278)	(SEQ ID NO: 8994)
iPS:586558	17724-G6	NA	AAGTCCTGGATGAAC	CGTGTGGCTGGAGATGGAGATACTACG TACAATGGGAAGTTCAAGGCC	GGCAATTACTTCGGTAGTAGCGAGGCGCTAC TTTGACTAC
			(SEQ ID NO: 7563)	(SEQ ID NO: 8279)	(SEQ ID NO: 8995)
		AA	KSWMN	RIVPGDGDITLYNEKFKG	GNYFGSEAYFDY
			(SEQ ID NO: 7564)	(SEQ ID NO: 8280)	(SEQ ID NO: 8996)
iPS:586574	17731-H8	NA	AGCTCCTGGATGAAC	CGGATTATCTGGAGATGGAGATACTAAC TACAATGGGAAGTTCAAGGCC	CGACAACITTAACACCGTCTTTGCTATGGAC TAC

		AA	(SEQ ID NO: 7565)	(SEQ ID NO: 8281)	(SEQ ID NO: 8997)
		SSWMN		RYPGDGDTNYNGKFKD	RQLNHVFAMDY
			(SEQ ID NO: 7566)	(SEQ ID NO: 8282)	(SEQ ID NO: 8998)
iPS:586576	17732-A8	NA	AGTTATGATATCAAC	TGGATGAACCCCTAACAGTGGTAAACACAGGC	GGGGTGGATACAGCAATGGTTACGACTA
			(SEQ ID NO: 7567)	TATGCACAGAAAGTTCAGGGC	CGGTATGGACGTC
		AA	SYDIN	(SEQ ID NO: 8283)	(SEQ ID NO: 8999)
			(SEQ ID NO: 7568)	WMNPSGNTGYAQKFG	GGGYSNGYDYGMDV
		NA	AGTTATGATATCAAC	(SEQ ID NO: 8284)	(SEQ ID NO: 9000)
			(SEQ ID NO: 7569)	TGGATGAACCCCTAACAGTGGTAAACACAGGC	GGGGTGGATACAGCTATGGTTACGACTAC
		AA	SYDIN	TATGCACAGAAAGTTCAGGGC	GGTATGGACGTC
			(SEQ ID NO: 7570)	(SEQ ID NO: 8285)	(SEQ ID NO: 9001)
		NA	GGTTACTACTGGAAC	WMNPSGNTGYAQKFG	GGGYSNGYDYGMDV
			(SEQ ID NO: 7571)	(SEQ ID NO: 8286)	(SEQ ID NO: 9002)
		AA	GYWYN	GAAATCAGTCAATAGTGAAGCAACCACTAC	GGCGTGGATACAGCTATGGTTATGACTAC
			(SEQ ID NO: 7572)	AACCCGTCCTCAAGAGT	GGTATGGACGTC
		NA	AGCTATGCCATGAGC	(SEQ ID NO: 8287)	(SEQ ID NO: 9003)
			(SEQ ID NO: 7573)	EHSISGNTNPNPLKS	GGGYSNGYDYGMDV
		AA	SYAMS	(SEQ ID NO: 8288)	(SEQ ID NO: 9004)
			(SEQ ID NO: 7574)	GCTATTAGTGGTAGTGGTGAATACATAC	CACCTACGATATTTTGACTGGCCCCCTTGAC
		NA	AGCTATGCCATGAGC	TACGCAGACTCCGTGAAGGGC	TAC
			(SEQ ID NO: 7575)	(SEQ ID NO: 8289)	(SEQ ID NO: 9005)
		AA	SYRMIH	AISGSDIITYYADSVKG	HLRYFDWPLDY
			(SEQ ID NO: 7576)	(SEQ ID NO: 8290)	(SEQ ID NO: 9006)
		NA	GGTTACTACTGGAAC	GTTATATCATATGATGGAGGTAAATAATAC	GACGAGTGGCCCACTACTACTACGGTATG
			(SEQ ID NO: 7577)	TATGCAGACTCCGTGAAGGGC	GACGTC
		AA	GYWYN	(SEQ ID NO: 8291)	(SEQ ID NO: 9007)
			(SEQ ID NO: 7578)	VISYDGNKYYADSVKG	EQWPNYYGMDV
		NA	GGTTACTACTGGAAC	(SEQ ID NO: 8292)	(SEQ ID NO: 9008)
			(SEQ ID NO: 7579)	GAAATCAATCATAGTGAAGCAACCACTAC	GGCGTGGATACAGCTATGGTTACGACTAC
		AA	SYAMS	AACCCGTCCTCAAGAGT	GGTATGGACGTC
			(SEQ ID NO: 7580)	(SEQ ID NO: 8293)	(SEQ ID NO: 9009)
		NA	TCCTATGCCATGAGC	EHSISGNTNPNPLKS	GGGYSNGYDYGMDV
			(SEQ ID NO: 7581)	(SEQ ID NO: 8294)	(SEQ ID NO: 9010)
		AA	GYDIN	ACTATTAGTGGTAGTGGTGAAGCAAGAC	GATGGGGCAGTGGCTGGTTCCTTAAACTA
			(SEQ ID NO: 7582)	TACGCAGACTCCGTGAAGGGC	CTACACTACGGTCTGGACGTC
		NA	GGTTATGATATCAAC	(SEQ ID NO: 8295)	(SEQ ID NO: 9011)
			(SEQ ID NO: 7583)	TISGSGSDIITYYADSVKG	DGSGWPKLLHYGLDV
		AA	SYDIN	(SEQ ID NO: 8296)	(SEQ ID NO: 9012)
			(SEQ ID NO: 7584)	TGGATGAACCCCTAACAGTGGTGAAGCAAGGC	GGGGTGGCTACAGCTATGGTTACGACTAT
		NA	AGCTATGCCATGAGC	TATGCACAGAAAGTTCAGGGC	GGTATGGACGTC
			(SEQ ID NO: 7585)	(SEQ ID NO: 8297)	(SEQ ID NO: 9013)
		AA	GYWYN	WMNPSGNTGYAQKFG	GGGYSNGYDYGMDV
			(SEQ ID NO: 7586)	(SEQ ID NO: 8298)	(SEQ ID NO: 9014)
		NA	GGTTACTACTGGAAC	GCTATTAGTGGTAGTGGTGAATACATAC	CACCTACGATATTTTGACTGGCCCCCTTGAC
			(SEQ ID NO: 7587)	TACGCAGACTCCGTGAAGGGC	TAC
		AA	SYAMS	(SEQ ID NO: 8299)	(SEQ ID NO: 9015)
			(SEQ ID NO: 7588)	AISGSDIITYYADSVKG	HLRYSDWPLDY
		NA	GGTTACTACTGGAAC	(SEQ ID NO: 8300)	(SEQ ID NO: 9016)
			(SEQ ID NO: 7589)	GAAATCAATCAGTGAAGCAACCACTA	GGCGTGGATACAGCTATGGTTACGACTAC
		AA	SYRMIH	CAATCCGTCCTCAAGAGT	GGTATGGACGTC
			(SEQ ID NO: 7590)	(SEQ ID NO: 8301)	(SEQ ID NO: 9017)

iPS:593046	17784-G10	NA	(SEQ ID NO: 7606) GGTTACTACTGGAGC	(SEQ ID NO: 8322) GAAATCACTCATAGTGGAGGACCAACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9038) GGCGGTGGATACAGCGATGGTTACGACTAC GGTATGGACGTC
		AA	(SEQ ID NO: 7607) GYYWS	(SEQ ID NO: 8323) ELHSGSTINYNPSLKS	(SEQ ID NO: 9039) GGGYSYGYDYGMVDV
iPS:593062	17784-B9	NA	(SEQ ID NO: 7608) AGCTATGCCATGAGC	(SEQ ID NO: 8324) GCTATTAGTGGTGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 9040) GTGATGACTCCGAGCTACTACTACGATATG GACGTC
		AA	(SEQ ID NO: 7609) SYAMS	(SEQ ID NO: 8325) AISGSGSTYYADSVKG	(SEQ ID NO: 9041) VMTPDYYYDMDV
iPS:593034	17784-C7	NA	(SEQ ID NO: 7610) AGCTATGGCATGAGC	(SEQ ID NO: 8326) GCTATTAGTGGTGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 9042) GTGATGACTCCGAGCTACTACTACGATATG GACGTC
		AA	(SEQ ID NO: 7611) SYGMS	(SEQ ID NO: 8327) AISGSGSTYYADSVKG	(SEQ ID NO: 9043) VMTPDYYYDMDV
iPS:593042	17784-C11	NA	(SEQ ID NO: 7612) GGTTACTACTGGAGC	(SEQ ID NO: 8328) GAAATCAATCATAGTGGAGGACCAACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9044) GGCGGTGGATACAGCTATGGTTACGACTAC GGTATGGACGTC
		AA	(SEQ ID NO: 7613) GYYWS	(SEQ ID NO: 8329) EINHSGSTINYNPSLKS	(SEQ ID NO: 9045) GGGYSYGYDYGMVDV
iPS:593036	17784-G10	NA	(SEQ ID NO: 7614) CGTGATCCTTACTACTGGAGC	(SEQ ID NO: 8330) TACATCTATTACAGTGGGAGCACCTACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9046) GATAAATCTATGTTCCGGAAATTAACCTAC TACTACGGTATGGACGTC
		AA	(SEQ ID NO: 7615) RDPYYWS	(SEQ ID NO: 8331) YIYSGSTINYNPSLKS	(SEQ ID NO: 9047) DKLWFGKLNYYGYMDV
iPS:593018	17784-H5	NA	(SEQ ID NO: 7616) GGTTACTACTGGAGC	(SEQ ID NO: 8332) GAAATCAATCATAGTGGAGGACCAACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9048) GGCGGTGGATACAGCTATGGTTACGACTAC GGTATGGACGTC
		AA	(SEQ ID NO: 7617) GYYWS	(SEQ ID NO: 8333) EINHSGSTINYNPSLKS	(SEQ ID NO: 9049) GGGYSYGYDYGMVDV
iPS:593030	17785-D12	NA	(SEQ ID NO: 7618) GGTTACTACTGGAAC	(SEQ ID NO: 8334) GAAATCAATCATAGTGGAGGACCAACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9050) GGCGGTGGATACAGCTATGGTTACGACTAC GGTATGGACGTC
		AA	(SEQ ID NO: 7619) GYYWN	(SEQ ID NO: 8335) EINHSGSTINYNPSLKS	(SEQ ID NO: 9051) GGGYSYGYDYGMVDV
iPS:592136	17813-D8	NA	(SEQ ID NO: 7620) AGCTTTGCCATGAGC	(SEQ ID NO: 8336) GCTATTAGTGGTGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 9052) ATGGTAACTCCGAGCTACTACTACGATATG GACGTC
		AA	(SEQ ID NO: 7621) SFAMS	(SEQ ID NO: 8337) AISGSGSTYYADSVKG	(SEQ ID NO: 9053) VMTPDYYYDMDV
iPS:592170	17813-E3	NA	(SEQ ID NO: 7622) GGTTACTACTGGAGC	(SEQ ID NO: 8338) GAAATCAATCATAGTGGAGGACCAACTAC CAATCCGTCCTCAAGAGT	(SEQ ID NO: 9054) GGCGGTGGATACAGCGATGGTTACGACTAC GGTATGGACGTC
		AA	(SEQ ID NO: 7623) GYYWS	(SEQ ID NO: 8339) EINHSGSTINYNPSLKS	(SEQ ID NO: 9055) GGGYSYGYDYGMVDV
iPS:592166	17813-E5	NA	(SEQ ID NO: 7624) GGTTACTACTGGAGC	(SEQ ID NO: 8340) GAAATCAATCATAGTGGAGGACCAACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9056) GGCGGTGGATACAGCTATGGTTACGACTAC GGTATGGACGTC
		AA	(SEQ ID NO: 7625) GYYWS	(SEQ ID NO: 8341) EINHSGSTINYNPSLKS	(SEQ ID NO: 9057) GGGYSYGYDYGMVDV
			(SEQ ID NO: 7626) GGTTACTACTGGAGC	(SEQ ID NO: 8342) GAAATCAATCATAGTGGAGGACCAACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 9058) GGCGGTGGATACAGCTATGGTTACGACTAC GGTATGGACGTC

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IPS:601106	18079-H4	NA	AGTTATGATATCAAC	TGGATGAACCTTAACAGTGGTAACACAGAG TATGCACAGAAATTCCAGGC	GGCTGGGGAAGGTTCTTATTCTCTACGGTATG GACGTC
		AA	SYDIN	(SEQ ID NO: 7647)	(SEQ ID NO: 8363)
IPS:601064	18079-H11	NA	AGTTATGATATCAAC	TGGATGAACCTTAACAGTGGTAACACAGAG TATACACAGAAATTCCAGGC	GGCTGGGGAACCTACTACTACTACCGGTATG GACGTC
		AA	SYDIN	(SEQ ID NO: 7649)	(SEQ ID NO: 8365)
		AA	SYDIN	(SEQ ID NO: 7650)	(SEQ ID NO: 8366)
		NA	AGTGTGATTACTACTGGAGC	TACATCAATGACAGTGGGAGCACCTACTAT AACCGTCCCTCAAGAGT	GATTTACTATGGTTCGGGAAGTTAAACTAC TACTACGGTATGGACGTC
IPS:601108	18080-C5	AA	SGDYYS	(SEQ ID NO: 7651)	(SEQ ID NO: 8367)
		AA	SGDYYS	(SEQ ID NO: 7652)	(SEQ ID NO: 8368)
IPS:601090	18080-H9	NA	AGCTATGCCATGAGC	GGTATTAGTGGTAGTGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGC	GTGATGACTCCGGACTACTACTACGATATG GACGTC
		AA	SYAMS	(SEQ ID NO: 7653)	(SEQ ID NO: 8369)
IPS:601096	18081-A6	NA	AGTAGTCGTACTACTGGGGC	AGTATCTATTATAGTGGGAGCACCTACTAC AACCGTCCCTCAAGAGT	GGGATTTTGGAGTGATTACGTACTTTGAC TAC
		AA	SRYYWG	(SEQ ID NO: 7655)	(SEQ ID NO: 8371)
		NA	AGCAACAGTCTGCTTGGAAC	AGGACATACAGGTCCAAGTGGTATAAT GATTATGCAGTACTGTGAAAAGT	GAGGTACTATGGTTCGGGAAGTTAAACTAC TACTACGGTATGGACGTC
		AA	SNSAAWN	(SEQ ID NO: 7657)	(SEQ ID NO: 8373)
IPS:601078	18081-C10	NA	AGTAGTAGTCTCTACTGGGGC	AGTATCTATTATGGTGGGAGCACCTACTAC AACCGTCCCTCAAGAGT	ACGATTTTGGAGTGGTAGGATGGTTCGAC CCC
		AA	SRSYWG	(SEQ ID NO: 7659)	(SEQ ID NO: 8375)
IPS:601114	18081-D6	NA	ACTCATAAATGGGTGGGAC	CTCATTTATTGGAATGATATACGCGCTAC AGCCCATCTCGCAGAGT	AGACGGTATAACTGGAACACGAGAACTG GTTCCACCCC
		AA	THKMGVD	(SEQ ID NO: 7661)	(SEQ ID NO: 8377)
IPS:601098	18081-D12	NA	ATCTATGCTTGGAGC	GCTATTAGTGGTAGTGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGC	GGGGAGGCTATAGCAGCTCGGTACTACTAC TACGGTATGGACGTC
		AA	IYALS	(SEQ ID NO: 7663)	(SEQ ID NO: 8379)
		AA	AGATATGGCATGGAT	(SEQ ID NO: 7664)	(SEQ ID NO: 8380)
		NA	AGATATGGCATGGAT	(SEQ ID NO: 7665)	(SEQ ID NO: 8381)
IPS:601130	18082-F5	AA	RYGMD	(SEQ ID NO: 7666)	(SEQ ID NO: 8382)
		AA	RYGMD	(SEQ ID NO: 7666)	(SEQ ID NO: 8382)

PS:601068	18084-E4	NA	AGCTATGCCATGAGC	GCTATTAGTGGTAGTGGTAGTACACATAC TACGCAGACTCCGTGAAGGC	CACCTACGATAATTCGACTGGCCCTTTGAC TAC
		AA	SYAMS (SEQ ID NO: 7667)	AISGSSTYYADSVKG (SEQ ID NO: 8383)	(SEQ ID NO: 9099) HLRYSDWPLDY
PS:603159	18086-H4	NA	AGTTATGATACAAC	TGGATGAACCTTAAGAGTGGTAAACACAGG CTATGCACAGAAGTTCAGGAC	GGCTGGGGAACCTTACTACTACTACGGTATG GACGTC
		AA	SYDIN (SEQ ID NO: 7669)	AISGSSTYYADSVKG (SEQ ID NO: 8385)	(SEQ ID NO: 9100) HLRYSDWPLDY
PS:603151	18088-B10	AA		WMNPKSGNTGYAQKFQD (SEQ ID NO: 8386)	(SEQ ID NO: 9101) GWGTYYYYGMDV
		NA	AGCTATGCCATGAGC	GCTATTAGTGGTAGTGGTAGTATACATAC TACGCAGACTCCGTGAAGGC	(SEQ ID NO: 9102) CACCTACGATAATTTGACTGGCCCTTTGAC TAC
PS:603189	18088-E4	AA	SYAMS (SEQ ID NO: 7672)	AISGSDIYYADSVKG (SEQ ID NO: 8388)	(SEQ ID NO: 9103) HLRYFDWPLDY
		NA	GGTTACTACTGGAGC	GAAATCAATCATAGTGAAGCACCACCACTAC AACCCGTCCCTCAAGAGT	GGCGGTGGATACAGCTATGGTTACGACTAC GGTATGGACGTC
		AA	GYYS (SEQ ID NO: 7673)	EINHSGSTNYNPSLKS (SEQ ID NO: 8389)	(SEQ ID NO: 9105) GGYSYGYDYGMDV
			AGTACTAGGTCCTACTGGGGC	AGTATCTATTATGGTGGGAGCACCTACTAC AACCGTCCCTCAAGAAT	(SEQ ID NO: 9106) ACGATTTTGGAGTGGTAGGATGGTTTCGAC CCC
PS:603131	18089-B8	AA	SSRSYWG (SEQ ID NO: 7675)	SIYYGSTYYNPSLKN (SEQ ID NO: 8391)	(SEQ ID NO: 9107) THFVVGWFPD
		NA	ACTAATAAATGGCTGTGGGT	CTCATTTATTGGAATGATGATAAGCGCTAC AGTCCATCTCTGAAGAGC	(SEQ ID NO: 9108) AGACGGTATAACTGGAACTACGAAAACTG GTTCGACCCC
PS:603139	18089-C8	AA	TKNMAVG (SEQ ID NO: 7677)	LIYWNDKRYSPSLKS (SEQ ID NO: 8393)	(SEQ ID NO: 9109) RRYNWNYNWFDP
		NA	ACTCATAAAATGGGTGTGGAC	CTCATTTATTGGAATGATGATAAGCGCTAC AGCCATCTCTGCAGAGT	(SEQ ID NO: 9110) AGACGGTATAACTGGAACTACGAGAACTG GTTCGACCCC
PS:603169	18089-C7	AA	THKMGVD (SEQ ID NO: 7679)	LIYWNDKRYSPSLOS (SEQ ID NO: 8395)	(SEQ ID NO: 9111) RRYNWNYNWFDP
		NA	AGCTATGCCATGAGC	GGTATTAGTGGTAGTGGTGGTAGCTCATAC TACGCAGACTCCGTGAAGGC	(SEQ ID NO: 9112) ACTTTAACCCCTGACTACTACTACTACGATATG GACGTC
PS:603179	18089-G11	AA	SYAMS (SEQ ID NO: 7681)	GISGSGSYADSVKG (SEQ ID NO: 8397)	(SEQ ID NO: 9113) TLTPDYDDMDV
		NA	AGCTATGCCGTGAGC	GGTATTAGTGGTAGTGGTGGTAGCACATAC TACGCAGACTCCGTGAAGGC	(SEQ ID NO: 9114) GCTTTAACCCCTGACTACTACTACTACGATATG GACGTC
PS:603191	18089-H9	AA	SYAVS (SEQ ID NO: 7683)	GISGSGSTYYADSVKG (SEQ ID NO: 8399)	(SEQ ID NO: 9115) ALTPDYDDMDV
		NA	AACCTATGCCATGAGC	GCTATTAGTGGTAGTGGTGGTAGTACATAC TACGCAGACTCCGTGAAGGC	(SEQ ID NO: 9116) CAGGGGGGTATAGCAGCAGCTTACTACTACTAC TACGACCGTATGACGCTC
PS:603205	18089-H12	AA	NYAMS (SEQ ID NO: 7685)	AISGSGSTYYADSVKG (SEQ ID NO: 8401)	(SEQ ID NO: 9117) QGIAAAYYYYDGMV
			AGTACTAGGTCCTACTGGGGC	AGTATCTATTATGGTGGGAGCACCTACTAC AACCGTCCCTCAAGAGT	(SEQ ID NO: 9118) GGYSYGYDYGMDV

iPS:604972	18090-H9	NA	AGATATGGCATGGAT	GTTATATCATATGATGAAGTAATAATAC	AATATGTTGCGGGAGTATGCGGCTAC
			(SEQ ID NO: 7687)	TATGCAGACTCCGTGAAGGC	TACTACTACGGTATGGACGTC
iPS:604980	18093-E2	AA	RYGMD	VISYDGSNKYYADSVKG	NYSGSYGAYYYYGMDV
			(SEQ ID NO: 7688)	(SEQ ID NO: 8403)	(SEQ ID NO: 9119)
iPS:604966	18093-E5	NA	TCCTATGGCATGAGC	ACTATTAGTCATAGTGGTGGTAGCACATAC	GATGGGGCAGTGGCTGGTTCCTAAACTA
			(SEQ ID NO: 7689)	TACGCAGACTCCGTGAAGGC	CTACACTACGGTCTGGACGTC
iPS:604975	18093-F5	AA	SYAMS	TISHSGGSYYADSVKG	DGSGWFPKLHLYGLDV
			(SEQ ID NO: 7690)	(SEQ ID NO: 8405)	(SEQ ID NO: 9121)
iPS:604976	18093-F5	NA	ATCTATGGCATGAGC	GCTATTAGTGGTAGTGGTGGTAGCACATAC	GGGAGGGATATACAGCTCGGTACTACTAC
			(SEQ ID NO: 7691)	TACGCAGACTCCGTGAAGGC	TACGGTATGGACGTC
iPS:613775	18179-A3	AA	IYGMS	AISGSGSYTYADSVKG	CEGISARYYYYGMDV
			(SEQ ID NO: 7692)	(SEQ ID NO: 8406)	(SEQ ID NO: 9122)
iPS:613775	18179-A3	NA	AGTAATCCTTACTACTGGAGC	TACATCTCTTACAGTGGGAGCACCTTCTAC	GATCGTCTTGGTTCGGAGTGTAAACTAC
			(SEQ ID NO: 7693)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613783	18179-A5	AA	SNPYYS	YISYSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7694)	(SEQ ID NO: 8407)	(SEQ ID NO: 9123)
iPS:613783	18179-A5	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GAGAAAGATGTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7695)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613707	18179-A9	AA	SGDYYS	YDKSGSYTYNPSLKS	EKMWFGVNLNYYYGMDV
			(SEQ ID NO: 7696)	(SEQ ID NO: 8411)	(SEQ ID NO: 9127)
iPS:613707	18179-A9	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7697)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613697	18179-A10	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7698)	(SEQ ID NO: 8412)	(SEQ ID NO: 9128)
iPS:613685	18179-B7	NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGTTGGGACA	CCATCGAATAGTGGGAGCTATTATAATTAC
			(SEQ ID NO: 7699)	ACAGACTACGCTGCACCCGTAAGGC	TTCTCCGTTATGGACGTC
iPS:613711	18179-B8	AA	NAWMS	RIKNTYGGTTDYAAPVKG	PSNSGSYNYFSVMDV
			(SEQ ID NO: 7700)	(SEQ ID NO: 8413)	(SEQ ID NO: 9129)
iPS:613711	18179-B8	NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGTTGGGACA	CCATCGAATAGTGGGAGCTATTATAATTAC
			(SEQ ID NO: 7701)	ACAGACTACGCTGCACCCGTAAGGC	TTCTCCGTTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7702)	(SEQ ID NO: 8414)	(SEQ ID NO: 9130)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7703)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7704)	(SEQ ID NO: 8415)	(SEQ ID NO: 9131)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7705)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7706)	(SEQ ID NO: 8416)	(SEQ ID NO: 9132)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7707)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7708)	(SEQ ID NO: 8417)	(SEQ ID NO: 9133)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7709)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7710)	(SEQ ID NO: 8418)	(SEQ ID NO: 9134)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7711)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7712)	(SEQ ID NO: 8419)	(SEQ ID NO: 9135)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7713)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7714)	(SEQ ID NO: 8420)	(SEQ ID NO: 9136)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7715)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7716)	(SEQ ID NO: 8421)	(SEQ ID NO: 9137)
iPS:613765	18179-C4	NA	AGTGTGATTACTACTGGAGC	TACATCGATAAGAGTGGGAGCACCTACTAC	GATCGTCTTGGTTCGGGTGTAAACTAC
			(SEQ ID NO: 7717)	AACCCGTCCCTCAAGAGT	TACTACGGTATGGACGTC
iPS:613765	18179-C4	AA	SGDYYS	YDKSGSYTYNPSLKS	DRLWFGVNLNYYYGMDV
			(SEQ ID NO: 7718)	(SEQ ID NO: 8422)	(SEQ ID NO: 9138)

iPS:613777	18179-C6	NA	AGTGGTGAATCTACTGGAGC	(SEQ ID NO: 7706)	TACATCGATAAGAGTGGGAGCACCTACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 8422)	GATCAACTATGGTTCGGGGTTTAAACTAC TATTACGGTATGGACGTC	(SEQ ID NO: 9138)
		AA	SGDYYS	(SEQ ID NO: 7707)	YDKSGSYNPSLKS	(SEQ ID NO: 8423)	DOLWFGVLNYYGMDV	(SEQ ID NO: 9139)
iPS:613687	18179-C7	NA	AGTAATCTTACTACTGGAGC	(SEQ ID NO: 7708)	TACATCTCTACAGTGGGAGCACTTATTAC AATCCGTCCTCAAGAGT	(SEQ ID NO: 8424)	GAGAAGATGTTGGTTCGGGGTGTAAACTAC TACTACGGTATGGACGTC	(SEQ ID NO: 9140)
		AA	SNPYYS	(SEQ ID NO: 7709)	YISHSGSYNPSLKS	(SEQ ID NO: 8425)	EKMWFVLNYYGMDV	(SEQ ID NO: 9141)
iPS:613787	18179-C10	NA	AGTAATCTTACTACTGGAGC	(SEQ ID NO: 7710)	TACATCTCTACAGTGGGAGCACTTATTAC AATCCGTCCTCAAGAGT	(SEQ ID NO: 8426)	GATCGTCTATGGTTCGGAGTGTAAACTAC TACTACGGTATGGACGTC	(SEQ ID NO: 9142)
		AA	SNPYYS	(SEQ ID NO: 7711)	YISHSGSYNPSLKS	(SEQ ID NO: 8427)	DRLWFGVLNYYGMDV	(SEQ ID NO: 9143)
iPS:613675	18179-D8	NA	AACGCTGGATGAGC	(SEQ ID NO: 7712)	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTAAGGC	(SEQ ID NO: 8428)	CCATCGAATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC	(SEQ ID NO: 9144)
		AA	NAWMS	(SEQ ID NO: 7713)	RIKNTYGGTTDYAAPVKG	(SEQ ID NO: 8429)	PSNSGSYNYFSVMDV	(SEQ ID NO: 9145)
iPS:613753	18179-D9	NA	AACGCTGGATGAGC	(SEQ ID NO: 7714)	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTAAGGC	(SEQ ID NO: 8430)	CCTTCGTATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC	(SEQ ID NO: 9146)
		AA	NAWMS	(SEQ ID NO: 7715)	RIKNTYGGTTDYAAPVKG	(SEQ ID NO: 8431)	PSYSGSYNYFSVMDV	(SEQ ID NO: 9147)
iPS:613689	18179-E6	NA	AACGCTGGATGAGC	(SEQ ID NO: 7716)	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTAAGGC	(SEQ ID NO: 8432)	CCATCGAATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC	(SEQ ID NO: 9148)
		AA	NAWMS	(SEQ ID NO: 7717)	RIKNTYGGTTDYAAPVKG	(SEQ ID NO: 8433)	PSNSGSYNYFSVMDV	(SEQ ID NO: 9149)
iPS:613679	18179-F3	NA	AGTTACTACTGGAGC	(SEQ ID NO: 7718)	CATATCTATACAGTGGGAGCACCAACTAC AACCCCTCCCTCAAGAGT	(SEQ ID NO: 8434)	GAGAAGATGTTGGTTCGGGGTGTAAACTAC TACTACGGTATGGACGTC	(SEQ ID NO: 9150)
		AA	SYYS	(SEQ ID NO: 7719)	HIYTSNSTNPSLKS	(SEQ ID NO: 8435)	EKMWFVLNYYGMDV	(SEQ ID NO: 9151)
iPS:613701	18179-F4	NA	AGTAATCTTACTACTGGAGC	(SEQ ID NO: 7720)	TACATCTCTACAGTGGGAGCACCTTCTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 8436)	GATCGTCTTGGTTCGGAGTGTAAACTAC TACTACGGTATGGACGTC	(SEQ ID NO: 9152)
		AA	SNPYYS	(SEQ ID NO: 7721)	YISHSGSYNPSLKS	(SEQ ID NO: 8437)	DRLWFGVLNYYGMDV	(SEQ ID NO: 9153)
iPS:613715	18179-F6	NA	AGTGGTGAATCTACTGGAGC	(SEQ ID NO: 7722)	TACATCGATAAGAGTGGGAGCACCTACTAC AACCCGTCCTCAAGAGT	(SEQ ID NO: 8438)	GATCAACTATGGTTCGGGGTTTAAACTAC TATTACGGTATGGACGTC	(SEQ ID NO: 9154)
		AA	SGDYYS	(SEQ ID NO: 7723)	YDKSGSYNPSLKS	(SEQ ID NO: 8439)	DOLWFGVLNYYGMDV	(SEQ ID NO: 9155)
iPS:613731	18179-F10	NA	GATTCTCTGGAGC	(SEQ ID NO: 7724)	TATATCTATTACAGAGGGAGCACCAACTAC CACCCCTCCCTCAAGAGT	(SEQ ID NO: 8440)	GAGAAGATGTTGGTTCGGGGTGTAAACTAC TACTACGGTATGGACGTC	(SEQ ID NO: 9156)

		AA	(SEQ ID NO: 7745) SHAMS	(SEQ ID NO: 8461) AISGSGGTYYADSVKG	(SEQ ID NO: 9177) GKGVHLNFDY
		NA	(SEQ ID NO: 7746) AGCTATGCCATGAGC	(SEQ ID NO: 8462) ACTATTAGTGGAAAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9178) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7747) SYAMS	(SEQ ID NO: 8463) TISGSGGTYYADSVKG	(SEQ ID NO: 9179) GKGVHLGFDY
		NA	(SEQ ID NO: 7748) AGCTATGCCATGAGC	(SEQ ID NO: 8464) GCTATTAGTGGAAAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9180) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7749) SYAMS	(SEQ ID NO: 8465) AISGSGGTYYADSVKG	(SEQ ID NO: 9181) GKGVHLGFDY
		NA	(SEQ ID NO: 7750) AGCTATGCCATGAGC	(SEQ ID NO: 8466) GCTATTAGTGGTAGTGGTGGTGGCACATAC AACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9182) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7751) SHAMS	(SEQ ID NO: 8467) AISGSGGTYYADSVKG	(SEQ ID NO: 9183) GKGVHLGFDY
		NA	(SEQ ID NO: 7752) AGCTATGCCATGAGC	(SEQ ID NO: 8468) GCTATTAGTGGAAAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9184) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7753) SYAMS	(SEQ ID NO: 8469) AISGSGGTYYADSVKG	(SEQ ID NO: 9185) GKGVHLGFDY
		NA	(SEQ ID NO: 7754) AGCTATGCCATGAGC	(SEQ ID NO: 8470) GCTATTAGTGGTAGTGGTGGTGGCACATAC AACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9186) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7755) SHAMS	(SEQ ID NO: 8471) AISGSGGTYYADSVKG	(SEQ ID NO: 9187) GKGVHLGFDY
		NA	(SEQ ID NO: 7756) AGCTATGCCATGAGC	(SEQ ID NO: 8472) GCTATTAGTGGTAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9188) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7757) SYAMS	(SEQ ID NO: 8473) AISGSGGTYYADSVKA	(SEQ ID NO: 9189) GKGVHLGFDY
		NA	(SEQ ID NO: 7758) AGCTATGCCATGAGC	(SEQ ID NO: 8474) GCTATTAGTGGTAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9190) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
		AA	(SEQ ID NO: 7759) SYAMS	(SEQ ID NO: 8475) AISGSGGTYYADSVKG	(SEQ ID NO: 9191) GKGVHLGFDY
		NA	(SEQ ID NO: 7760) AGCTATGCCATGAGC	(SEQ ID NO: 8476) GCTATTAGTGGTAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9192) GGAAAGGGAGTACATCTGGGCTTTTGACCAC
		AA	(SEQ ID NO: 7761) SYAMS	(SEQ ID NO: 8477) AISGSGGTYYADSVKG	(SEQ ID NO: 9193) GKGVHLGFDH
		NA	(SEQ ID NO: 7762) AGCTATGCCATGAAC	(SEQ ID NO: 8478) GCTATTAGTGGTAGTGGTGGTGGCACTTAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9194) GGAAAGGGAGTACATCTGAACCTTTTGACTAC
		AA	(SEQ ID NO: 7763) SYAMIN	(SEQ ID NO: 8479) AISGSGGTYYADSVKG	(SEQ ID NO: 9195) GKGVHLNFDY
		NA	(SEQ ID NO: 7764) AGCTATGCCATGAGC	(SEQ ID NO: 8480) GCTATTAGTGGAAAGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC	(SEQ ID NO: 9196) GGAAAGGGAGTACATCTGGGCTTTTGACTAC
			(SEQ ID NO: 7765)	(SEQ ID NO: 8481)	(SEQ ID NO: 9197)

		AA	SYAMS (SEQ ID NO: 7766)	AISGSGGTYADSVKG (SEQ ID NO: 8482)	CRKGVHLGHDY (SEQ ID NO: 9198)
iPS:613607	18182-C3	NA	AGCCATGCCATGAGC	GCTATTAGTGGAAAGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8483)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9199)
		AA	SHAMS (SEQ ID NO: 7768)	AISGSGGTYADSVKG (SEQ ID NO: 8484)	CRKGVHLGHDY (SEQ ID NO: 9200)
iPS:613571	18182-C4	NA	AGCTATGCCATGAGC	GCTATTAGTGGAAAGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8485)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9201)
		AA	SYAMS (SEQ ID NO: 7770)	AISGSGGTYADSVKG (SEQ ID NO: 8486)	CRKGVHLGHDY (SEQ ID NO: 9202)
iPS:613661	18182-C5	NA	AGCTATGCCATGAGC	ACTATTAGTGGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8487)	GGAAAGGGAGTACATCTGAACTTTGACTAC (SEQ ID NO: 9203)
		AA	SYAMS (SEQ ID NO: 7772)	TISGSGGTYADSVKG (SEQ ID NO: 8488)	CRKGVHLNFDY (SEQ ID NO: 9204)
iPS:613621	18182-C10	NA	AGCTATGCCATGAGC	ACTATTAGTGGAAAGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8489)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9205)
		AA	SYAMS (SEQ ID NO: 7774)	TISGSGGTYADSVKG (SEQ ID NO: 8490)	CRKGVHLGHDY (SEQ ID NO: 9206)
iPS:613629	18182-C12	NA	AGCTATGCCATGAGC	GCTATTAGTGGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8491)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9207)
		AA	SYAMS (SEQ ID NO: 7776)	AISGSGGTYADSVKG (SEQ ID NO: 8492)	CRKGVHLGHDY (SEQ ID NO: 9208)
iPS:613549	18182-D4	NA	AGCTATGCCATGAGC	ACTATTAGTGGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8493)	GGAAAGGGAGTACATCTGAACTTTGACTAC (SEQ ID NO: 9209)
		AA	SYAMS (SEQ ID NO: 7778)	TISGSGGTYADSVKG (SEQ ID NO: 8494)	CRKGVHLNFDY (SEQ ID NO: 9210)
iPS:613645	18182-D8	NA	AGCTATGCCATGAGC	GCTATTAGTGGAAAGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8495)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9211)
		AA	SYAMS (SEQ ID NO: 7780)	AISGSGGTYADSVKG (SEQ ID NO: 8496)	CRKGVHLGHDY (SEQ ID NO: 9212)
iPS:613537	18182-D9	NA	AGCTATGCCATGAGC	ACTATTAGTGGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8497)	GGAAAGGGAGTACATCTGAACTTTGACTAC (SEQ ID NO: 9213)
		AA	SYAMS (SEQ ID NO: 7782)	TISGSGGTYADSVKG (SEQ ID NO: 8498)	CRKGVHLNFDY (SEQ ID NO: 9214)
iPS:613541	18182-D11	NA	AGCTATGCCATGAAC	GCTATTAGTGGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8499)	GGAAAGGGAGTACATCTGAACTTTGACTAC (SEQ ID NO: 9215)
		AA	SYAMN (SEQ ID NO: 7784)	AISGSGGTYADSVKG (SEQ ID NO: 8500)	CRKGVHLNFDY (SEQ ID NO: 9216)
iPS:613657	18182-E2	NA	AGCTATGCCATGAGC	GCTATTAGTGGTGGTGGTGGCACATAC TACGCAGACTCCGTGAAGGCC (SEQ ID NO: 8501)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9217)
		AA	SYAMS (SEQ ID NO: 7785)	AISGSGGTYADSVKG	CRKGVHLGHDY

PS:613519	18182-E3	NA	(SEQ ID NO: 7786)	AGCTATGCCATGAGC	(SEQ ID NO: 8502)	GCTATTAGTGGTAGTGGTGGGCACATAC	(SEQ ID NO: 9218)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7787)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8503)	(SEQ ID NO: 9219)		
			SYAMS	AISGGGGTYADSVKG	GKGVHLGFDY			
PS:613595	18182-E8	NA	(SEQ ID NO: 7788)	AGCTATGCCATGAGC	(SEQ ID NO: 8504)	GCTATTAGTGGAAAGTGGTGGGCACATAC	(SEQ ID NO: 9220)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7789)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8505)	(SEQ ID NO: 9221)		
			SYAMS	AISGGGGTYADSVKG	GKGVHLGFDY			
PS:613667	18182-E11	NA	(SEQ ID NO: 7790)	AGCTATGCCATGAGC	(SEQ ID NO: 8506)	GCTATTAGTGGTAGTGGTGGGCACATAC	(SEQ ID NO: 9222)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7791)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8507)	(SEQ ID NO: 9223)		
			SYAMS	AISGGGGTYADSVKA	GKGVHLGFDY			
PS:613529	18182-F1	NA	(SEQ ID NO: 7792)	AGCTATGCCATGAGC	(SEQ ID NO: 8508)	GCTATTAGTGGAAAGTGGTGGGCACATAC	(SEQ ID NO: 9224)	GGAAAGGGAGTACATCTGAACITTTGACTAC
			(SEQ ID NO: 7793)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8509)	(SEQ ID NO: 9225)		
			SYAMS	AISGGGGTYADSVKG	GKGVHLNFDY			
PS:613531	18182-F6	NA	(SEQ ID NO: 7794)	AGCTATGCCATGAGC	(SEQ ID NO: 8510)	GCTATTAGTGGTAGTGGTGGGCACATAC	(SEQ ID NO: 9236)	GGAAAGGGAGTACATCTGAACITTTGACTAC
			(SEQ ID NO: 7795)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8511)	(SEQ ID NO: 9227)		
			SYAMS	AISGGGGTYADSVKG	GKGVHLNFDY			
PS:613623	18182-F8	NA	(SEQ ID NO: 7796)	AGCTATGCCATGAGC	(SEQ ID NO: 8512)	ACTATTAGTGGTAGTGGTGGGCACATAC	(SEQ ID NO: 9228)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7797)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8513)	(SEQ ID NO: 9229)		
			SYAMS	TISGGGGTYADSVKG	GKGVHLGFDY			
PS:613641	18182-G3	NA	(SEQ ID NO: 7798)	AGCTATGCCATGCAC	(SEQ ID NO: 8514)	GCTATTAGTGGAAAGTGGTGGGCACATAC	(SEQ ID NO: 9230)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7799)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8515)	(SEQ ID NO: 9231)		
			SYAMH	AISGGGGTYADSVKG	GKGVHLGFDY			
PS:613527	18182-G4	NA	(SEQ ID NO: 7800)	AGCTATGCCATGACC	(SEQ ID NO: 8516)	GCTATTAGTGGTAGTGGTGGCACTTAC	(SEQ ID NO: 9232)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7801)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8517)	(SEQ ID NO: 9233)		
			SYAMT	AISGGGGTYADSVKG	GKGVHLGFDY			
PS:613651	18182-G5	NA	(SEQ ID NO: 7802)	AGCTATGCCATGAGC	(SEQ ID NO: 8518)	GCTATTAGTGGTAGTGGTGGGCACATAC	(SEQ ID NO: 9234)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7803)	AACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8519)	(SEQ ID NO: 9235)		
			SYAMS	AISGGGGTYNADSVKG	GKGVHLGFDY			
PS:613625	18182-G9	NA	(SEQ ID NO: 7804)	AGCTATGCCATGAGC	(SEQ ID NO: 8520)	GCTATTAGTGGAAAGTGGTGGGCACATAC	(SEQ ID NO: 9236)	GGAAAGGGAGTACATCTGGGCTTTGACTAC
			(SEQ ID NO: 7805)	TACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 8521)	(SEQ ID NO: 9237)		
			SYAMS	AISGGGGTYADSVKG	GKGVHLGFDY			
		AA	(SEQ ID NO: 7806)		(SEQ ID NO: 8522)		(SEQ ID NO: 9238)	

IPS:613589	18182-G11	NA	AGCTATGCCATGAGC	GCTATTAGTGGTAGTGGTGGTGACACATAC TACGCAGACTCCCGTGAAGGCC	(SEQ ID NO: 7807)	SYAMS	(SEQ ID NO: 8523)	GCTATTAGTGGTAGTGGTGGTGACACATAC TACGCAGACTCCCGTGAAGGCC	(SEQ ID NO: 9239)
		AA							(SEQ ID NO: 9240)
		NA							
IPS:613587	18182-H5	AA							
		NA							
		AA							
IPS:603153	18089-D12	NA							
		AA							
		AA							
IPS:613717	18179-G12	NA							
		AA							
		AA							
IPS:613759	18179-C1	NA							
		AA							
		AA							
IPS:604976	18093-B11	NA							
		AA							
		NA							
IPS:613599	18182-B5	AA							
		NA							
		AA							
IPS:613567	18182-H9	NA							
		AA							
		AA							
IPS:613583	18182-E6	NA							
		AA							
		AA							
IPS:613565	18182-G6	NA							
		AA							
		AA							

iPS:613647	18182-G2	NA	AGCCATGCCATGAGC	GCTATTAGTGGTAGTGGTGGGCACATAC AACGCAGACTCCGTGAAGGGC (SEQ ID NO: 7827)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9259)
		AA	SHAMS	AISGSGGTYNADSVKG (SEQ ID NO: 8543)	GKGVHLGHDY (SEQ ID NO: 9260)
iPS:613517	18182-H12	NA	AGCTATGCCATGAGC	ACTATTAGTGGAAAGTGGTGGTGGGCACATAC TACGCAGACTCCGTGAAGGGC (SEQ ID NO: 7828)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9261)
		AA	SYAMS	TISGSGGTYYADSVKG (SEQ ID NO: 8545)	GKGVHLGHDY (SEQ ID NO: 9262)
iPS:613523	18182-G8	NA	AGCTATGCCATGAAC	GCTATTAGTGGTAGTGGTGGGCACATAC TACGCAGACTCCGGGAAGGGC (SEQ ID NO: 7830)	GGAAAGGGAGTTCATCTGAACTTTGACTAC (SEQ ID NO: 9263)
		AA	SYAMN	AISGSGGTYYADSVKG (SEQ ID NO: 8547)	GKGVHLNFDY (SEQ ID NO: 9264)
iPS:613521	18182-E10	NA	AGCCATGCCATGAGC	TCTATTAGTGGTAGCGGTGGTGGGCACATAC TACGCAGCTCCGTGAAGGGC (SEQ ID NO: 7832)	GGAAAGGGAGTACATCTGAACTTTGACTAC (SEQ ID NO: 9265)
		AA	SHAMS	SISGSGGTYYAASVKG (SEQ ID NO: 8549)	GKGVHLNFDY (SEQ ID NO: 9266)
iPS:613627	18182-B12	NA	AGCTATGCCATGAGC	GCTATTAGTGGAAAGTGGTGGTGGGCACATAC TACGCAGACTCCGTGAAGGGC (SEQ ID NO: 7834)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9267)
		AA	SYAMS	AISGSGGTYYADSVKG (SEQ ID NO: 8551)	GKGVHLGHDY (SEQ ID NO: 9268)
iPS:613525	18182-E5	NA	AGCTATGCCATGAGC	ACTATTAGTGGAAAGTGGTGGTGGGCACATAC TACGCAGACTCCGTGAAGGGC (SEQ ID NO: 7836)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9269)
		AA	SYAMS	TISGSGGTYYADSVKG (SEQ ID NO: 8553)	GKGVHLGHDY (SEQ ID NO: 9270)
iPS:613555	18182-A4	NA	AGCTATGCCATGACC	TCTATTAGTGGTAGTGGTGGTGGGCACATAC TACGCAGCTCCGTGAAGGGC (SEQ ID NO: 7838)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9271)
		AA	SYAMT	SISGSGGTYYAASVKG (SEQ ID NO: 8555)	GKGVHLGHDY (SEQ ID NO: 9272)
iPS:613545	18182-E1	NA	AGCCATGCCATGAGC	GCTATTAGTGGTAGTGGTGGTGGGCACATAC AACGCAGACTCCGTGAAGGGC (SEQ ID NO: 7840)	GGAAAGGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 9273)
		AA	SHAMS	AISGSGGTYNADSVKG (SEQ ID NO: 8557)	GKGVHLGHDY (SEQ ID NO: 9274)
iPS:601102	18081-B9	NA	AGTAGTCGTACTACTGGGC	AGTATCTATTATAGTGGGAGCACCTACTAC AACCCGTCCTCAAGAGT (SEQ ID NO: 7842)	GGGATTTTGGAGTGATTACGTACTTTGAC TAC (SEQ ID NO: 9275)
		AA	SSRYWVG	SIYYSSTYINPFLKS (SEQ ID NO: 8559)	GIFGVITYFDY (SEQ ID NO: 9276)
iPS:601120	18081-E7	NA	AGTAGTCGTACTACTGGGC	AGTATCTATTATAGTGGGAGCACCTACTAC AACCCGTCCTCAAGAGT (SEQ ID NO: 7844)	GGGATTTTGGAGTGATTACGTACTTTGAC TAC (SEQ ID NO: 9277)
		AA	SSRYWVG	SIYYSSTYINPFLKS (SEQ ID NO: 8561)	GIFGVITYFDY (SEQ ID NO: 9278)

		AA	NAWMS (SEQ ID NO: 7866)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8582)	PSNSGSYNYFVSVM DV (SEQ ID NO: 9298)
IPS:613733	18179-D11	NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGC	CCTTCGTATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC
		AA	NAWMS (SEQ ID NO: 7867)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8583)	PSYSGSYNYFVSVM DV (SEQ ID NO: 9299)
IPS:613723	18179-D7	AA	NAWMS (SEQ ID NO: 7868)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8584)	PSYSGSYNYFVSVM DV (SEQ ID NO: 9300)
		NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGC	CCTTCGTATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC
IPS:613769	18179-A7	AA	NAWMS (SEQ ID NO: 7869)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8585)	PSYSGSYNYFVSVM DV (SEQ ID NO: 9301)
		NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGC	CCTTCGTATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC
IPS:615240	18181-H7	AA	NAWMS (SEQ ID NO: 7871)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8587)	PSYSGSYNYFVSVM DV (SEQ ID NO: 9303)
		NA	AGTAATCCTTACTACTGGAGC	TACATCTCTACAGTGGGATCACCAACTAC AACCCCTCCCTCAAGAGT	GAGAAGATGTGCTCGGGGTGTTAAACTAC TACTACGGTATGGACGTC
IPS:615266	18181-G10	AA	SNPYYS (SEQ ID NO: 7874)	YISYSGTINYPSLKS (SEQ ID NO: 8590)	EKMWFVLNYYYGMDV (SEQ ID NO: 9306)
		NA	AGTAATCCTTACTACTGGAGC	TACATCTCTACAGTGGGAGCACCTTCTAC AACCCGTCCTCAAGAGT	GATCGTCTTTGGTTCGGAGTGTAAACTAC TACTACGGTATGGACGTC
IPS:615250	18181-G8	AA	SNPYYS (SEQ ID NO: 7875)	YISYSGTIFYNPSLKS (SEQ ID NO: 8591)	DRLWFGVLNYYYGMDV (SEQ ID NO: 9307)
		NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGC	CCATCGAATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC
IPS:615194	18181-E3	AA	NAWMS (SEQ ID NO: 7877)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8593)	PSNSGSYNYFVSVM DV (SEQ ID NO: 9309)
		NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGC	CCTTCGTATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC
IPS:615180	18181-F1	AA	NAWMS (SEQ ID NO: 7879)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8595)	PSYSGSYNYFVSVM DV (SEQ ID NO: 9311)
		NA	AACGCTGGATGAGC	CGTATTAAAGGCAACACTTATGGTGGGACA ACAGACTACGCTGCACCCGTGAAAGGC	CCTTCGTATAGTGGGAGCTATTATAATTAC TTCTCCGTTATGGACGTC
IPS:615184	18181-E2	AA	NAWMS (SEQ ID NO: 7882)	RIKGNTYGGTTIDYAAPVKG (SEQ ID NO: 8598)	PSYSGSYNYFVSVM DV (SEQ ID NO: 9314)
		NA	AGTAATCCTTACTACTGGAGC	TACATCTCTACAGTGGGAGCACTTATAC AATCCGTCCTCAAGAGT	GATCGTCTATGGTTCGGAGTGTAAACTAC TACTACGGTATGGACGTC

		AA	SNPYYS	YISHSSTYNNPSLKS	DRLWFGVNLNYYGMDV
		(SEQ ID NO: 7884)	(SEQ ID NO: 8600)	(SEQ ID NO: 9316)	
IPS:615252	18181-C9	NA	AGTAATCTTACTACTGGAGC	TACATCTTACAGTGGGAGCACCTTCTAC	GATCGCTTGGTTCGGAGTGTAAACTAC
		(SEQ ID NO: 7885)	(SEQ ID NO: 8601)	(SEQ ID NO: 9317)	TACTACGATGACGCTC
		AA	SNPYYS	YISYSGSTYNNPSLKS	DRLWFGVNLNYYGMDV
		(SEQ ID NO: 7886)	(SEQ ID NO: 8602)	(SEQ ID NO: 9318)	
IPS:615242	18181-B8	NA	AGTGGTGGTTACTACTGGAGC	TACATCTTACAGTGGGAGCACCTTCTAC	GAGAAAGATGTTGGTTCGGAGTGTAAACTAC
		(SEQ ID NO: 7887)	(SEQ ID NO: 8603)	(SEQ ID NO: 9319)	TACTACGATGACGCTC
		AA	SGGYYS	YISHSSTYNNPSLKS	EKMWFGVNLNYYGMDV
		(SEQ ID NO: 7888)	(SEQ ID NO: 8604)	(SEQ ID NO: 9320)	
IPS:615222	18181-A6	NA	AACGCTGGATGAGC	CGTATTAAAGCAACACTTATGGTGGGACA	CCTTCGTATAGTGGGAGCTATTATAATTAC
		(SEQ ID NO: 7889)	(SEQ ID NO: 8605)	(SEQ ID NO: 9321)	TTCTCCGTTATGACGCTC
		AA	NAWMS	RIKNTYGGTTDYAAPVK	PSYSGSYNNYFSVMDV
		(SEQ ID NO: 7890)	(SEQ ID NO: 8606)	(SEQ ID NO: 9322)	
IPS:1855072	18403-F12-AS	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	SYAMS	AISGSGGTYYAASVKG	GKGVHLGHDY
		(SEQ ID NO: 7891)	(SEQ ID NO: 8607)	(SEQ ID NO: 9323)	
IPS:1855074	18403-G10-AS	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	SYAMS	AISGSGGTYYAASVKG	GKGVHLGHDY
		(SEQ ID NO: 7892)	(SEQ ID NO: 8608)	(SEQ ID NO: 9324)	
IPS:1855054	02-C1-86-A4-N-F5_final	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	TYGMH	VISYDAETVKYAESVKG	GQLLTGY
		(SEQ ID NO: 7893)	(SEQ ID NO: 8609)	(SEQ ID NO: 9325)	
IPS:1855068	03-F3-88-B3-F9_final	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	DYYMS	YISKSSYTVTYADAVKG	YNYGHFDY
		(SEQ ID NO: 7894)	(SEQ ID NO: 8610)	(SEQ ID NO: 9326)	
IPS:1855106	81-H7-SG-F28_final	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	SNPYYS	YISYSGITNNPSLKS	EKMWFGVNLNYYGMDV
		(SEQ ID NO: 7895)	(SEQ ID NO: 8611)	(SEQ ID NO: 9327)	
IPS:1891845	18081-B9_final	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	SSRYWYG	SIYSGSTYNNPSLKS	GFGVTYFDY
		(SEQ ID NO: 7896)	(SEQ ID NO: 8612)	(SEQ ID NO: 9328)	
IPS:1891847	18398-C7_final	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	SHAMS	SISGSGGTYYAASVKG	GKGVHLGHDY
		(SEQ ID NO: 7897)	(SEQ ID NO: 8613)	(SEQ ID NO: 9329)	
IPS:1891849	18403-D8_final	NA	No int. seq. available	No int. seq. available	No int. seq. available
		AA	SHAMS	TISGSGGTYYADSVKG	GKGVHLGHDY
		(SEQ ID NO: 7898)	(SEQ ID NO: 8614)	(SEQ ID NO: 9330)	
IPS:1855064	18403-D8_AS_final	NA	No int. seq. available	No int. seq. available	No int. seq. available

		AA	SHAMS (SEQ ID NO: 7899) <i>No time seq available</i>	TISGGGGTYAASVKG (SEQ ID NO: 8615) <i>No time seq available</i>	GKGVHLGHDY (SEQ ID NO: 9331) <i>No time seq available</i>
iPS:1855066	18403-E11_AS_final	NA			
		AA	SHAMS (SEQ ID NO: 7900) <i>No time seq available</i>	AISGGGGTYAASVKG (SEQ ID NO: 8616) <i>No time seq available</i>	GKGVHLGHDY (SEQ ID NO: 9332) <i>No time seq available</i>
iPS:1891851	18403-F12_final	NA			
		AA	SYAMS (SEQ ID NO: 7901) <i>No time seq available</i>	AISGGGGTYADSVKG (SEQ ID NO: 8617) <i>No time seq available</i>	GKGVHLGHDY (SEQ ID NO: 9333) <i>No time seq available</i>
iPS:1855072	18403-F12-AS_final	NA			
		AA	SYAMS (SEQ ID NO: 7902) <i>No time seq available</i>	AISGGGGTYAASVKG (SEQ ID NO: 8618) <i>No time seq available</i>	GKGVHLGHDY (SEQ ID NO: 9334) <i>No time seq available</i>
iPS:1891853	18403-G10_final	NA			
		AA	SYAMS (SEQ ID NO: 7903) <i>No time seq available</i>	AISGGGGTYADSVKG (SEQ ID NO: 8619) <i>No time seq available</i>	GKGVHLGHDY (SEQ ID NO: 9335) <i>No time seq available</i>
iPS:1855074	18403-G10-AS_final	NA			
		AA	SYAMS (SEQ ID NO: 7904) <i>No time seq available</i>	AISGGGGTYAASVKG (SEQ ID NO: 8620) <i>No time seq available</i>	GKGVHLGHDY (SEQ ID NO: 9336) <i>No time seq available</i>
iPS:1891855	18409-E2_final	NA			
		AA	NAWMS (SEQ ID NO: 7905) <i>No time seq available</i>	RIKSKTYGGTIDYAAPVKG (SEQ ID NO: 8621) <i>No time seq available</i>	PSYSGSYNYFVSMDV (SEQ ID NO: 9337) <i>No time seq available</i>
iPS:1891857	18409-F12_final	NA			
		AA	THKMGVD (SEQ ID NO: 7906) <i>No time seq available</i>	LIYWDDDKRYSPSLQS (SEQ ID NO: 8622) <i>No time seq available</i>	RRYNWNYENWFDP (SEQ ID NO: 9338) <i>No time seq available</i>
iPS:1891859	18409-G10_final	NA			
		AA	THKMGVD (SEQ ID NO: 7907) <i>No time seq available</i>	GIHYDDKRYSPSLQS (SEQ ID NO: 8623) <i>No time seq available</i>	RRYNWNYENWFDP (SEQ ID NO: 9339) <i>No time seq available</i>
iPS:1891861	18409-H7_final	NA			
		AA	THKMGVD (SEQ ID NO: 7908) <i>No time seq available</i>	LIYWDDDKRYSPSLQS (SEQ ID NO: 8624) <i>No time seq available</i>	RRYNWNYENWFDP (SEQ ID NO: 9340) <i>No time seq available</i>
iPS:1891863	18409-H10_final	NA			
		AA	THKMGVD (SEQ ID NO: 7909) <i>No time seq available</i>	LIYWDDDKRYSPSLQS (SEQ ID NO: 8625) <i>No time seq available</i>	RRYNWNYENWFDP (SEQ ID NO: 9341) <i>No time seq available</i>
iPS:1891865	18410-B5_final	NA			
		AA	NAWMS (SEQ ID NO: 7910) <i>No time seq available</i>	RIKSKTYGGTIDYAAPVKG (SEQ ID NO: 8626) <i>No time seq available</i>	PSYSGSYNYFVSMDV (SEQ ID NO: 9342) <i>No time seq available</i>
iPS:1891867	18410-B6_final	NA			
		AA	NAWMS (SEQ ID NO: 7911) <i>No time seq available</i>	RIKSKTYGGTIDYAAPVKG (SEQ ID NO: 8627) <i>No time seq available</i>	PSYSGSYNYFVSMDV (SEQ ID NO: 9343) <i>No time seq available</i>

IPS:1891869	18410-D3_final	NA	<i>No num. seq available</i>	<i>No num. seq available</i>	<i>No num. seq available</i>
		AA	NAWMS (SEQ ID NO: 7912)	RITSSRYGGTTDYAAPVKG (SEQ ID NO: 8628)	PSYSGSYNYFVSMDV (SEQ ID NO: 9344)
IPS:1891871	18410-D6_final	NA	<i>No num. seq available</i>		<i>No num. seq available</i>
		AA	NAWMS (SEQ ID NO: 7913)	RILNNAYGGTTDYAAPVKG (SEQ ID NO: 8629)	PSYSGSYNYFVSMDV (SEQ ID NO: 9345)
IPS:1891873	18410-G10_final	NA	<i>No num. seq available</i>		<i>No num. seq available</i>
		AA	SHAMS (SEQ ID NO: 7914)	AISGGGGTYNADSVKG (SEQ ID NO: 8630)	GKGVHLGFDY (SEQ ID NO: 9346)
IPS:1855092	18410-G10_AS_final	NA	<i>No num. seq available</i>		<i>No num. seq available</i>
		AA	SHAMS (SEQ ID NO: 7915)	AISGGGGTYNAASVKG (SEQ ID NO: 8631)	GKGVHLGFDY (SEQ ID NO: 9347)
IPS:1891875	18410-H1_final	NA	<i>No num. seq available</i>		<i>No num. seq available</i>
		AA	NAWMS (SEQ ID NO: 7916)	RITSGIYGGTTDYAAPVKG (SEQ ID NO: 8632)	PSYSGSYNYFVSMDV (SEQ ID NO: 9348)
IPS:1891877	18410-H3_final	NA	<i>No num. seq available</i>		<i>No num. seq available</i>
		AA	NAWMS (SEQ ID NO: 7917)	RURSPYGGTTDYAAPVKG (SEQ ID NO: 8633)	PSYSGSYNYFVSMDV (SEQ ID NO: 9349)
IPS:1891879	18486-A4_final	NA	<i>No num. seq available</i>		<i>No num. seq available</i>
		AA	TYGMH (SEQ ID NO: 7918)	VISYDASNKYYAESVKG (SEQ ID NO: 8634)	GQLLTGY (SEQ ID NO: 9350)

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IPS:58/6576	17732-A8	NA	GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCCGTCTCCCTGAGAGCCCGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCCTGTATAGTATGATGATACAACTATGTGGATTGGTACTTGCAAGACCGACGGCAGTCTCACAGCTCTGATCTATTTGGGTCTAATCGGGCTCCGGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAGCAAAAGTGGAGGCT	(SEQ ID NO: 9357)	ELVMTQSLPLSPVSPGEPASISCRSSQSLLYSNGYNYVDWYLYLQKPGSQPLILYLGSRASGVDPDRFSGSGSDTFLTKISKVEAEDVGYYVCMQALQTPPIFGQGTREIK	(SEQ ID NO: 9358)	GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCCGTCAACCCCTGGAAGCCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCCTGTATAGTAATGGATACCACTATTTGGATTGTACCTGCAGAAAGCCAGGACAGTCTCCACAGCTCTCGATCTATTTGGGTCTATCCGGGCTCCGGGGTCCCTGACAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCACAGAGTGGAGGCT	NA	(SEQ ID NO: 9359)	ELVMTQSLPLSPVTPGEPASISCRSSQSLLYSNGYHYLDWYLYLQKPGSQPLILYLGSRASGVDPDRFSGSGSDTFLTKISRVEAEDVGYYVCMQPLQTPPIFGP/TKLEIK	(SEQ ID NO: 9360)	GAGCTCGTGTGATGACCCAGACTCCACTCTCCCTGCCCCGTCACTCCCTGGAAGCCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCCTGTATAGTAATGGATACAACTATTTGGATTGTACTCTGCAGAAAGCCAGGGCAGTCTCCACAGCTCTGATCTATTTGGGTCTAAAGCGGCTCTCCGGGTCCCTGACAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCACGAGAGTGGAGGCT	NA	(SEQ ID NO: 9361)	ELVMTQTLPLSPVTPGEPASISCRSSQSLLYSNGYNYLDWYLYLQKPGSQPLIYLKSRASGVDPDRFSGSGSDTFLTKISRVEAEDVGYYVCMQGTHTWPRITFGQGTKEIK	(SEQ ID NO: 9362)	GAGCTCACACTCACGAGTCTCCAGGCACCTGTGTCTTGTCTCCAGGGGAAAGAGCCACCTCTCTCGAGGGCAGTCAGAGTGTATAGCAGCAGCTACTTAGCTGGTACAGCAGAAACTGGCAGGCTCCAGGCTCCTCTACTTAGTGTGCATCCAGCAGGCCACTGGCATCCAGACAGAGTTTCAGTGGCAGTGGTCTGGGACAGACTTCACTCTCAATCAGCAGACTGGAGCCTGAAGATTTTGA	NA
		AA	(SEQ ID NO: 9715)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9716)	GAGGTGCAGCTGCTCGAGTCTGAGCTGAGGTGAGTGAAGAAGCTTGGGCTCTCATGAAAGGTCTCTGGAAGGTTCTGGATACACCTTACCAGTTATGATATCAACTGGGTGCGACAGGCCACTGGACAAGGCTTGAGTGGATGGATGGATGAACCTTAACAGTGGTAAACACAGGCTATGCACAGAAAGTTCCAGGCAGAGTCAACCATGACCAAGAACACCTCCATAAGCACAGCCTAATGGAGCTGAGCAGC	(SEQ ID NO: 9717)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9718)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9719)	EVQLLEWAGLLKPSLETSLTCAVYGGSFSGYYWNWIRPPKGLIEWIGHSHSGSTNYPNLSLRYSISGDTSKNQSLKLSVTAADTAIVYYCARGGGYSHGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9720)	GAGGTGCAGCTGCTCGAGTCTCGGGGAGGCTTGTGTACAGCTGGGGGTCCCTGAGACTCTCTGTGCGCCTTGGATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGACAGGCTCCAGGAAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGTATACACATACTACGACAGCTCCGTGAAGGCGGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGC				
		IPS:58/7871	17745-E5	NA	(SEQ ID NO: 9715)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9716)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9717)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9718)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9719)	EVQLLEWAGLLKPSLETSLTCAVYGGSFSGYYWNWIRPPKGLIEWIGHSHSGSTNYPNLSLRYSISGDTSKNQSLKLSVTAADTAIVYYCARGGGYSHGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9720)	GAGGTGCAGCTGCTCGAGTCTCGGGGAGGCTTGTGTACAGCTGGGGGTCCCTGAGACTCTCTGTGCGCCTTGGATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGACAGGCTCCAGGAAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGTATACACATACTACGACAGCTCCGTGAAGGCGGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGC		
		IPS:58/7897	17745-E8	NA	(SEQ ID NO: 9715)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9716)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9717)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9718)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9719)	EVQLLEWAGLLKPSLETSLTCAVYGGSFSGYYWNWIRPPKGLIEWIGHSHSGSTNYPNLSLRYSISGDTSKNQSLKLSVTAADTAIVYYCARGGGYSHGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9720)	GAGGTGCAGCTGCTCGAGTCTCGGGGAGGCTTGTGTACAGCTGGGGGTCCCTGAGACTCTCTGTGCGCCTTGGATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGACAGGCTCCAGGAAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGTATACACATACTACGACAGCTCCGTGAAGGCGGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGC		
IPS:58/7885	17745-G8	NA	(SEQ ID NO: 9715)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9716)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9717)	EVQLLESGAEVKKPGASVKVSCKASGYTFITSYDINWVRQATGQGLEWMVGWNPNSGNTGYAQKFGQGRVTMTRNTSISTAYMELSSLRSEDIAVYYCARGGYSGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9718)	GAGGTGCAGCTGCTCGAGTGGGGCCGAGGACTGTITGAAGCCTTCGGAGACCTGTCCCTCACTGCTGTATGGTGGGTCTTCAAGTGGTACTACTGAACTGGATCCGCCACCCAGGAAAGGGCTGGAGTGGATTGGGAAATCAGTATAGTGAAGACCAACTCAACCCCTCCCTCAAGAGTCGAGTCAGCATATCAGGAGACAGCTCCAAAGAACAGGCTTCTCCCTGAAGCTGAGCTCTGTG	(SEQ ID NO: 9719)	EVQLLEWAGLLKPSLETSLTCAVYGGSFSGYYWNWIRPPKGLIEWIGHSHSGSTNYPNLSLRYSISGDTSKNQSLKLSVTAADTAIVYYCARGGGYSHGYDYGMVDVWVGQGTITVVS	(SEQ ID NO: 9720)	GAGGTGCAGCTGCTCGAGTCTCGGGGAGGCTTGTGTACAGCTGGGGGTCCCTGAGACTCTCTGTGCGCCTTGGATTCACTTTAGCAGCTATGCCATGAGCTGGGTCCGACAGGCTCCAGGAAAGGGCTGGAGTGGGTCTCAGCTATTAGTGGTGGTGTATACACATACTACGACAGCTCCGTGAAGGCGGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGC				

		AA	(SEQ ID NO: 9363) ELTLTQSPGTLISLSPGERATILSCRASQSVSSSYLAWYQKPGQAPRLIYIG ASSRATGIPDRFSGSGTDFLITISRLPEDFAVYQCQYGRSLFTFGPGT KVDIK	(SEQ ID NO: 9721) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVS AISGSDITYYADSVKGRFTISRDNKNLTLQMNLSRAEDTAVYYCAKH LRYFDWPLDLYWGQGLTVTVSS
iPS:588445	17748-D12	NA	(SEQ ID NO: 9364) GAGCTCGTGTGACGCAGTCTCCAGGCACCCCTGTCTTGTCTCCAGGG GAAAGAGCCACCCTCTCTCGAGGCCAGTACAGAGTGTAGCAGCAGC TACTTAGCTGGTACAGAGAAAGCTGGCCAGGTCCAGGCTCTCTC ATCTATGGTGCATCCAGCAGGCCAGTGCATCCAGACAGGTTCAGT GGCAGTGGGTCTGGACAGAGATTCACCTCACCATCAGCAGACTGGAG CCTGAAGATTITGCA	(SEQ ID NO: 9722) GAGTGCAGTCTCTCGAGTCCGGGGGAGGGTGTCTCCAGCTGGGAG GTCCCTCAGACTCTCTCTGTGAGCTCTCGATTCACCTTCCGTAGCTAT CGCATGCACTGGGTCCGCGAGCTCCAGGCAAGGGGCTGGAGTGGGT GGCAGTTATATCATATAGTAGGAGTAAATACTATGCAGACTCCGT GAAGGCCGATTCACCATCTCCAGAGACAAATTCACAGAACACCTGTAT TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 9365) ELVLTQSPGTLISLSPGERATILSCRASQSVSSSYLAWYQKPGQAPRLIYIG ASSRATGIPDRFSGSGTDFLITISRLPEDFAVYQCQYGRSLFTFGGGT KLEIK	(SEQ ID NO: 9723) EVQLLESGGGLVQPGSLRLSCAASGFTFSYRMHWWVRQAPGKGLEWVA VISYDGNKYADSVKGRFTISRDNKNLTLQMNLSRAEDTAVYYCAR EQWPNYYGMVDVWGQGLTVTVSS
iPS:589113	17753-F4	NA	(SEQ ID NO: 9366) GAGCTCGTGTGATGACCCAGTCTCCCTGCTCCGCTCACCCCTGGA GAGCCGCCCTCATCTCTCTGAGGTCTAGTCAGAGCCCTCTCTGTATAGT AATGGATACAACTATTGGATTGTACCTGCAGAACCCAGGCGAGTCT CCACAGCTCTGTATCTATTGGGTCTAATCGGGCTCCGGGTCTCTG ACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9724) GAGTGCAGTCTCTCGAGTGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCAGCTCCGCTGTCTATGGTGGGTCTTCAAGTGTACT ACTTGAACCTGGATCCGCGAGCCCGAGGAGGGCTGGAGTGGATT GGGAAATCAATCATATAGTGAAGACCACTACACCCCTCCCTCAAG AGTCCAGTCAACCATATCAGTAGACACGCTCCAGAACCACTTCCCTG AAGCTGAGCTCTGTG
		AA	(SEQ ID NO: 9367) ELVMTQSPSLPVPFGEPAISCRSSQSLYSNGYNLYDWYLOKPGQSPQL LIYLGSNRASGVPRFSGSGTDFLTKISRVEAEDVGYVYCMQALQTPFT FGPGTKVEIK	(SEQ ID NO: 9725) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYVWVRQPPGKGLEWIGE INHSGSTNYPNLSKSRVITISVDTSKNQFSLKLSVTAADTAVYYCARGGGY SYGDIYGMVDVWGQGLTVTVSS
		NA	(SEQ ID NO: 9368) GAGCTCCAGATGACCCAGTCTCCATCTCCGTCTGCTGATCTGTAGGAG ACAGAGTCACCATCACTTGTCCGGCGAGTCAGGTATTAGCAGCTGGT TAGCTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCTGATCT ATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTCAGCGGCA GTGGATCTGGGACAGATTTCATCTCACCATCAGCAGCTGCAGCCTG AAGAATTTGCAACT	(SEQ ID NO: 9726) GAGTGCAGTCTCTCGAGTCCGGGGGAGGGTGTGTACAGCCTGGGG GTCCCTCAGACTCTCTCTGTGAGCTCTCGATTCACCTTACCTTACCTCTAT GCCATGAGTGGTCCGCGAGCTCCAGGCTCCAGGAGGGGCTGGAGTGGGT CTCAACTATTAGTGGTAGTGGTGGTACACACTACGACACTACGACACTCCGT GAAGGCCGCTTACCCTCTCCAGAGACAAATTCACAGAACACCTGTAT TCTGCAAAATGAACAGC
iPS:590622	17771-D2	NA	(SEQ ID NO: 9369) ELQMTQSPSSVSASVGDRTVITCRASQGISWLAHYQKPGKAPKLLIYA ASSLQSGVPSRFSGSGTDFLITISLQPEDFATYYCQANSPFTFGQGT KVEIK	(SEQ ID NO: 9727) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVST ISGSGSDITYADSVKGRFTISRDNKNLTLQMNLSRAEDTAVYYCAKDG GSGWFPKLLHYGLDVGQGLTVTVSS
		AA	(SEQ ID NO: 9370) ELVMTQSPSLPVPFGEPAISCRSSQSLYSNGYNLYDWYLOKPGQSPQL LIYLGSNRASGVPRFSGSGTDFLTKISRVEAEDVGYVYCMQALQTPFT FGPGTKVEIK	(SEQ ID NO: 9728) EVQLLEWGAGLLKPSETLSLTCAVYGGSFSGYVWVRQPPGKGLEWIGE INHSGSTNYPNLSKSRVITISVDTSKNQFSLKLSVTAADTAVYYCARGGGY SYGDIYGMVDVWGQGLTVTVSS

iPS:593066	17777-B4	NA	GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCCTGTATAGTGA ATGGATACAACTATTGGATTGGTACCTGCAGAACGCCAGGCAGTCTC CACAGCTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9371) ELVMTQSPSLSPVTPGEPASISCRSSQSLYSNGYNVLDWYLQKPGQSPQL LIYLSNRASGVPDRFSGSGGTDFTLKISRVEAEDVGVYCMQALQIPLT FGGGTKVEIK	(SEQ ID NO: 9729) EVQLLESGAEVKKPGASVKVSCMASGYTFTGYDINWVRQATGQGLEWM GWMNPNRGITGYAQKQFRVTIMRNTISISTAYMELSSRSIEDTAVYYCA RGGYSYGYDYGMDVWGQGTITVTVSS
		AA	(SEQ ID NO: 9372) GAGCTCGTGTGAGCCAGTCTCCAGGCACCTGTCTTGTCTCCAGGG GAAAGAGCCACCTCTCTGAGGCCAGTCAGAGTGTTAGCAGCAGC TACTTAGCTGTGACAGCAGAAACCTGGCCAGGCTCCAGGCTCTC ATCTATGGTGCATCCAGCAGGGCCACTGGCATCCAGACAGAGTTTCAGT GGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAGCAGACTGGAG CCTGAAGATTITGCA		(SEQ ID NO: 9730) GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTCGGGG GTCCCTGAGACTCTCTGTGCGACCTCTGGATTACCTTTAGCAGCTAT GCCATGAGTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGTAGTGGTATTACATATACTAGCAGCAGACTCCGTG AAGGCCGGTTCACCATCTCCAGAGACAAATTCCAAGAACACCGCTGTAT CTGCAAAITGAACAGC
iPS:593048	17777-C4	NA	(SEQ ID NO: 9373) ELVLTQSPGTLISLSPGERATILSCRASQSVSSSYLAWYQKPGQAPRLIY ASSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYYCQYQSSPLITFGG KLEIK	(SEQ ID NO: 9731) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSDYTYVADSVKGRFTISRDNKNTILYQLMNSLR AEDTAVYYCAKH LRYSDWPLDYWGQGTILVTVSS	
		AA	(SEQ ID NO: 9374) GAGCTCGTGTGACTCAGTCTCAGTCTCCCTGCCCGTCTCCCTGGAG AGCCGGCTCCATCTCTGCAGGTCTAGTCAGAGCCTCCTGTATAGTA ATGGATACAACTATGTGGATTGGTACTTGCAGAAAGCCAGGCAGTCTC CACAGTCTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9732) GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTITGAAGCCTTCGGAG ACCTGTCCCTCACTCGGCTGTCTATGGTGGTCTTTCAGTGGTTACT ACTGGACCTGGATCCGCCAGCCGCCAGGGAAGGGCTGGAGTGGATT GGGGAATCAATACAGTGGAAAGAACCACTACAATCCGTCCTCCCTCAAG AGTCGCTCACCATGTGAGAGACACGGCCCAAGAACCACTTCTCCCTG AAGCTGAGCTCTGTG	
iPS:593044	17777-C5	NA	(SEQ ID NO: 9375) ELVLTQSPSLSPVSPGEPASISCRSSQSLYSNGYNVVDWYLYQKPGQSPQL IYLSNRASGVPDRFSGSGGTDFTLKISRVEAEDVGVYCMQGHWPILT FGGGTKVDIK	(SEQ ID NO: 9733) EVQLLEWAGLLKPSETLSLTCAVYGGSFSGYVWVIRPPKGLWEIGE INHSGRITNPNPILSKSRVTMSIEDTAKNQPSLSSVTAADTAVYYCARGGG YSDGYDYGMDVWGQGTITVTVSS	
		AA	(SEQ ID NO: 9376) GAGCTCGTGTGATGACTCAGACTCCACTCTCCTGCCCGTCTCCCTGGAG AGCCGGCTCCATCTCTGCAGGTCTAGTCAGAGCCTCCTGTATAGTA ATGGATACAACTATGTGGATTGGTACTTGCAGAAAGCCAGGCAGTCTC CACAGTCTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAAAGTGGAGGCT	(SEQ ID NO: 9734) GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTITGAAGCCTTCGGAG ACCTGTCCCTCACTCGGCTGTCTATGGTGGTCTTTCAGTGGTTACT ACTTGAAGTGGATCCGCCAGCCGCCAGGGAAGGGCTGGAGTGGATT GGGGAATCAATCACTGTGGAAGCACCACCTACAAACCCGTCCTCCCTCAAG AGTCGAGTCACCATATCATGACGCGCTCCAAAGAACCACTTCTCCCTG AAGCTGAGTCTCTGTG	
iPS:591971	17778-C9	NA			

PS:593050	17779-E1	NA	GAGCTCGTGTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA ATGGATACCACTATTGTGATTTGGTAACTCAGGAAGCCAGGCAGTCT CACAGCTCTGATCTTTTGGGTCTAAATCGGCCCTCCGGGTCCTCTGA CAGGTTGAGTGGCAGTAGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9385) ELVLTQSPLSLPVTPGEPASISCRSSQSLLSYNGYHYLDWYLQKPGQSPQLI IFLGSNRASGVPDRFSASRSGIDFTLKISRVEAEDVGVYYCMQALQTPTF GPGTKVEIK	(SEQ ID NO: 9743) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWSWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSVDTSKNQFSLKLSSTVAADTAVYYCARGGGY SYGYDYGMDVWVGQTTVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTCTATGTTGGGTCTTTCAGTGGTACT ATGGAACTCAATCATAGTGAAGACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACACGTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGCTCTGTG
		AA	(SEQ ID NO: 9386) GAGCTCGTGTGATGACTCAGACTCCACTCTCCCTGCCCGTCTCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA ATGGATACAACTATTGTGATTTGGTACCTGCAGGAAGCCAGGCAGTCTC CACAGCTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTGA CAGGTTGAGTGGCAGTAGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9744) GAGGTGCAGCTGCTCGAGTGGAGCAGAGGTGAAAAAGCCTGGGGC CTCAGTGAAGGTCTCTCGAAGGTTCTGGATACACCTTCACCACTGAT GATATCAACTGGGTGGCAGAGCCACTGGCAAGGCTTGGAGTGGATT GGATGGATGAACCTTAACAGTGGTGAACACAGGCTATGCACAGAAAGTT CAGGCGAGAGTCAACCATGACCAAGGAACACCTCCATAAGCACAGCCTCAQ ATGGAGCTGAGCAGC		
		NA	(SEQ ID NO: 9387) ELVMTQPLSLPVSPGEPASISCRSSQSLLSYNGYNLYLDWYLQKPGSQPL LIYLGNSRASGVPDRFSGSGIDFTLKISRVEAEDVGVYYCMQALQTPIT FGQGTREIK	(SEQ ID NO: 9745) EVQLLESGAEVKKPKGASVKVSKASGYTFTSYDINWVROATGQGLEWVMG WMNPNSGNTGYAQKFGQRVTIMRTNISTAYMELSLRSEDIAVYYCAR GGGYSNGYDYGMDVWVGQTTVTVSS	(SEQ ID NO: 9746) GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTGTCTATGGTGGGTCTTTCAGTGGTACT ACTGGAACCTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATAGTGAAGACCACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCAGAAACACGTCCAGGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG	
		AA	(SEQ ID NO: 9388) GAGCTCGTGTGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA ATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCTC CACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTGA CAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGCAAAATCAG CAGGTTGGAGGCT	(SEQ ID NO: 9748) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS		
PS:591851	17780-E6	NA	(SEQ ID NO: 9389) ELVMTQSPLSLPVTPGEPASISCRSSQSLLSYNGYNLYLDWYLQKPGQSPQL LIYLGNSRASGVPDRFSGSGIDFTLQISRVEAEDVGVYYCMQTHWPF TFPGTKVEIK	(SEQ ID NO: 9389) ELVMTQSPLSLPVTPGEPASISCRSSQSLLSYNGYNLYLDWYLQKPGQSPQL LIYLGNSRASGVPDRFSGSGIDFTLQISRVEAEDVGVYYCMQTHWPF TFPGTKVEIK	(SEQ ID NO: 9747) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTCAGAGCCTCTGTATAGTGA ATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCTC CACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTGA CAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGCAAAATCAG CAGGTTGGAGGCT
		AA	(SEQ ID NO: 9390) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9748) GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTGGGTCTTTCAGTGGTCTTTCAGTGGTACT ACTGGAACTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATCTGTGGAAGCACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACGCGCTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG		
		NA	(SEQ ID NO: 9391) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9749) GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTGGGTCTTTCAGTGGTCTTTCAGTGGTCT ACTGGAACTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATCTGTGGAAGCACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACGCGCTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG		
		AA	(SEQ ID NO: 9392) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9750) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS		
PS:591859	17781-B3	NA	(SEQ ID NO: 9393) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9393) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9751) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTGGGTCTTTCAGTGGTCTTTCAGTGGTCT ACTGGAACTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATCTGTGGAAGCACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACGCGCTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG
		AA	(SEQ ID NO: 9394) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9752) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTGGGTCTTTCAGTGGTCTTTCAGTGGTCT ACTGGAACTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATCTGTGGAAGCACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACGCGCTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG	
		NA	(SEQ ID NO: 9395) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9753) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTGGGTCTTTCAGTGGTCTTTCAGTGGTCT ACTGGAACTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATCTGTGGAAGCACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACGCGCTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG	
		AA	(SEQ ID NO: 9396) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGTATAGTGA AATGGATACAACTATTGTGATTTGGTACCTGCAGAAAGCCAGGCAGTCT CCACAGTCTGATCTATTTGGGTCTAAATCGGCCCTCCGGGTCCTCTG ACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9754) EVQLLEWGAGLLKPSFETLSLTCAVYGGFSFGYYWNIWIRQPPQKGLEWIGE INHSGTYYNPSLKSRTVTSIDTSRNQFSLKLSSTVAADTAVYYCTRGGY SHGYDYGMDVWVGQTTVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAG ACCTGTCCCTCACTCGCGTCTAGTGGGTCTTTCAGTGGTCTTTCAGTGGTCT ACTGGAACTGGATCCGCCAGCCCCCAGGAAGGGCTGGAGTGGATT GGGGAATCAATCATCTGTGGAAGCACCAACTACAACTCAACCCGCTCCCTCAAG AGTCGAGTCAACCATATCATAGTAGACGCGCTCCCAAGAACCAAGTTCTCCCTG AAGCTGAGTTCTGTG	

iPS:593062	17784-B9	NA	GAGCTCCAGATGACCCAGTCTCCATCTTCCGTGTCGCACTCTGAGGAG ACAGAGTCAACCATCACTTGC CGGCAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAAGCTCCTGATCT ATGCTGCATCCAGTTTGC AAAGTGGGTCCCATCAAGTTTCAGTGGCA GTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTGCAGCT	GAGGTGCAGTCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGCAAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTTGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGT CTCAGCTATTAGTGGTAGTGGTAGCAGACATACACTACGACAGCTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAAATTCCAAGAACACAGCTGTA TCTGCAATGAACAGC
		AA	(SEQ ID NO: 9399) ELQMTQSPSSVSASVGDRTVITCRASQSISSYLNWYQKPKAPKLLIYAA SSLQSGVPSRFSGSGGDFTLTISSLQPEDFAAYYCCQSYSTPFTFGQGTK VEIK (SEQ ID NO: 9400) GAGCTCCAGATGACCCAGTCTCCATCTCCTCTGTCTGCACTCTGAGGAG ACAGAGTCAACCATCACTTGC CGGCAAGTCAGGCAATTAGCAATATT TAGCCTGTGATCAGCAGAAACAGGAAAGTTCTTAAGCTCCTGATCT ATGCTGCATCCAGTTTGC AAAGTGGGTCCCATCAAGTTTCAGTGGCA GTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTGCAACT	(SEQ ID NO: 9757) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLWEWS AISGSGSYIYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYFCAKV MTPDYIYDMDVWVGQGITTVTVSS (SEQ ID NO: 9758) GAGGTGCAGCTCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGCAAGCCTCTGGATTACCTTTAGCAGCTAT GGCATGAGCTGGTCCGCAAGCTCCAGGAAAGGGACTGGAGTGGT CTCAGCTATTAGTGGTAGTGGTAGCAGACATACACTACGACAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAAATTCCAAGAACACAGCTGTA TCTGCAATGAACAGC
iPS:593034	17784-C7	NA	(SEQ ID NO: 9401) ELQMTQSPSSLSASVGDRTVITCRASQGISNVLAWYQKPGKVPKLLIYAA SSLQSGVPSRFSGSGGDFTLTISSLQPEDFATYYCQSYSTPFTFGPTKV EIK (SEQ ID NO: 9402) GAGCTCGTGAAGACCCAGACTCCACTCTCCTGCCCCGTCACCCCTGGA GAGCCGGCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTCTGTATAGT AATGGATACAACTATTGGATTGGTACCTGCAGAAAGCCAGGGCAGTCT CCACAGCTCTGATCTATTGGTCTTAATCGGGCTCTCCGGGTCCCTG ACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9759) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYGMSWVRQAPKGLWEWS AISGSGSYIYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYFCAKV MTPDYIYDMDVWVGQGITTVTVSS (SEQ ID NO: 9760) GAGGTGCAGCTCTCGAGTGGGGCGCAGGACTGTITGAAGCCTTCGGAG ACCTGTCCCTCACTGCGCTGTCTATGGTGGGTCTTTCAGTGGTTACT ACTGGAGCTGGATCCGCCAGCCCCAGGAAAGGGCTGGAGTGGATT GGGAAATCAATATAGTGGAAAGCACCAACTACACCCCTCCCTCAAG AGTCGAGTACCATATACGTAGACACGTCACAGAACCAAGTCTTCCCTCG AAGCTGAGCTCTGTG
	17784-C11	NA	(SEQ ID NO: 9403) ELVMTQTPLSLPVTGPEPASISCRSSQSLIYSGNYNLYDWYLQKPGQSPL LIYLGSRASGVDPDRFSGSGGDFTLTKSRVEAEDVGVVYCMQGTHTWPF TFGPGTKVEIK (SEQ ID NO: 9404) GAGCTCGTGAATGACTCAGACTCCACTCTCCTGCCCCGTCACCCCTGGA GAGCCGGCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTCTGATAGT AATGGATACAACTATTGGATTGGTACCTGCAGAAAGCCAGGGCAGTCT CCACAGCTCTGATCTATTGGTCTTAATCGGGCTCTCCGGGTCCCTG ACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9761) EVQLLEWAGLLKPSLESLTCAVYGGSFSGYVWSWIRQPPKGLWEWIGE INHSGSTNYPNLSKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGGY SYGYDYGMDEVWVGQGITTVTVSS (SEQ ID NO: 9762) GAGGTGCAGCTCTCGAGTCTGGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACTGCGCTGTCTGTGAGTCCATCAGCCCGTGATC CTTACTACTGGAGCTGGATCCGCCAGCACCAGGAAAGGGCCTGGAGT CTTACTACTGGAGCTGGATCCGCCAGCACCAGGAAAGGGCCTGGAGT GGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCCTGCC TCAAGAGTGCAGTTACCATATCAGTAGACACGCTCTAAGAACACAGTTCT CCCTGAAGCTGAGC
iPS:593036	17784-G10	NA	(SEQ ID NO: 9405) ELVMTQTPLSLPVTGPEPASISCRSSQSLIYSGNYNLYDWYLQKPGQSPL LIYLGSRASGVDPDRFSGSGGDFTLTKSRVEAEDVGVVYCMQGTHTWPF TFGPGTKVEIK (SEQ ID NO: 9406) GAGCTCGTGAATGACTCAGACTCCACTCTCCTGCCCCGTCACCCCTGGA GAGCCGGCTCCATCTCCTGCAGGTCTAGTCAGAGCCTCCTCTGATAGT AATGGATACAACTATTGGATTGGTACCTGCAGAAAGCCAGGGCAGTCT CCACAGCTCTGATCTATTGGTCTTAATCGGGCTCTCCGGGTCCCTG ACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9763) EVQLLEWAGLLKPSLESLTCAVYGGSFSGYVWSWIRQPPKGLWEWIGE INHSGSTNYPNLSKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGGGY SYGYDYGMDEVWVGQGITTVTVSS (SEQ ID NO: 9764) GAGGTGCAGCTCTCGAGTCTGGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACTGCGCTGTCTGTGAGTCCATCAGCCCGTGATC CTTACTACTGGAGCTGGATCCGCCAGCACCAGGAAAGGGCCTGGAGT CTTACTACTGGAGCTGGATCCGCCAGCACCAGGAAAGGGCCTGGAGT GGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCCTGCC TCAAGAGTGCAGTTACCATATCAGTAGACACGCTCTAAGAACACAGTTCT CCCTGAAGCTGAGC

iPS:592170	17813-E3	NA	GAGCTCGTGAATGACCCAGACTCCACTCTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCCATCTCTCGAGGTAGTCAGAGCCTCCTGTATAGTAAATGGATACAACTATTGGATTGGTACCTGCAAGAACGAGGAGTCTCCACAGCTCCTGATCTATTGGGTCTAATCGGGCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAACAGAGTGGAGGCT	GAGGTGCAGTCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCACCTGGCGTGTCTATGGTGGTCCCTCAGTGGTTACTACTGGAGAGTATCCGCGAGCCCAAGGAAGGGCTGGAGTGGATGGGAAATCAATACAGTGGGAAGAACCAACAATCCGTCCTCAAGAGTCGGTCAACATGTTCAGAGACACGCGCAAGAACCAAGTCTCCCTGAAGCTGAGCTCTGTG
		AA	(SEQ ID NO: 9413) ELVMTQTPLSLVPVTPGEPASISCRSSQSLLYSNGYNLYLDWYLQKPGQSPQLLIYLGSRASGVDPDRFSGSGSDFTFLKISRVEAEDVGVYCYMQUALQSLTFGGGTKLEIK	(SEQ ID NO: 9771) EVQLLEWGAGLLKPSLESLTCAVYGGSLSGYYWSWIRQPPKGLIEWEINHSGRITNYPNLSKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARGGGYSDGYDYGMDDVWGQGITTVTVSS
iPS:592166	17813-E5	NA	(SEQ ID NO: 9414) GAGCTCGTGAATGACTCAGACTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCTCCATCTCTCGAGGTAGTCAGAGCCTCCTGTATAGTAAATGGATACAACTATTGGATTGGTACCTGCAGAACCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTCTAAGCGGGCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAACAGAGTGGAGGCT	(SEQ ID NO: 9772) GAGGTGCAGTCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCACCTGGCGTGTCTATGGTGGTCCCTCAGTGGTTACTACTGGAGCTGGATCCGCGAGCCCAAGGAAGGGCTGGAGTGGATGGGAAATCAATCAATAGTGGGAAGCAACAATACAACTCCCTCAAGAGTCGAGTCAACATATCAGTAGACACGCTCCCAAGAACCAAGTCTCCCTGAAGCTGAGCTCTGTG
		AA	(SEQ ID NO: 9415) ELVMTQTPLSLVPVTPGEPASISCRSSQSLLYSNGYNLYLDWYLQKPGQSPQLLIYLGSKRASGVDPDRFSGSGSDFTFLKISRVEAEDVGVYCYMQUALQSLTFGGGTKVDIK	(SEQ ID NO: 9773) EVQLLEWGAGLLKPSLESLTCAVYGGSFSGYYWSWIRQPPKGLIEWEINHSGRITNYPNLSKSRVTISVDTSKNQFSLKLSSTVAADTAVYYCARGGGYSYGYDYGMDDVWGQGITTVTVSS
iPS:592154	17813-F1	NA	(SEQ ID NO: 9416) GAGCTCGTGAATGACCCAGTCTCCACTCTCTCTGTCGCTCACCCCTGGAGAGCCGGCTCCATCTCTCGAGGTAGTCGAGCCTCCTGTATAGTAAATGGATACAACTATTGGATTGGTACCTGCAGAACCCAGGGCAGTCTCACAGCTCCTGATCTATTGGGTCTAATCGGGCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCATAGATTTTACACTGAAATCAGCAGAGTGGAGGCT	(SEQ ID NO: 9774) GAGGTGCAGTCTCGAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCTGTCCCTCACCTGGCGTGTCTATGGTGGTCCCTCAGTGGTTACTACTGGAACTGGATCCGCGAGCCCAAGGAAGGGCTGGAGTGGATGGGAAATCAATCAATCGTGGGAAGCAACAATCAAACTCCCTCAAGAGTCGAGTCAACATATCAGTAGACGCTCCCAAGAACCAAGTCTCCCTGAAGCTGAGTCTGTG
		AA	(SEQ ID NO: 9417) ELVMTQSPSLSVTPGEPASISCRSSRLHSNGYNLYLDWYLQKPGQSPQLLIYLGSRASGVDPDRFSGSGSDFTFLKISRVEAEDVGVYCYMQUALQTPHFGGGTVKLEIK	(SEQ ID NO: 9775) EVQLLEWGAGLLKPSLESLTCAVYGGSFSGYYWSWIRQPPKGLIEWEINHSGRITNYPNLSKSRVTISVDASKNQFSLKLSSTVAADTAVYYCARGGGYSDGYDYGMDDVWGQGITTVTVSS
iPS:592150	17814-D9	NA	(SEQ ID NO: 9418) GAGCTCGTGAATGACTCAGTCTCCACTCTCTCTGTCGCTCACCCCTGGACAGCCGGCTCCATCTCTCGAGGTAGTCAGAGCCTCCTGTATAGTAAATGGATACAACTATTGGATTGGTACCTGCAGAACCCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTCTAATCGGGCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGCAGGGTGGAGGCT	(SEQ ID NO: 9776) GAGGTGCAGTCTCGAGTGGGGCGCAGGACTGAGGTGAAGAACCTGGGCTCTCAGTGAAGGTCTCTCGAAGCTTCTGGATACACTTCAACAGTGTATGATCAACTGGTGGCAGAGCCCACTGGACAAGGGCTTGGTGGATGGATGGATGAACCTAACTAAGTGGTAACAGAGGTATGCACAGAGTTCAGGGCAGAGTCAACCTAGCAAGAACCTCCATAAGCACAGCTACATGGAGCTGAGCAGC

			(SEQ ID NO: 9419) ELVMTQSPDLSVTPGPASISCKSSQSLYSNGYNLYLDWYLKPGQSPQL LIYLSNRASGVDPDRFSGSGGTDFLTKISRVEAEDVGYYCMQALQITPT FGQGRLEIK (SEQ ID NO: 9420) GAGCTGCGCTGACTCAGCTCCCTCCGTGCTGGGTCTCTGGACAGT CGATCACCCTCTCTGCACTGGAACACGACGTCAGTGTGGTGTATA ACTATGCTCTCTGGTACCAACAGACCCAGGCAAGCCGCCAAACTCA TGATTTATGAGGTCAAGTAAAGCGCTCAGGGGTTCCTAATCGCTCTC TGGCTCAAAGTCTGGCAACACGGGCTCCCTGACCATCTCTGGGCTCCA GGCTGAGGACGAG	(SEQ ID NO: 9777) EVQLLESGAEVKKPGASVKYSCKASGYFTSYDINWVRQATGQGLEWMG WMNPNNGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDYAVYYCAR GGYSYGYDYGMVWVGQGTITVSS (SEQ ID NO: 9778) GAGTGCAGCTGCTCGAGTCTGGGGAGGGCGTGTCCAGCCTGGGAG GTCCCTCAGACTCTCTGTCGAGCGTCTGGATTCACCTTCAGCAGATAC GGCATGGACTGGGTCCGACAGGCTCCAGGCAAGGGGCTGGAGTGGGT GGCATTTATGTGATAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG GAAGGGCCGATTCACCATCTCCAGAGACAAATTCACAGAACACGCTGTA TCTGCAAAATGAACAGC
iPS:603175	18071-B1	NA		
		AA	(SEQ ID NO: 9421) ELALTPPSVSGSPGQSITISCTGSSDVGGYVYVSWYQQHPGKAPKLMIY EVSKRPSGVNRFSGSKSGNTASLTISGLQAEADYYCSSYTSSTLVFGG GTKLTIVL (SEQ ID NO: 9422) GAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGCCACCATCACTGCAAGTCCAGCAGAGTGTITTTATACAGC TCCAACAATAAGAACTACTAGTGTGACAGCAGAAACAGCAGACAG CCTCTAAGTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCC CTGACCGATTCACTGGCAGCGGTCTGGACAGATTTCCTCTCACCA TCAGCAGCCTGCAG	(SEQ ID NO: 9779) EVQLLESGGVVYADSVKGRFTISRDNSKNTLYLQMINSLRAEDYAVYYCAR NYGSGSYGAYYHGMVDVWVGQGTITVSS (SEQ ID NO: 9780) GAGTGCAGCTGCTCGAGTCTGGAGTCTGAGTGAAGAAAGCCTGGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTGCGACAGGCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATGCACAGAGTTTC CAGGGCAGATCACTACATGACAGGAACACTCCATCAAGCAGCAGCTAC ATGGAGCTGAGCAGC
iPS:603181	18071-C4	NA		
		AA	(SEQ ID NO: 9423) ELVMTQSPDLSAVSLGERATINCKSSQSLYSSNNKNYLAWYQOKPGQPP KLLIYWASTRESGVDPDRFSGSGGTDFLTIISLQAEDVAVYYCQYYSTP WTFGQGTKVEIK (SEQ ID NO: 9424) GAGCTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGCCACCATCACTGCAAGTCCAGCAGAGTGTITTTATACAGC TCCAACAATAAGAACTACTAGTGTGACAGCAGAAACAGCAGACAG CCTCTAAGTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCC CTGACCGATTCACTGGCAGCGGTCTGGACAGATTTCCTCTCACCA TCAGCAGCCTGCAG	(SEQ ID NO: 9781) EVQLLESGAEVKKPGASVKYSCKASGYFTSYDINWVRQATGQGLEWMG WMNPNNGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDYAVYYCVR WGTYYYYGMVDVWVGQGTITVSS (SEQ ID NO: 9782) GAGTGCAGCTGCTCGAGTCTGGGGTGAAGTGAAGAAAGCCTGGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTGCGACAGGCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATGCACAGAGTTTC CAGGGCAGATCACTACATGACAGGAACACTCCATCAAGCAGCAGCTAC ATGGAGCTGAGCAGC
iPS:603133	18071-D4	NA		
		AA	(SEQ ID NO: 9425) ELVMTQSPDLSAVSLGERATINCKSSQSLYSSNNKNYLAWYQOKPGQPP KLLIYWASTRESGVDPDRFSGSGGTDFLTIISLQAEDVAVYYCQYYSTP WTFGQGTKVEIK (SEQ ID NO: 9426) GAGCTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGCCACCATCACTGCAAGTCCAGCAGAGTGTITTTATACAGC TCCAACAATAAGAACTACTAGTGTGACAGCAGAAACAGCAGACAG CCTCTAAGTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGTCC CTGACCGATTCACTGGCAGCGGTCTGGACAGATTTCCTCTCACCA TCAGCAGCCTGCAG	(SEQ ID NO: 9783) EVQLLESGAEVKKPGASVKYSCKASGYFTSYDINWVRQATGQGLEWMG WMNPNNGNTGYAQKFQGRVTMTTRNTSISTAYMELSSLRSEDYAVYYCAR WGRTYSGYGMVDVWVGQGTITVSS (SEQ ID NO: 9784) GAGTGCAGCTGCTCGAGTCTGGGGTGAAGTGAAGAAAGCCTGGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTGCGACAGGCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATGCACAGAGTTTC CAGGGCAGATCACTACATGACAGGAACACTCCATCAAGCAGCAGCTAC ATGGAGCTGAGCAGC

iPS:603207	18072-D6	NA	GAGCTCACACTCAGCAGTCTCCAGGCCACCTGCTGTTTGTCTCCAGGG GAAAGAGCCACCTCTCTCGAGGGCCAGTCAGAGTGTTAGCAGCAGC TACTTAGCTGGTACAGCAGAACTCTGGCAGGCTCCCAAGGCTCCTC ATCTATGGTGCATCCGCCAGGCCACTGGCATCCAGACAGGTTTCAGT GGCAGTGGGTCTGGGACAGACTTTCATCTCAACCATCAGCAGACTGGAG CCTGAAGATTITGCA	(SEQ ID NO: 9427) ELJLTQSPGILSLSPGERATLSRASQSVSSYLAWYQKPGQAPRLIYG ASARATGIPDRFSGSGGTDFLTISRLEPEDEFAVYYCQYGSLLTFGGGTK VDIK	(SEQ ID NO: 9428) GAGCTGCTGTGACTCAGCCACCTCAGCGTCTGGGACCCCGGGCAG AGGATCACCAATCTCTTGTGCGAGCAGTCCAACATCGGAAAGTAATT ATGTATCTGGTATCAGCATCTCCAGGAACGCCGCCCAAACTCTCTCA TCTATAGGAATAATCAGCGGCCCTCAGGGTCCCTGACCGAATCTCTG GCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGT CCGAGGATGAGGCT	(SEQ ID NO: 9429) ELVLTQPPSASGTPGQRUTISCSGSSNIGSNYVYVYQHLPGTAPKLLIYRN NQRPSGVDRFSGSKSGTASLAISGLRSEDEADYYCAAWDDSLSGVVF GGTKLTVL	(SEQ ID NO: 9430) GAGCTCGTGATGACCCAGTCTCCATCTCTCCCTGCTGCTGTCATCTGAGGAG ACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATT TAAATTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCT ACGATGCATCCAAATTTGGAACAGGGTCCCATCAAGGTTTCAGTGCCA GTGGATCTGGGACAGATTTTACTTTTCAACCATCAGCAGTCTGCAACCTGA AGATTTTGCAACT	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTCACTTACCTTTAGCTCTAT GCCATGAGCTGGGTCCGCCAGGCTCCAGGAGGGGCTGGAGTGGGT CTCAAGCATAACTATTACTGGTGTAGCACATACTACGACAGACTCCGT GAAGGGCCGTTTCACCATCTCCAGAGACAATTCCAAGAACACCGCTGAA TCTGCAAAATGAACAGC	(SEQ ID NO: 9785) EVQLLESGGGLVOPGGSRLRLSCAASGFTFSYAMSWVRQAPQKGLWEVWS AISGSDITYYADSVKGRFTISRDNKNTILYLQMNLSRAEDTAVYYCAKH LRVFDWPLDYWGQGTLVTVSS	(SEQ ID NO: 9786) GAGGTGCAGCTCTCGAGTCTGGGGAGGCTTGGTCAAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTCACTTTCAGTTCAGTGGCTAT AGCATGAACCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCGTCCATTAGTAGTAGTAGTATTACATATACTACGACAGACTCAGT AAGGGCCGCTTTCACCATCTCCAGAGACAACGCCCAAGAACTCACTGTAT CTGCAAAATGAACAGC	
		AA					(SEQ ID NO: 9787) EVQLLESGGGLVKPGGSRLRLSCAASGFTFSGYSMNVVRQAPQKGLWEVWS SISSSSYYIYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCVRSK AARPDGDMVDVWGQGTITVTVSS	(SEQ ID NO: 9788) GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTCACTTTCAGCTCTCTAT GCCATGAGCTGGGTCCGCCAGGCTCCAGGAGGGGCTGGAGTGGGT CTCAAGCATAACTATTACTGGTGTAGCACATACTACGACAGACTCCGT GAAGGGCCGTTTCACCATCTCCAGAGACAATTCCAAGAACACCGCTGAA TCTGCAAAATGAACAGC	(SEQ ID NO: 9789) EVQLLESGGGLVOPGGSRLRLSCAASGFTFSYAMSWVRQAPQKGLWEVWS ITITGGSTYYADSVKGRFTISRDNKNTILNLMNSLRRAEDTAVYYCAKDG GSGWFPKLLHYGLDVWGQGTITVTVSS	(SEQ ID NO: 9790) GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTTCAGCCTGGGAG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTCACTTTCAGTTCAGTAGATAT GGCATGAGTGGGTCCGCCAGGCTCCAGGAAAGGGGCTGGAGTGGGT GGCATGTATATCATATGATGGAAGTAAATAAATACTATGACAGACTCCGT GAAGGGCCGATTTCACCATCTCCAGAGACAATTCCAAGAACACCGCTATA TCTGCAAAATGAACAGC	
iPS:603185	18072-G9	NA									
		AA									
iPS:603201	18074-G12	NA									
iPS:601126	18078-H6	NA									

			(SEQ ID NO: 9433) ELVLTQPPSVSKGLRQTATLTCTGNSNNVGNQGAWLQHQHGHPPKLLS YRNNRPSGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLAWV FGGTTKLTIVL (SEQ ID NO: 9434) GAGCTCGTGTGACTGACCATCTCGGTGTCCAAAGGACTTGAGACAG ACCGCCACACTCACTGCACTGGGAACAGCAACAATGTTGGCAACCAA GGAGCAGCTTGGCTGACGAAACACGAGGGCCACCTTCCAAACTCTTA TCCTACAGGAATAACAACCGCCCTCAGGATCTCAGAGAGATTATCT GCATCCAGTTCAGGAAACACAGCCTCCCTGACCAATTACTGGACTCCAG CTTGAGGACGAGGCT	(SEQ ID NO: 9791) EVQLLESGGGVVQPGHSLRLSCAASGFTFSRYGMQWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRSEDYAVYYCAR NYGSGSYGAYYYHGMDVWGQGTITVTVSS (SEQ ID NO: 9792) GAGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGTCCAGCCTGGGAG GTCCCTCGAGACTCTCTGTGAGCTCTGGATTCACCTTCAGTAGCTAT GGCATGCACTGGGTCCGACGGTCCAGGCAAGGGGCTGAGTGGGT GGCAGTTATATCATATAGTGAAGTAAATAGTACTATGCAGACTCCGT GAAGGGCCGATTCACCATCTCCAGAGACAAATTCACAGAACACGCTGT TCTGCAAAATGAACAGC
iPS:601094	18079-C8	NA	(SEQ ID NO: 9435) ELVLTQPPSVSKDLRQTATLTCTGNSNNVGNQGAWLQHQHGHPPKLLS YRNNRPSGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLAWV FGGTTKLTIVL (SEQ ID NO: 9436) GAGCTCGTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGGCCACCATCACTGAAGTCCAGCAGAGTGTGTTTATACAGC TCCAACAATAAGAACTACTTAGTCTGGTACCAGCAAAACAGGACAG CCTCTAAGTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTGAGTGGCAGCGGTCTGGGACAGATTCTCACTCTCACCA TCAGCAGCCTGCAG	(SEQ ID NO: 9793) EVQLLESGGGVVQPGHSLRLSCAASGFTFSRYGMHVVVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRSEDYAVYYCAR QWPNYYGLGVWVGQGTITVTVSS (SEQ ID NO: 9794) GAGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTCCGACGGCCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATGCACAGAGTTC CAGGGCAGAGTCACTGACCCAGGAACACTCCATACAGCAGCAGCTAC ATGGAGCTGAGAAAGC
iPS:601106	18079-H4	NA	(SEQ ID NO: 9437) ELVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPP KLLIYWASTRESGVDPDRFSGSGTDFTLTISLQAEDVAVYYCQYYSTP WTFGQGTGLEIK (SEQ ID NO: 9438) GAGCTCGTGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGCCACCATCACTGAAGTCCAGCAGAGTGTGTTTATACAGC TCCAACAATAAGAACTACTTAGTCTGGTACCAGCAAAACAGGACAG CCTCTAAGTGTCTATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTGAGTGGCAGCGGTCTGGGACAGATTCTCACTCTCACCA TCAGCAGCCTGCAG	(SEQ ID NO: 9795) EVQLLESGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYAQKFQGRVTMTRTNISITAYMELSLRSEDYAVYYCAR GWGRFYSYGMDVWGQGTITVTVSS (SEQ ID NO: 9796) GAGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTCCGACGGCCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATACACAGAGTTC CAGGGCAGAGTCACTGACCAAGGAACACTCCATAGGACAGCCTAC ATGGAGCTGAGCAGC
iPS:601064	18079-H11	NA	(SEQ ID NO: 9439) ELVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPP KLLIYWASTRESGVDPDRFSGSGTDFTLTISLQAEDVAVYYCQYYSTP WTFGQGTGLEIK (SEQ ID NO: 9440) GAGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTCCGACGGCCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATACACAGAGTTC CAGGGCAGAGTCACTGACCAAGGAACACTCCATAGGACAGCCTAC ATGGAGCTGAGCAGC	(SEQ ID NO: 9797) EVQLLESGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYAQKFQGRVTMTRTNISITAYMELSLRSEDYAVYYCAR GWGRFYSYGMDVWGQGTITVTVSS (SEQ ID NO: 9798) GAGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTCCGACGGCCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATACACAGAGTTC CAGGGCAGAGTCACTGACCAAGGAACACTCCATAGGACAGCCTAC ATGGAGCTGAGCAGC
		AA	(SEQ ID NO: 9439) ELVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQOKPGQPP KLLIYWASTRESGVDPDRFSGSGTDFTLTISLQAEDVAVYYCQYYSTP WTFGQGTGLEIK (SEQ ID NO: 9440) GAGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTCCGACGGCCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATACACAGAGTTC CAGGGCAGAGTCACTGACCAAGGAACACTCCATAGGACAGCCTAC ATGGAGCTGAGCAGC	(SEQ ID NO: 9797) EVQLLESGAEVKKPGASVKVSCKASGYFTSYDINWVRQATGQGLEWMG WMNPNSGNTDYAQKFQGRVTMTRTNISITAYMELSLRSEDYAVYYCAR GWGRFYSYGMDVWGQGTITVTVSS (SEQ ID NO: 9798) GAGTGCAGCTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCCTGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGATACACCTTCACCACTTAT GATATCAACTGGGTCCGACGGCCACTGGACAAAGGGCTTGAGTGGATG GGATGGATGAACCTTAACAGTGTAAACAGACTATACACAGAGTTC CAGGGCAGAGTCACTGACCAAGGAACACTCCATAGGACAGCCTAC ATGGAGCTGAGCAGC

iPS:601108	18080-C5	NA	GAGTCGTGCTGACTCAGTCTCCACTCTCCCTGCCGCTCACCCCTGGAG AGCCGCCCTCCTCCTGCAAGTCTAGTCAGAGCCTCCTGCTAGTA ATGGATACAACTATTGGATTGGTACCTGCAGAAAGCAAGGCGAGTCTC CACAGTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9441) ELVLTQSPSLPVTPEPASISCRSSQSLHNSGYNLYDWLYQKPGSQPLL IYLGSNRASGVNDRFSGSGGTDFILKISRVEAEDVGVVYCMQALQTRTF GQGTKEIK	(SEQ ID NO: 9442) GAGTCACACTCAGCAGTCTCCAGGCACCTGCTTTGCTCTCCAGGG GAAAGAGCCACCTCTCTGCGAGGCCAGTCAGAGTGTAGCAGCGGC TACTTAGCTGGTACCAGAGAAACCTGGCCAGGCTCCAGGCTCTC ATCTATGTTGTCATCCAGCAGGGCACTGGCATCCAGACAGGTTTCAGT GGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAGCAGACTGGAG CCTGAAGATTTCGA	GAGGTGCAGCTGCTCGAGTCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTG ATTACTACTGGAGTGGATCCGACCCAGCAGCCAGGAGGCGCTGGAGT GGATTGGGTACATCAATGACAGTGGGAGCACCTACTATAACCCGTCCC TCAAGAGTCCAGTACCTTATACGTAGACTCGTCTAAGAACCAAGTCTC CCTGAAGCTGAGC	(SEQ ID NO: 9799) EVQLLESGPGLVKPSEILSLTCTVSGSSISGDYYWVIRQHPGKGLEWIG YINDSGTYNPNLSKSRVTLSDSSKNQFSLKLSSTVAADTA VYYCAARDLL WFGKLNYYYGMDVWVGQGTITVYSS
		AA					(SEQ ID NO: 9800) GAGGTGCAGCTGCTCGAGTCGGGCCAGGCTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGCGCCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGTCCGCGCAGGCTCCAGGGAAGGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTACACATACCTACGCGACTCCGT GAAGGGCCGTTCCACTCTCCAGAGACAATTCACAGAACACCTGTGA TCTGCAAAATGAACAGC
iPS:601090	18080-H9	NA		(SEQ ID NO: 9443) ELTILQSPGTLISLSPGERATLSCRASQSVSSGYLAWYQKPGQAPRLIYG ASSRATGIPDRFSGSGGTDFILITSLRLEPEDFAVYYCQYQYSSPFTFGPGT KVEIK	(SEQ ID NO: 9444) GAGTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTITTTATACAGC TCCAACAATAAGAACTACTTGTGTGTACAGCAGAAACCCAGGACAG CCTCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTCAAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCA TCAGCAGCCTGCAG	(SEQ ID NO: 9801) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVS GISGSGSYADSVKGRFTISRDNKNTLYLQMNSLRADTA VYYCAKV MTDPYYDMDVWVGQGTITVYSS	(SEQ ID NO: 9802) GAGGTGCAGCTGCTCGAGTCGGGCCAGGACTGGTGAAGCCTTCGGA GACCTGTCCCTCACCCTGCACTGTCTCTGGTACTCCATCAGTAGTAGT CGTACTACTGGGCTGGATCCGCCAGCCCGCAGGGAAGGGGCTGGA GTGGATTGGGAGTATCTATTATAGTGGGAGCACTACTACAAACCCGTC CCTCAAGAGTCGAGTACCATACTCCGTAGACAGCTCCAGAACCAAGT CTCCCTGAAGCTGAGT
	18081-A6	NA		(SEQ ID NO: 9445) ELVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA WYQKPGQPP KLLIYWASTRESGVNDRFSGSGGTDFILITSLRLEPEDFAVYYCQYQYSSP LTFGGGTKEIK	(SEQ ID NO: 9446) GAGTCGTGCTGACTCAGTCTCCACTCTCCCTGCCGCTCACCCCTGGAG AGCCGCCCTCCTCCTGCAAGTCTAGTCAGAGCCTCCTGCTAGTA ATGGATACAACTATTGGATTGGTACCTGCGAGAGCCAGGCGAGTCTC CACAGCTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9803) EVQLLESGPGLVKPSEILSLTCTVSGDSISSRYWVIRQHPGKGLEWIG SIYSGSTYYPNLSKSRVITISVDTSKNQFSLKLSSTVAADTA VYYCARGIFG VITYFDYWGQGTITVYSS	(SEQ ID NO: 9804) GAGGTGCAGCTGCTCGAGTCAGTCCAGGACAGGTCAGGCCCCCTCGCA GACCTCTCACTCACTGCTGCTGCTCCGGGAGAGTGTCTCTAGCAAC AGTGTGCTTGGAACTGGATCAGGCACTCCCATCGAGAGGCGCTTGA TGGCTGGGAAGACATACCTAGGTCCTCAAGTGGTATATGATTATGCA GTATCTGTGAAAGTCCAAATACCATCAACCCAGACACATCCAAGAAC CAGTCTCTCCCTGCAG
iPS:601070	18081-B5	NA					

	AA		(SEQ ID NO: 9447) ELVLTQSPSLPVTGEPASISCRSSQSLHNRNGYNLDWYLOKPGQSPQLI IYLGSNRASGVDPDRFSGSGGTDFILTKISRVEAEDVGYYCMQALQPIITF GQGTIRLEIK	(SEQ ID NO: 9805) EVQLLESGPGQVKPSQTLSTLCAISGDSVSSNSAAWNWIRQSPRGLWLG RTYRYSKWYNDYAVSVKSRITNPDTSKNQSLQLNSVTPEDTAVYYCAR EVLWFGKLNYYGMDVWVGQGTITVYSS
			(SEQ ID NO: 9448) GAGCTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGC GAGAGGCCACCATCAACTCAAGTCCAGCAGAGAGTGTITATACAGC TCCAAACAATAAGAACTACTTACCTGACAGAGAGAAACAGGACAG CTCTTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTGAGTGGCAGGGGTCTGGGACAGATTCTACTCTCACCA TCAGCAGCGCTGCAG	(SEQ ID NO: 9806) GAGGTGCAGTCTCTGAGTCCGGCCAGGACTGGTGAAGCCTTCGGGA GACCTGTCCCTCACCTGCGCATTTGTCTGTGTCTCCATCAGCAGTGT AGGTCTACTGGGGTGGATCCGCCAGCCCCAGGGAAGGAGTGGGA GTGGATTGGGAGTATCTATTATGGTGGGAGACCTACTACAAACCCGTC CTCAAGAGTCGAGTCAACATATCCGTTGACACGTCCAAAGAACCAAGTT CTCCCTGAAGCTGAGC
iPS:601078 18081-C10	AA		(SEQ ID NO: 9449) ELVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPP KLLIYWASTRESGVDPDRFSGSGGTDFILTISSLQAEDVAVYYCQYYSTP LTFGGGTKVEIK	(SEQ ID NO: 9807) EVQLLESGPGLVKPSEITLSLTIVSGVSISSRSYWGWIQPPKGLIEWIGSI EYGGSTYNNPSLKSRYTISVDTSKNQSLKSSVTAADTAVYYCATITFGV VGWFDPPWQGQNLVTYSS
			(SEQ ID NO: 9450) GAGCTCGTGATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGGAG ACAGATCACCATCACTTGGCGGGAAGTCAAGAGCATTAAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCTCTGATCT ATGCTGCATCCAGTTTGAAGTGGGTCCCATCAAGGTTCACTGAGCA GTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9808) GAGGTGCAGTCTGCTGAGTCTGCTGCGCTGGTGAACCCACACAG ACCTCAGCTGACCTGACACCTTCTGTGTCTTCATTCACCATCATA AAATGGGTGTGGAGTGGATCCGTCAGCCCGAGAAAGGCCCTGGAGT GGCTTGCACTCAATTTATTGGAATGATAGCGGCTACAGCCATCTCT GCAGATAGCTCACCATCACCAGGACACCTCCAAAAACCAAGTGGT CCTCACAATGACC
iPS:601114 18081-D6	AA		(SEQ ID NO: 9451) ELVMTQSPSSLSASVGDRTITCRASQISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGGTDFILTISSLQPEDFATYYCQQSYSTPFTFGPGTKL EIK	(SEQ ID NO: 9809) EVQLLESGPALVKPIQTLTLCTFSGFSFTHKMGVDWIRQPPKALEWLA LIYWNDDTRYSPSLQSRLTIKDTSKNQVVLTMTNMDPVDITATYYCVYR RYNNWYENWFDPPWQGQTLVTYSS
			(SEQ ID NO: 9452) GAGCTCGTGATGACCCAGTCTCCATCTCCCTGTCTGCACTCTGAGGAG ACAGATCACCATCACTTGGCGGGAAGTCAAGAGCATTAAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCTGATCT ATGCTACATCCAGTTTGCAGAGTGGGTCCCATCAAGGTTCACTGAGCA GTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9810) GAGGTGCAGTCTGCTGAGTCCGGGGAGGCTGGTCAAGCCTGGGG GTCCCTGAGACTCTCTGTGCGAGCTCTGGATTCACCTTAGCATCTAT GCCTTGAGCTGGTCCCGCAGGTCCAGGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGTGGTGGTGGTACACATACACGACAGCTCCGT GAAGGGCCGGTTCACCATCTCCAGAGACAAATTCAGAACACCTGTGA TCTGCAAAATGAACAGC
iPS:601098 18081-D12	AA		(SEQ ID NO: 9453) ELVMTQSPSSLSASVGDRTITCRASQISSYLNWYQQKPGKAPKLLIYAT SSLQSGVPSRFSGSGGTDFILTISSLQPEDFATYYCQQSYSTPFTFGQGTK VEIK	(SEQ ID NO: 9811) EVQLLESGGLVKPGGSLRLSCAASGFTFSYALSWVRQAPGKGLWVSAI SCSGGSTYYADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVYYCAKGE GIAARYYYGMDVWVGQGTITVYSS
			(SEQ ID NO: 9454) ELVMTQSPSSLSASVGDRTITCRASQISSYLNWYQQKPGKAPKLLIYAT SSLQSGVPSRFSGSGGTDFILTISSLQPEDFATYYCQQSYSTPFTFGQGTK VEIK	(SEQ ID NO: 9812) EVQLLESGGLVKPGGSLRLSCAASGFTFSYALSWVRQAPGKGLWVSAI SCSGGSTYYADSVKGRFTISRDNSKNTLYQMNSLRRAEDTAVYYCAKGE GIAARYYYGMDVWVGQGTITVYSS

IPS:601130	18082-F5	NA	GAGTCGCCCTGACTAGCTGCTCCGCTGCTGGGTCTCCTGGACAG TCGATCACCATCTCTGCACTGGAACACAGAGTGAAGTGTGGTTAT AACTATGCTCTGCTGTAACACACAGCACCAGCAAGCCCAAACTC ATGATTTAGAGTCAAGTAAAGCGCCCTCAGGGTCCCTGATGCTTCT CTGGCTCAAGTCTGGCAACACGCGCTCCTGACCGCTCTCTGGGCTCC AGGCTGAGGATGAG	(SEQ ID NO: 9455) ELALTPASASGSGSQTITCTGSSDVGGYNVSWYQQHPGKAPKLMY EVSKRPSGVPRFSGSKSNTASLTVSGLQAEDEADYCYSSYAGSNVVF GGGTKLTVL	(SEQ ID NO: 9456) GAGTCACACTCAGCAGTCTCAGGCCACCTGCTGTTGCTTCCAGGG GAAAGAGCCACCTCTCTGCGAGGCCAGTCAAGTGTTAGCAGCAGC TACTTAGCTGTGACAGAGAAACCTGGCCAGGCTCCAGGCTCTC ATCTATGTTGCTATCCAGCAGGCCACTGGTATCCAGCAGGTTTCACT GGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAGCAGACTGGAG CCTGAAGATTITGCC	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGAG GTCCCTGAGACTCTCTGTGAGCGCTCTGGATTCACCTTACAGTATAT GGCATGGATTGGTCCGCGCAGGCTCCAGCAAGGAGCTGGAGTGGGT GGCAGTTATAGTATGATGAGTAAAGTAAATAACTATGACAGACTCCGT GAAGGGCCGATTCACCATCTCCAGAGACAAATCCAAAGAAATACGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9813) EVQLLESGGGVVPQPSRLSLSCAASGFTFSRYGMDWVRQAPGKGLEWVA VIWYDGSNKYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAR NYGSGSYGAYYYHGMDEVWGQGTITVTVSS	(SEQ ID NO: 9814) GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTGTGCGCCCTCTGGATTCACCTTACAGCAGCTAT GCCATGAGCTGGTCCGCGCAGGCTCCAGGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGTAGTGTAGTACACATACGACAGACTCCGT GAAGGGCCGTTACCATCTCCAGAGACAAATCCAAAGAAACAGCCTGTA TCTGCAAAATGAACAGC
	AA		(SEQ ID NO: 9457) ELTLTQSPGTLISLSPGERATLSRASQSVSSSYLA WYQQKPGQAPRLIYG ASSRATGIPARFSGSGTDFTLTISRLEPEDFAVYYCQQYGSPLTFGGGT KLEIK	(SEQ ID NO: 9458) GAGTCGTGATGACCCAGTCTCCAGACTCCCTGGCTGTCTCTGGGC GAGAGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTITATACAGC TCCAACAATAAGAACTACTTGTGTGTAACAGAGAAACCCAGGACAG CCTCTAAGCTGCTATTACTGGGCATCTACCCGGGAATCCGGGGTCC CTGACCGATTGAGTGGCAGCGGTCTGGGACAGATTTCATCTCTACCA TCAGCAGCTGCAG	(SEQ ID NO: 9815) EVQLLESGGGLVQPSGSLRLSCAASGFTFSRYAMSWVRQAPGKGLEWVS AISGDSSTIYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKH LRYSDWPLDYWGQGTITVTVSS	(SEQ ID NO: 9816) GAGGTGCAGCTGCTCGAGTCTGGAGCTGAGGTGAAGAGCCTGGGGC CTCAGTGAAGTCTCTGCAAGCTTCTGGATACACCTTACACAGTTAT GATATCAACTGGTGGCGCAGCGCCTGAGCAAGGGCTTGAAGTGGATG GGATGGATGAACCTTAAGTGGTAAACAGAGGTATGCACAGAAATTC CAGGACAGAGTCACTACCATGACAGGAACACCTCCATAAGCACAGCTAC ATGGAGCTGAGCAGC	(SEQ ID NO: 9817) EVQLLESGAEVVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWVG WMNPKSGNTGYAQKFQDRVTMTRNTSISTAYMELSLRSDDTAVYYCYVR GWGTYYYGMDVWGQGTITVTVSS	(SEQ ID NO: 9818) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTGTGCGCCCTCTGGATTCACCTTACAGCAGCTAT GCCATGAGCTGGTCCGCGCAGGCTCCAGGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGTAGTGTAGTACATACGACAGACTCCGTG AAGGGCCGTTACCATCTCCAGAGACAAATCCAAAGAAACAGCCTGTA TCTGCAAAATGAACAGC
IPS:601159	18086-H4	NA		(SEQ ID NO: 9459) ELVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLA WYQQKPGQPP KLLIYWASTRESGVPRFSGSGTDFTLTISLQAEDEVAVYYCQQYYSITP WTFGQGTKVDIK	(SEQ ID NO: 9460) GAGTCGTGATGACAGACTCCAGGCCACCTGCTGCTGCTCCAGGG GAAAGAGCCACCTCTCTGCGAGGCCAGTCAAGTGTITAGCAGCAGC TACTTAGCTGTGACAGAGAAACCTGGCCAGGCTCCAGGCTCTC ATCTATGTTGCTATCCAGCAGGCCACTGGTATCCAGCAGGTTTCACT GGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAGCAGACTGGAG CCTGAAGATTITGCA			
	AA							
IPS:603151	18088-B10	NA						

[illegible]

PS:603169	18089-G7	NA	GAGCTCCAGATGACCCAGTCTCCATCTCTCCCTGTTCTGCATCTGTAGGAG ACAGAGTCAACCATCACTTGC CGGCAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAAGCTCTCTGATCT ATGCTACATCCAGTTTGCAAAGTGGGTCCCATCCAGGTTCAGTGGCA GTGGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9469)	ELQMTQSPSSLASVGDRLVTITCRASQSISSYLNWYQOKPGKAPKLLIYAT SSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQQSYSPFTFGPGTKV EIK	(SEQ ID NO: 9470)	GAGCTCCAGATGACCCAGTCTCCATCTTCCGTGTTCTGCATCTGTAGGAG ACAGAGTCAACCATCACTTGCAGGCGAGTCAGGACATTAGAACTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAAGCTCTCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCCAGGTTCAGTGGCA GTGGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9471)	ELQMTQSPSSVSASVGDRLVTITCOASQDISNYLNWYQOKPGKAPKLLIYA ASSLQSGVPSRFSGSGTDFTLTISSLQPEDFATYYCQSQSYSTPLTFGGGT KVDIK	(SEQ ID NO: 9472)	GAGCTCCAGATGACCCAGTCTCCATCTCTCCCTGTTCTGCATCTGTAGGAG ACAGAGTCAACCATCACTTGTGCGGCGAGTCAGGCAATTAGCAATATT TGCGATGGTATCAGCAGAAAGCCAGGAAAGTTCTCTAATCTCTGATCT ATGGTGCATCCATTTGCAATTAGGGGTCCCATCTCGGTTCAGTGGCAG TGCTCTGGGACAGATTTCATCTCTCACCATCAGCAGCCTGCAGCCTGA AGATGTTTGCAACT	(SEQ ID NO: 9473)	ELQMTQSPSSLASVGDRLVTITCRASQISNYLAWYQOKPGKVPNLLIYGAA STLQLGVPSRFSGSGTDFTLTISSLQPEDVATYYCQKYSPFTFGPGTK VDIK	(SEQ ID NO: 9474)	GAGCTCCAGATGACCCAGTCTCCATCTCTCCCTGTTCTGCATCTGTAGGAG ACAGAGTCAACCATCACTTGC CGGCAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAAGCTCTCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAGTGGCA GTGGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	NA	18089-IH12	PS:603205
		AA	(SEQ ID NO: 9827)	EVQLLESPVLVKPTQLTLTCTIFSFSFTTHKMGVDWIRQPPGKALEFLWA LIYNWDDKRYSPSLQSRLLTIKDTSKNQVVLTMNMDPVDATYYCAVR RYNWNVENWFDPPWQGQGLVTYSS	(SEQ ID NO: 9828)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9829)	EVQLLESGGLVQPGGSLRLSCAASGFTTSSYAMSVMVRQAPGKGLEWVS GISGSGSYTYADSVKGRFTISRDNLSKNTLYLQMNLSRAEDTAVYYCAKT LTPDYDDMDVWVGQGTITVYSS	(SEQ ID NO: 9830)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAGCTAT GCCGTGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9831)	EVQLLESGGLVQPGGSLRLSCAASGFTTSSYASVMVRQAPGKGLEWVSC ISGSGSYTYADSVKGRFTISRDNLSKNTLYLQMNLSRAEDTAVYYCAKAL TPDYDDMDVWVGQGTITVYSS	(SEQ ID NO: 9832)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAACTAT GCCATGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC				
		NA	(SEQ ID NO: 9827)	EVQLLESPVLVKPTQLTLTCTIFSFSFTTHKMGVDWIRQPPGKALEFLWA LIYNWDDKRYSPSLQSRLLTIKDTSKNQVVLTMNMDPVDATYYCAVR RYNWNVENWFDPPWQGQGLVTYSS	(SEQ ID NO: 9828)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9829)	EVQLLESGGLVQPGGSLRLSCAASGFTTSSYAMSVMVRQAPGKGLEWVS GISGSGSYTYADSVKGRFTISRDNLSKNTLYLQMNLSRAEDTAVYYCAKT LTPDYDDMDVWVGQGTITVYSS	(SEQ ID NO: 9830)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAGCTAT GCCGTGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9831)	EVQLLESGGLVQPGGSLRLSCAASGFTTSSYASVMVRQAPGKGLEWVSC ISGSGSYTYADSVKGRFTISRDNLSKNTLYLQMNLSRAEDTAVYYCAKAL TPDYDDMDVWVGQGTITVYSS	(SEQ ID NO: 9832)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAACTAT GCCATGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC				
		AA	(SEQ ID NO: 9827)	EVQLLESPVLVKPTQLTLTCTIFSFSFTTHKMGVDWIRQPPGKALEFLWA LIYNWDDKRYSPSLQSRLLTIKDTSKNQVVLTMNMDPVDATYYCAVR RYNWNVENWFDPPWQGQGLVTYSS	(SEQ ID NO: 9828)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9829)	EVQLLESGGLVQPGGSLRLSCAASGFTTSSYAMSVMVRQAPGKGLEWVS GISGSGSYTYADSVKGRFTISRDNLSKNTLYLQMNLSRAEDTAVYYCAKT LTPDYDDMDVWVGQGTITVYSS	(SEQ ID NO: 9830)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAGCTAT GCCGTGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGGTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9831)	EVQLLESGGLVQPGGSLRLSCAASGFTTSSYASVMVRQAPGKGLEWVSC ISGSGSYTYADSVKGRFTISRDNLSKNTLYLQMNLSRAEDTAVYYCAKAL TPDYDDMDVWVGQGTITVYSS	(SEQ ID NO: 9832)	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTGTGCAGCCTCTGGATTACCTTTAGCAACTAT GCCATGAGCTGGGTCCGCAAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCCAAAGAACACCGCTGTA TCTGCAAAATGAACAGC				

			(SEQ ID NO: 9475) ELQMTQSPSSLSASVGDRTVITICRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGTDFTLTIISLQPEDFATYYCQSYSTPPTFGQGTK EIK	(SEQ ID NO: 9833) EVQLLESGGGLVQPGSLRLSCAASGFTISYAMSWVRQAPGKGLEWVS AISGSGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKQ GGIAAAAYYYDGMVWVGQGTITVSS
			(SEQ ID NO: 9476) GAGCTCGTGTGACTGACTACCTCGGTGTCCAAAGGGCTTGAGACAG ACCGCCACACTCACTGCACTGGGAACAGCAACAATGTTGGCAACCAA GGAGCAGCTTGGCTGACGACGACCCAGGGCCACCTTCCAAACTCCTA TCCTACAGAAATAACAACCGCCCTCAGGATCTCAGACAGATTATCT GCATCCAGTTCAGGAAACACAGCCTCCCTGACCAATTACTGGACTCCAG CCTGAGGACGAGGCT	(SEQ ID NO: 9834) GAGTGCAGCTGCTCGAGTCCGGGGGAGGGCTTGCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGAGCTGTGATTCACCTTCAGTAGATAT GGCATGGATTGGGTCCGACAGGCTCCAGGCAAGGACTTCGAGTGGGT GGCATGTTATATCATATAGTAAAGTAAATAATATATGTCAGACTCCGT GAAGGGCCGATTCACCATCTCCAGAGACAAATTCACAGAACACGCTGTA TCTGCAAAATGAACAGC
			(SEQ ID NO: 9477) ELVLTLQPSVSKGLRQTATLTCTGNSNNVGNQGAALQQHQHPPKLLS YRNNRPSGISERLSASRSGNTASLTITGLQPEDEADYYCSAWDSSLASVV FGGGLTKLTVL	(SEQ ID NO: 9835) EVQLLESGGVVQPGSLRLSCAASGFTISRYGMDWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR NYGSGSYGAYYYGMDVWVGQGTITVSS
			(SEQ ID NO: 9478) GAGCTCGTGATGACCCAGTCTCCATCTCCTCTGTCTGCACTCTGAGGAG ACAGAGTCACTACCTTGGCAGGGAGTCAAGACATTAGCAACTATT TAAATTGGTATCAGCAGAAACAGGAGGCCCTTAAGCTCTCTGATCT ATGCTGCATCCAGTTTGAAGTGGGTCCCATCAAGGTTCAAGCGCA GTGGATCTGGGACAGAAATTCATCTCACAATCAGCAGCCTGCAGCCTG AAGATTTTGCAACT	(SEQ ID NO: 9836) GAGTGCAGCTGCTCGAGTCCGGGGGAGGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGAGCCCTGTGATTCACCTTACCTCTAT GCCATGAGCTGGGTCCGACAGGCTCCAGGAAGGGCTGGAGTGGGT CTCAACTATTAGTCACTAGTGGTGGTAGCACATACTACGACACTCCGT GAAGGGCCGTTCCACATCTCCAGAGACAAATTCACAGAACACGCTGTA TCTGCAAAATGAACAGC
			(SEQ ID NO: 9479) ELVMTQSPSSLSASVGDRTVITICQASQDISNYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGTDFTLTIISLQPEDFATYYCQSYSTPPTFGQGTKV DIK	(SEQ ID NO: 9837) EVQLLESGGGLVQPGSLRLSCAASGFTISYAMSWVRQAPGKGLEWVS ITISHSGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARD GGSGWFPKLLHYGLDVWVGQGTITVSS
			(SEQ ID NO: 9480) GAGCTCGTGATGACCCAGTCTCCATCTCCTCTGTCTGCACTCTGAGGAG ACAGAGTCACTACCTTGGCAGGGCAAGTCAAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTTAAGCTCTGATCT ATGCTGCATCCAGTTTGAAGTGGGTCCCATCAAGGTTCAAGTGGCA GTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9838) GAGTGCAGCTGCTCGAGTCCGGGGGAGGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGAGCCCTGTGATTCACCTTGAGCATCTAT GGCATGAGCTGGGTCCGACAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGACACTCCGT GAAGGGCCGTTCCACATCTCCAGAGACAAATTCACAGAACACGCTGTA TCTGCAAAATGAACAGC
			(SEQ ID NO: 9481) ELVMTQSPSSLSASVGDRTVITICRASQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGTDFTLTIISLQPEDFATYYCQSYSTPPTFGQGTK VDIK	(SEQ ID NO: 9839) EVQLLESGGGLVQPGSLRLSCAASGFTISYAMSWVRQAPGKGLEWVA ISGSGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKGE GISARYYYGMDVWVGQGTITVSS
			(SEQ ID NO: 9482)	(SEQ ID NO: 9840)

IPS:613775	18179-A3	NA	GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGCACAGAA ATGGATCAACATATTGGATTGGTACCTGACAGAGCCAGGCGAGTCTC CACAGCTCGATCTATTGGGTCTTAATCGGGCTCCGGGGTCCCTGA CAGGTTACAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT (SEQ ID NO: 9483) ELVMTQSPSLPVTGPEPASISCRSSQSLLRHNGYNYLDWYLYKPGQSPQL LIVLGSNRASGVPDFRFGSGSGDTFTLKISRVEAEDVGYYVCMQALQPTFT FGPGTKVDIK (SEQ ID NO: 9484) GAGCTCGTGTGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGCATAGTA ATGGATACAACTATTGGATTGGTACCTGCAGAGCCAGGCGAGTCTC CACAACCTCGATCTATTGGGTCTTAATCGGGCTCCGGGGTCCCTGA CAGGTTACAGTGGCAGTGGATCAGGCACAGATTTTACACTAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9841) EVQLLESGPGLVKPSQTLTCTVSGDISSNPPYYSWIRQLPGKGLEWIG YISYSGSTFYNPISKRSVTISVDTSKNQFSLNLTSLTAADTAVYYCARDRL WFGVNLNYYYGMDVWVWGQGITVTVSS (SEQ ID NO: 9842) GAGGTGCGAGCTGCTCGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGA GACCTGTCCCTCACTGCTCACTGCAGCTGTCTTGGTGGCGCATCAGCAGTGGT GATTACTCTGGAGCTGGATCCGACAGCCAGCCAGGAGGCGCTGGA GTGGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAAACCCGTC CCTCAAGAGTCGAGTACCATAATCAGTAGACACGCTCTAAGGAGCACGAGT CTCCTGAAGCTGACC
IPS:613783	18179-A5	NA	(SEQ ID NO: 9485) ELVLTSQPSLSPVTGPEPASISCRSSQSLHSHNGYNYLDWYLYKPGQSPQL IYLGSRASGVPDFRFGSGSGDTFTLKISRVEAEDVGYYVCMQALQPTFT GPGTKVEIK (SEQ ID NO: 9486) GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCCGTACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTGCATAGTA ATGGATACAACTATTGGATTGGTACCTGCAGAGCCAGGCGAGTCTC CACAGCTCGATCTATTGGGTCTTAATCGGGCTCCGGGGTCCCTGA CAGGTTACAGTGGCAGTGGATCAGGCAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9843) EVQLLESGPGLVKPSQTLTCTVSGDISSNPPYYSWIRQLPGKGLEWIG YIDKSGSTYYNPISLKSRTISVDTSKQFSLKLTSLTAADTAVYYCAREKM WFGVNLNYYYGMDVWVWGQGITVTVSS (SEQ ID NO: 9844) GAGGTGCGAGCTGCTCGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACTGCTCACTGCAGCTGTCTTGGTGGCGCATCAGCAGTGGT ATTACTCTGGAGCTGGATCCGACAGCCAGCCAGGAGGCGCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAAACCCGTC TCAAGAGTCGAGTACCATAATCAGTTGACACGCTCTAAGAACCCAGTTCT CCCTGAATCTGACC
IPS:613707	18179-A9	NA	(SEQ ID NO: 9487) ELVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLYKPGQSPQL LIVLGSNRASGVPDFRFGSGSGADFTLKISRVEAEDVGYYVCMQALQPTLT FGGGTKVEIK (SEQ ID NO: 9488) GAGCTCGTGTGACCGAGTCTCAGGCACCTGTCTTGTCTCCAGGG GAAAGCCACCTCTCTGCAGGTCTAGTCAGAGCCTCTGCATAGTA AATGGATACAACTATTGGATTGGTACCTGCAGAGCCAGGCGAGTCTC CCACAGCTCGATCTATTGGGTCTTAATCGGGCTCCGGGGTCCCTG ACAGGTTACAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9845) EVQLLESGPGLVKPSQTLTCTVSGDISSNPPYYSWIRQLPGKGLEWIG YIDKSGSTYYNPISLKSRTISVDTSKNQFSLNLTSLTAADTAVYYCARDRL WFGVNLNYYYGMDVWVWGQGITVTVSS (SEQ ID NO: 9846) GAGGTGCGAGCTGCTCGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACTGCTCACTGCAGCTGTCTTGGTGGCGCATCAGCAGTGGT ATTACTCTGGAGCTGGATCCGACAGCCAGCCAGGAGGCGCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAAACCCGTC TCAAGAGTCGAGTACCATAATCAGTTGACACGCTCTAAGAACCCAGTTCT CCCTGAATCTGACC
IPS:613697	18179-A10	NA	(SEQ ID NO: 9487) ELVMTQSPSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLYKPGQSPQL LIVLGSNRASGVPDFRFGSGSGADFTLKISRVEAEDVGYYVCMQALQPTLT FGGGTKVEIK (SEQ ID NO: 9488) GAGCTCGTGTGACCGAGTCTCAGGCACCTGTCTTGTCTCCAGGG GAAAGCCACCTCTCTGCAGGTCTAGTCAGAGCCTCTGCATAGTA AATGGATACAACTATTGGATTGGTACCTGCAGAGCCAGGCGAGTCTC CCACAGCTCGATCTATTGGGTCTTAATCGGGCTCCGGGGTCCCTG ACAGGTTACAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9845) EVQLLESGPGLVKPSQTLTCTVSGDISSNPPYYSWIRQLPGKGLEWIG YIDKSGSTYYNPISLKSRTISVDTSKNQFSLNLTSLTAADTAVYYCARDRL WFGVNLNYYYGMDVWVWGQGITVTVSS (SEQ ID NO: 9846) GAGGTGCGAGCTGCTCGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACTGCTCACTGCAGCTGTCTTGGTGGCGCATCAGCAGTGGT ATTACTCTGGAGCTGGATCCGACAGCCAGCCAGGAGGCGCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGCACCTACTACAAACCCGTC TCAAGAGTCGAGTACCATAATCAGTTGACACGCTCTAAGAACCCAGTTCT CCCTGAAGCTGACC

		AA	(SEQ ID NO: 9489) ELVLTQSPGTLSPGERATLSCRSSQLHHRNGYNLDWYLKPKGSPQL LIYLGNSNRASGVDPDRFSGSGGTDFTLKISRVEADVGYYVCMQALQTPRT FGQG/TKVEIK (SEQ ID NO: 9490) GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGTCTGGATCTGTAGGAG ACAGAGTCACCATCATCTGCCAGGAGGAGGACATTAGCGACTATT TAAATTGGTTTACAGCAGAAACAGGAGAGCCCTAAGCTCTGATCT TTGCTGCATCCAGTTTGCAAGGTGGGTCCTCATCTCGGTTTCAGTGGA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9847) EVQLLESGPGLVKPSQTLSLTCTVSGGAISSGDYYWSWIRQHPKGKLEWIG YIDKSGSTYYNPSLKRATISVDTSKDQFSLKLSSTVAADTAVVYCARDQL WFGVLNYYYGMDVWVGQGTITVTVSS (SEQ ID NO: 9848) GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTAAAGCCTGGGGG GTCCCTTAGACTCTCTGTGACGCTCTGGATTCACTTTTCAGTAACGCC TGGATGAGCTGGTCCGACAGCTCCAGGAAAGGGCTGGAGTGGGT TGCCCGTATTAAAGCAACACTTATGTTGGGACAAACAGACTACGCTGC ACCGGTAAAGGACAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTCTGCAAAATG	
PS:613685	18179-B7	NA		(SEQ ID NO: 9491) ELVMTQSPSSLASVGDRTVITTCARQDISDYLNWFOQKPKRAPKLLIFAA SSLQGGVPSRFSFGSGGTDFTLTISLQPEDFATYYCQQTYSMPFTFGPGTK VDIK (SEQ ID NO: 9492) GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCATCTGCCGAGCAAGTCAGAGCATTAACAGCTATT TAAATTGGTTTCAACAGAAACAGGAAAGCCCTAAGCTCTGATCT ATGCTGCATCCAGTTTGCAAGTGGGTCCTCATCAAGTTTCAGTGGA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACTG AAGATTTTGCAACT	(SEQ ID NO: 9849) EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVVC RIKGNITYGGTIDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCT TPSNSGSYNYFVSVMQVWVGQGTITVTVSS (SEQ ID NO: 9850) GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTGTGACGCTCTGGATTCACTTTTCAGTAACGCC TGGATGAGCTGGTCCGACAGCTCCAGGGAAGGGCTGGAGTGGGT TGCCCGTATTAAAGCAACACTTATGTTGGGACAAACAGACTACGCTGC ACCGGTAAAGGACAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTCTGCAAAATG
PS:613711	18179-B8	NA		(SEQ ID NO: 9493) ELVMTQSPSSLASVGDRTVITTCRSQSINLYNWFQKPKAPKLLIYAA SSLQSGVPSRFSFGSGGTDFTLTISLQPEDFATYYCQQSYSTPFTFGPGTKV DIK (SEQ ID NO: 9494) GAGCTCGTGATGACCCAGTCTCCACTCTCCCTGCGCCGTACCCCTGGA GAGCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGT ACTGGATCAACTATTGGATTGGTACTCGAGAAAGCCGGGCGAGTCT CCACAGCTCTGATCTATTGGTTTCTAATCGGCGCTCCGGGGTCCCTG ACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9851) EVQLLESGGGLVQPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVVC RIKGNITYGGTIDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCT TPSNSGSYNYFVSVMQVWVGQGTITVTVSS (SEQ ID NO: 9852) GAGGTGCAGCTGCTCGAGTCCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGACTCTCTGTGGTGGCCCATCAGCAGTGGTG ATTACTACTGGAGCTGGATCCGACAGCCAGGGAAGGGCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGGACCTACTACAAACCCGTCCC TCAAGAGTCGAGCTACCATATCATAGTACACACGCTCTAAGGACCACTTCT CCCTGAAGCTGAGC
PS:613765	18179-C4	NA		(SEQ ID NO: 9495) ELVMTQSPSLSPVTPGEPASISCRSSQLLHSTGYNLDWYLKPKGSPQL LIYLGNSNRASGVDPDRFSGSGGTDFTLKISRVEAGDVGFYYCMQALQTPRT FGQG/TKLEIK (SEQ ID NO: 9496) GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGCGCCGTACCCCTGGA GAGCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGT ACTGGATCAACTATTGGATTGGTACTCGAGAAAGCCGGGCGAGTCT CCACAGCTCTGATCTATTGGTTTCTAATCGGCGCTCCGGGGTCCCTG ACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9853) EVQLLESGPGLVKPSQTLSLTCTVSGGAISSGDYYWSWIRQHPKGKLEWIG YIDKSGSTYYNPSLKRATISVDTSKDQFSLKLSSTVAADTAVVYCARDRL WFGVLNYYYGMDVWVGPGGTITVTVSS (SEQ ID NO: 9854) GAGGTGCAGCTGCTCGAGTCCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGACTCTCTGTGGTGGCCCATCAGCAGTGGTG ATTACTACTGGAGCTGGATCCGACAGCCAGGGAAGGGCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGGACCTACTACAAACCCGTCCC TCAAGAGTCGAGCTACCATATCATAGTACACACGCTCTAAGGACCACTTCT CCCTGAAGCTGAGC

iPS:613777	18179-C6	NA	GAGCTCGTGTGATGACTCAGACTCCACTCTCCCTGCCGTCAACCCCTGGA GAGCGGCTCCATCTCTCGAGGTAGTCAGAGCCCTCTGCATAGA AATGGATACAAATTATTGGATTGGTACTGCAATAACAGAGGAGCTCTC CACAGTCTCGATCTATTGGGTCTAATCGGGCTCCGGGCTCCCTGA CAGGTTCATTGGCATTGGCTCAGGCACAGATTTTACACTGAAAATCAG CAAAGTGGAGGCT	GAGGTGCAGTCTCGAGTGGGCCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCAGTCTCTGTGGGCCATCAGCAGTGGTG ATTACTACTGGAGTCCGACCCAGCAGCCAGGAGGGCTGGAGT GGATTGGGTACATCGATAAGAGTGGGAGACCTACTACAACCCGTCCC TCAAGAGTCCAGCTACCATATCAGTAGACACGCTTAAGGACCACTTCT CCCTGAAGCTGAGC
		AA	(SEQ ID NO: 9497) ELVMTQ/PLSLPVTPGEPASISCRSSQSLHRNGYNVLDWYLHKPGSQPL LIYLSNRASGVDPDRFSGSGTDFTLKISKVEAEDVGIYYCMQALQTPFTF GPGTKVEIK	(SEQ ID NO: 9855) EVQLLESGPGLVKPSQTLSLTCTVSGDAISSGDYYWSWIRQHPGKLEWIG YIDKSGSTYYNPSSLKSRATISVDTSKDQFSLKLSVTAADTAVVYCARDRL WFGVLNYYYGMDVWVGQGTITVTVSS
iPS:613687	18179-C7	NA	GAGCTCGTGTGACTCAGTCTCCACTTCCCTGCCGTCAACCCCTGGAG AGCGGCTCCATCTCTCGAGGTAGTCAGAGCCCTCTGCATCGTA ATGGATACCACTATTGGATTGGTACCTGCAGAGCCAGGGCAGTCTC CACAACTCCTGATCTATTGGGTCTAATCGGGCTCCGGGCTCCCTGA CAGGTTCATTGGCAGTGGCTCAGGCACAGATTTTACACTGGAATCAG CAGAGTGGAGGCT	GAGGTGCAGTCTGCTCGAGTGGGCCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCAGTCTCTGTGGACTCCATCAGCAGTAATC CTTACTACTGGAGTGGATCCGCCAGCAGCCAGGAGGGCTGGAGT GGATTGGGTACATCTCTCACAGTGGGAGCACTTATACAAATCCGTCCT CAAGAGTCCAGTAACCATATCAGTAGACACGCTAAGAAATCAGTCTC CCTGAATCTGACC
		AA	(SEQ ID NO: 9499) ELVLTQSPSLPVTPGEPASISCRSSQSLHRNGVHYLDWYLQKPGSQPL IYLGSRASGVDPDRFSGSGTDFTLISRVEAEDVGYYCMQALQTPSFG QGTKEIK	(SEQ ID NO: 9857) EVQLLESGPGLVKPSQTLSLTCTVSGDSSSNPPYWSWIRQHPGKLEWIG YIHSKSTYYNPSSLKSRVTISVDTSKNQFSLNLTSTVTAADTAVVYCARDKM WFGVLNYYYGMDVWVGLTITVTVSS
iPS:613787	18179-C10	NA	GAGCTCGTGTGACTCAGTCTCCACTTCCCTGCCGTCAACCCCTGGAG AGCGGCTCCATCTCTCGAGGTAGTCAGAGCCCTCTGCATAGAA ATGGATACAACTATTGGATTGGTACCTGCAGAGCCAGGGCAGTCTC CACAGTCTCGATCTATTGGGTCTAATCGGGCTCCGGGCTCCCTGA CAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAG CAGAGTGGAGGCT	GAGGTGCAGTCTGCTCGAGTGGGCCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCAGTCTCTGTGGACTCCATCAGCAGTAATC CTTACTACTGGAGTGGATCCGCCAGCAGCCAGGAGGGCTGGAGT GGATTGGGTACATCTCTCACAGTGGGAGCACTTATACAAATCCGTCCT CAAGAGTCCAGTAACCATATCAGTAGACACGCTAAGAAATCAGTCTC CCTGAAGCTGACC
		AA	(SEQ ID NO: 9501) ELVLTQSPSLPVTPGEPASISCRSSQSLHRNGYNVLDWYLQKPGSQPL IYLGSRASGVDPDRFSGSGTDFTLKISRVEAEDVGVYYCMQALQTPFTF GPGTKVEIK	(SEQ ID NO: 9859) EVQLLESGPGLVKPSQTLSLTCTVSGDSSSNPPYWSWIRQHPGKLEWIG YIHSKSTYYNPSSLKSRVTISVDTSKNQFSLNLTSTVTAADTAVVYCARDRL WFGVLNYYYGMDVWVGLTITVTVSS
iPS:613675	18179-D8	NA	GAGCTCGTGTGATGACCCAGTCTCCATCTCCCTCTGTCATCTGTAGGAG ACAGATCAACATCACTTCCCGGACAAAGTCAGAGCAATTAAGCAGCTAT TAAATTGGTATCAGCAGAAACACAGGAGAGCCCTAAGCTCCTGATCT TTGCTGCTCAGTTCAGAGGTGGGTCCTCAATCAAGGTTCAGTGGCA GTGGATCTGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACTG AAGATTTTGCAACT	GAGGTGCAGTCTGCTCGAGTCCGGGGGAGGCTTGGTAAAGCCTGGGG GTCCCTTAGACTCTCTGTGAGCCCTCTGATTCATCTCAGTAACGCC TGGATGAGCTGGTCCCGCCAGGCTCCAGGAGGGGCTGGAGTGGGT TGGCCGTATTAAGAGCAACTTATGGTGGGACAACTACACTACGCTGC ACCGGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTTCGAAATG
			(SEQ ID NO: 9502) GAGCTCGTGTGATGACCCAGTCTCCATCTCCCTCTGTCATCTGTAGGAG ACAGATCAACATCACTTCCCGGACAAAGTCAGAGCAATTAAGCAGCTAT TAAATTGGTATCAGCAGAAACACAGGAGAGCCCTAAGCTCCTGATCT TTGCTGCTCAGTTCAGAGGTGGGTCCTCAATCAAGGTTCAGTGGCA GTGGATCTGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACTG AAGATTTTGCAACT	(SEQ ID NO: 9860) GAGGTGCAGTCTGCTCGAGTCCGGGGGAGGCTTGGTAAAGCCTGGGG GTCCCTTAGACTCTCTGTGAGCCCTCTGATTCATCTCAGTAACGCC TGGATGAGCTGGTCCCGCCAGGCTCCAGGAGGGGCTGGAGTGGGT TGGCCGTATTAAGAGCAACTTATGGTGGGACAACTACACTACGCTGC ACCGGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTTCGAAATG

			AA	ELVMTQSPSSLSASVGDRTVITICRTSQSISSVNLNWYQQKPGRAPKLLIFAAAS SLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQQTYSNMPTFTGPGTKV DIK	(SEQ ID NO: 9503)	(SEQ ID NO: 9861)	EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVC RIKGNTYGGTIDYAAPVKGRFTISRDKNTLFLQMNSLKLTEDTAVYYCT IPSNCSYNYFVSVMQGVTVVSS
			NA	GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTCCCGGACAAGTCAGAGCAATTAACAGCTATT TAAATTGGTTTCAACAGAAACAGGAAAGCCCTTAAGCTCTCTGATCT TTGCTGCATCCAGTTTACAAAGTGGGTCCTCAAGGTTCAAGTGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACGTG AAGAATTTGCAACT	(SEQ ID NO: 9504)	(SEQ ID NO: 9862)	GAGGTGCAGCTGCTCGAGTCCGGGAGGCTTGGTAAAGCCTGGGG GTCCCTTAGACTCTCTCTGTCAGCTCTGAGTTCAGTTCACTTCACTAACCGC TGATGAGCTGGTCCGACAGCTCCAGGTCCTCAAGGAAAGGGCTGGAGTGGT TGCCGTATTAAAGGCAACACTTATGGTGGGACAAACAGACTACGCTGC ACCGGTAAAGGAGATTCACCATCTCAAGAGATGATTCAAAAACAC GCTGTTCTGCAAAATG
			AA	ELVMTQSPSSLSASVGDRTVITICRTSQSISSVNLNWYQQKPGKAPKLLIFAAAS SLQSGVPSRFSGSGSGTDFTLTISSLQREDFATYYCQQSYSTPTFTGPGTKV DIK	(SEQ ID NO: 9505)	(SEQ ID NO: 9863)	EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVC RIKGNTYGGTIDYAAPVKGRFTISRDKNTLFLQMNSLKLTEDTAVYYCT IPSYSGSYNYFVSVMQGVTVVSS
			NA	GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTCCCGGACAAGTCAGAGCAATTAAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGAGAGCCCTTAAGCTCTCTGATCT TTGCTGCATCCAGTTTGCAGAGTGGGTCCTCAATCAAGTTCAGTGGA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACTG AAGAATTTGCAACT	(SEQ ID NO: 9506)	(SEQ ID NO: 9864)	GAGGTGCAGCTGCTCGAGTCCGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTCTGTCAGCTCTGAGTTCAGTTCACTTCACTAACCGC TGATGAGCTGGTCCGACAGCTCCAGGTCCTCAAGGAAAGGGCTGGAGTGGT TGCCGTATTAAAGGCAACACTTATGGTGGGACAAACAGACTACGCTGC ACCGGTAAAGGAGATTCACCATCTCAAGAGATGATTCAAAAACAC GCTGTTCTGCAAAATG
			AA	ELVMTQSPSSLSASVGDRTVITICRTSQSISSVNLNWYQQKPGRAPKLLIFAAAS SLQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQQTYSNMPTFTGPGTKL EIK	(SEQ ID NO: 9507)	(SEQ ID NO: 9865)	EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVC RIKGNTYGGTIDYAAPVKGRFTISRDKNTLFLQMNSLKLTEDTAVYYCT IPSNCSYNYFVSVMQGVTVVSS
			NA	GAGCTCGTGCTGACTCAGTCTCCATCCTCCCTGCGGTCACCCCTGGAG AGCCGCGCTCCATCTCTGAGGTCTAGTCAGAGCCTCTGCTGATCGTA ATGGATACAACTATTGGATTGGTACCTGCAGAGCAGCCAGGGCAGTCTC CACAGCTCTGATCTATTGGTTCTTAATCGGCGCTCCGGGTCCTCTGA CAGGTTCAITGGCAGTGGCTCAGGCACAGATTTTACACTGGAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9508)	(SEQ ID NO: 9866)	GAGGTGCAGCTGCTCGAGTCCGGGCCCAGGACTGGTGAAGCCTTCGGA GACCTGACCTCACCTCACCTGACTGCTCTGGTGGCTCCATCAGTAGTTAC TACTGGAGTGGATCCGCGAGCCGCGGGAAGGGAAGGACTGGAGTGGAT TGCCATATCTATACCACTGGGAGCACCACCTACACCCCTCCCTCAA GAGTCGATCACCATGTCAGTGGACTCGTCCAAAGAACAGTTCCTCCT GAAGCTGACCTCTCTG
			AA	ELVLTQSPSLSPVTPGEPASISCRSSQLLHRNGVNLVDWYLQKPGSQQLI IYLGSRASGVPDFRFGSGTDFTLTISRVEAEDVGVYYCMQALQTPSFG QGTKLEIK	(SEQ ID NO: 9509)	(SEQ ID NO: 9867)	EVQLLESGGLVKPSETLTCTVSGGSISSYYWVSWIRQAPKAGLEWIGHI YTSGTNYPNLSKSRVTMSVDSKNQSLKLTSLTAADTAVYYCAREKM WFGVLYYYGMDVWVGQGVTVVSS
					(SEQ ID NO: 9510)	(SEQ ID NO: 9868)	

iPS:613701	18179-F4	NA	GAGCTCGTGTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATCGTA ATGGATACCACTATTGGATTGGTACCTGCAAGAACCCAGGCGAGTCT CACAACTCCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9511) ELVLTQSPSLPVTPGEPASISCRSSQSLHNRNGYHYLDWYLQKPGQSPQLI IYLGSNRASGVDPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPFTF FGPTKVEIK	(SEQ ID NO: 9869) EVQLLESGPGLVKPSQTLSTLTCTVSGDSISSNPYYWSWIRQLPGKGLEWIG YISYSGSTFPNPSLKSRVTISVDTSKNQFSLNLTSLTAADTA VYYCARDRL WFGVLNYYYGMDVWVGLGTTVTIVSS
		AA		(SEQ ID NO: 9512) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGA GAGCGGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGT AATGGATACAACTATTGGATTGGTACCTGCAGAGCCAGGCGAGTCT CCACAGCTCCTGATCTATTGGGTCTAATCGGGCTCCGGGGTCCCTG ACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9870) GAGGTGCAGCTGCTCGAGTCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCAGTCTCTCTGGTGGGCCCATCAGCAGTGGTG ATTACTACTGGAGTGGATCCGCCAGCACCCAGGGAAGGCGCTGGAGT GGATTGGGTACATCATGAAGAGTGGGAGCACCTACTACAACCCGCTCC TCAAGAGTCCGAGTACCATATCATAGTAGACACGCTTAAGGACCAAGTTCT CCCTGAAGCTGAGC
iPS:613715	18179-F6	NA		(SEQ ID NO: 9513) ELVMTQSPSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQL LIYLGSRASGVDPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPRT FGQGTKVEIK	(SEQ ID NO: 9871) EVQLLESGPGLVKPSQTLSTLTCTVSGAISSGDYYWSWIRQHPKGLWIG YIDKSGSTYYNPSLKSRTATISVDTSKQFSLKLSVTAADTA VYYCARDQL WFGVLNYYYGMDVWVWQGTTVTIVSS
		AA		(SEQ ID NO: 9514) GAGCTCGTGTGATGACCCAGACTCCACTCTCCCTGCCCGTCACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGT AATGGATACAACTATTGGATTGGTACCTGCAGAAAGCCAGGCGAGTCT CCACAGCTCTGATCTATTGGGTCTAATCGGGCTCTCGGGGTCCCTG ACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTAAAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 9872) GAGGTGCAGCTGCTCGAGTCGGGCCAGGACTGGTGAAGCCTACGGA GACCTGTCCCTCACCTGCAGTCTCTCTGGTGGCTCCATCAGTGAATTTC TTCTGGAGCTGGATCCGCCAGGCCCCAGGAAAGGAGCTGGAGTGGATT GGATATCTATTACAGAGGAGGACCAACTACCAACCCCTCCCTCAAG AGTCGAGTCCACCATGTCAGTGGACACGCTCCAGAACCAAGTCTTCCTCCGTC AAGCTGACCTCTCTG
iPS:613731	18179-F10	NA		(SEQ ID NO: 9515) ELVMTQTPSLPVTPGEPASISCRSSQSLHNSNGYNYLDWYLQKPGQSPQL LIYLGSRASGVDPDRFSGSGGTDFTLKISRVEAEDVGVYYCMQALQTPRT FGQGTKVEIK	(SEQ ID NO: 9873) EVQLLESGPGLVKPTEITLSLTCTVSGGSISDFWWSWIRQPPKGLWIGYIY YRGSTNYHPSLKSRTVMTSDTSKNQFSLKLTSLTAADTA VYYCAREKMW FGLVNNYYYGMDVWVWQGTTVTIVSS
		AA		(SEQ ID NO: 9516) GAGCTCGTGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGA GAGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGA AATGGATACAACTATTGGATTGGTACTTGCATAAACCCAGGCGAGTCTG CACAGCTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCTGA CAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9874) GAGGTGCAGCTGCTCGAGTCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCAGTCTCTCTGGTGGGCCCATCAGCAGTGGTG ATTACTACTGGAGTGGATCCGCCAGCACCCAGGGAAGGCGCTGGAGT GGATTGGGTACATCATGAAGAGTGGGAGCACCTACTACAACCCGCTCC TCAAGAGTCCGAGTACCATATCATAGTAGACACGCTTAAGGACCAAGTTCT CCCTGAAGCTGAGC
iPS:613681	18179-C8	NA			

IPS:615270	18181-A11	NA	GAGCTCGTGAATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGAA ATGGATACAACTATTGGATTGGTACCTGCAGAAAGCCAGGGCAGTCTC CACAGCTCTCGATCTATTGGGTCTAATCGGGCTCCGGGGTCCCTGTA CAGGTTCAAGTCGGCAGTGGATCAGGCACAGATTTTCACGCTGAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9525) ELVMTQSPSLSPVTPGEPASISCRSSQSLHRRNGYNVLDWYLQKPGQSPQL LIYLGNSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQALQIPFTF GPGTKVEIK	(SEQ ID NO: 9526) GAGCTCGTGAATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCATAGTA CTGGATACAACTATTGGATTGGTACCTGCAGAAAGCCAGGGCAGTCTC CACAGCTCTCGATCTATTGGGTCTAATCGGGCTCCGGGGTCCCTGA CAGGTTCAAGTCGGCAGTGGATCAGGCACAGATTTTACACTAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9883) EVQLLESGPGLVKPSQTLSTLTCTVSGDSISSNPYYWSWIRQHPGKGLEWIG YISYSGSYTYPNPSLKSRTVISVDTSKNQFSLNLTSTVTAADTAVVYCARDRL WFGVLYNYGMDVWVGPGTITVTVSS	GAGGTGCAGCTGCTCGAGTGGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACTGCAGTCTCTCTGGTGACTCCATCAGCAGTAATC CTTACTACTGGAGCTGGATCCGACAGCAGCAGGAGGGCGCTGGAGT GGATTGGGTACATCTTACAGTGGGAGCACCTACTACAAACCCGCTCCC TCAAGAGTCGAGTTACCATATCAGTAGACACGCTCTAAGAACCCAGTTCT CCCTGAATCTGACC	
		AA						
IPS:615224	18181-C6	NA						
		AA	ELVMTQSPSLSPVTPGEPASISCRSSQSLHSTGYNYLDWYLQKPGQSPQL LIYLGNSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGFYCMQQLQIPRTI FQQGTKLEIK	(SEQ ID NO: 9527) ELVMTQSPSLSPVTPGEPASISCRSSQSLHSTGYNYLDWYLQKPGQSPQL LIYLGNSNRASGVDPDRFSGSGSGTDFTLKISRVEAEDVGFYCMQQLQIPRTI FQQGTKLEIK	(SEQ ID NO: 9885) EVQLLESGPGLVKPSQTLSTLTCTVSGDSISSNPYYWSWIRQHPGKGLEWIG YISYSGSYTYPNPSLKSRTVISVDTSKNQFSLNLTSTVTAADTAVVYCARDRL WFGVLYNYGMDVWVGPGTITVTVSS			
IPS:615238	18181-G7	NA	GAGCTCGTGAATGACCCAGTCTCCATCTCCCTGCTGCTGCACTCTGAGGAG ACAGAGTCACCAATCACTTGCCTGGACAAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGAGAAACAGGGAGAGCCCTAAGCTCCTGATCT TTGCTGCATCCAGTTTCAAGGTGGGTCCCATCAAGGTTCAGTGGCA GTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAAACCTG AAGATTTTGCACAT	(SEQ ID NO: 9528) GAGCTCGTGAATGACCCAGTCTCCATCTCCCTGCTGCTGCACTCTGAGGAG ACAGAGTCACCAATCACTTGCCTGGACAAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGAGAAACAGGGAGAGCCCTAAGCTCCTGATCT TTGCTGCATCCAGTTTCAAGGTGGGTCCCATCAAGGTTCAGTGGCA GTGGAATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAAACCTG AAGATTTTGCACAT	(SEQ ID NO: 9886) GAGGTGCAGCTGCTCGAGTCTGGGGAGGGCTTGGTAAAGCCTGGGGG GTCCCTTAGACTCTCTGTGCGACCTCTGGATTCATCTTTCAGTAACCGC TGGATGAGCTGGGTCCGCGAGGCTCCAGGAGGGGCTGGAGTGGGT TGCCCGTATTAAAGGCAACACTTATGGTGGGACCAACAGACTACGCTCG ACCCGTGAAAGGAGCAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTCTCTGCAAAATG	(SEQ ID NO: 9887) EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVVC RIKGNITYGGITDYAAPVKGRFTISRDTSKNTLFLQMNLSKLTEDTAVYYCT TPSNNGSYNYFVMDVWVGQGTITVTVSS		
		AA	ELVMTQSPSSLASVGDVVTTCRTSQSISSYLNWYQQKPKRAPKLLIFAAAS SLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYISMPFTFGPGTKV EIK	(SEQ ID NO: 9529) ELVMTQSPSSLASVGDVVTTCRTSQSISSYLNWYQQKPKRAPKLLIFAAAS SLQGGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQYISMPFTFGPGTKV EIK	(SEQ ID NO: 9888) GAGGTGCAGCTGCTCGAGTGGGGCCAGGACTGGTGAAGCCTTCGGA GACCTGTCCCTCACTGCAGTCTCTCTGGTGCTCCATCAGTAATTAAC TACTGGAGCTGGTCCGCGAGCCCGCCGGAAGGAGCTGAGTGGAT TGGTCAATCTATCATTACCATGAGGACCAACTTCAACCCCTCCCTCAA GAGTTCGAGTCCACATGTCAGTGGACACGCTCCAGAACCCAGATTCTCCCT GAAGCTGACCTCTCTG			
IPS:615268	18181-H10	NA						

iPS:613619	18182-A7	NA	GAGCTGCTGCTGACTCAGCTACCCCTCGGTGTCAGTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGGCACCAAGCAAGCCAGCCAGGCCCTGTGATGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	(SEQ ID NO: 9539) ELVLTLQPSVSVAPGQTARITCGGNNIGSKSVHWHQKPGQAPVMVVYD DNDPSGIPERFSGNSGNTATLITSRVEAGDEADYHCQVWSSSDHVV GGTKLTVL	(SEQ ID NO: 9897) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDN SKNTLYLQMNLSLR AEDTAVYYCATG KGVHLGFDYWGGQTLVTSS
		AA		(SEQ ID NO: 9540) GAGCTGCTGCTGACTCAATCATCTCGGTGTCAGTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGGTACCAGCAAGCAAGCCAGGCCCTGTGCTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTTT	(SEQ ID NO: 9898) GAGGTGCAGCTGCTCCTGAGTCCGGGAGGCTTGGTACAGCTGGGG GTCCCTGAGACTCTCTGTGCAAGCTCTGGATTACCTTTAGCAGCCAT GCCATGAGCTGGTCCGCCAGGCTCCAGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGGACATATCAACGACGACTCCGT GAAGGCCGGTTTACCATCTCCAGAGACAATTCGAAGAACACAGCTGTA TCTGCAAAATGAACAGC
iPS:613573	18182-A8	NA		(SEQ ID NO: 9541) ELVLTLQSSSVSVAPGQTARITCGGNNIGSKSVHWHYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLITSRVEAGDEADFYCQVWSSSDHVVFG GTKLTVL	(SEQ ID NO: 9899) EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPKGLWEVWS AISGSGGTYYNADSVKGRFTISRDN SKNTLYLQMNLSLR AEDTAAYYCVTG KGVHLGFDYWGGQTLVTSS
		AA		(SEQ ID NO: 9542) GAGCTGCTGCTGACTCAGCCACCCCTCGGTGTCAGTGACCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATCTGTACCAGCAAGCAAGCCAGGCCCTGTGCTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9900) GAGGTGCAGCTGCTCCTGAGTCCGGGAGGCTTGGTACAGCTGGGG GTCCCTGAGACTCTCTGTGCAAGCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGGACATATCAACGACGACTCCGT GAAGGCCGGTTTACCATCTCCAGAGACAATTCGAAGAACACAGCTGTA TCTGCAAAATGAACAGC
iPS:613513	18182-A11	NA		(SEQ ID NO: 9543) ELVLTLQPPSVSVTPGQTARITCGGNNIGSKSVHWHYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLITSRVEAGDEADYCYQVWSSSDHVVFG GGTKLTVL	(SEQ ID NO: 9901) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDN SKNTLYLQMNLSLR AEDTAVYYCATG KGVHLGFDYWGGQTLVTSS
		AA		(SEQ ID NO: 9544) GAGCTGCTGCTGACTCAGCTACCCCTCGGTGTCAGTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGGTACCAGCAAGCAAGCCAGGCCCTGTGCTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9902) GAGGTGCAGCTGCTCCTGAGTCTGGGGAGGCTTGGTACAGCTGGGG GTCCCTGAGACTCTCTGTGCAAGCTCTGGATTACCTTTAGCAGCCAT GCCATGAGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGGACATATCAACGACGACTCCGT GAAGGCCGGTTTACCATCTCCAGAGACAATTCGAAGAACACAGCTGTA TCTGCAAAATGAACAGC
iPS:613639	18182-B1	NA			

		AA	ELVLTQLPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVLVVYDD NDRPSGIPERFSGSNFGNTATLISRVEAGDEADYYCQVWDDSSDHVVF GGTKLTVL (SEQ ID NO: 9545)	EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCATG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9903)
18182-B4	18182-B4	NA	GAGCTCATGCTGACTCAGCCACCTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAGTGT GCATGGTACAGCAGAGCAGCCAGGCCCTGTGTGATGGTCTGTCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT (SEQ ID NO: 9546)	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGTGGGTCCGACAGGCTCCAGGGAAGGGGCTAGAGTGGGT CTCAGCTATTAGTGTGATGGTGGTGGCACATCTACGACGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC (SEQ ID NO: 9904)
		AA	ELMLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVLMVVYD DNDRPSGIPERFSGSNFGNTATLISRVEAGDEADYYCQVWDDSSDHVVF GGTKLTVL (SEQ ID NO: 9547)	EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCATG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9905)
18182-B6	18182-B6	NA	GAGCTCATGCTGACTCAGCCCACTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAACAGAGCAGCCAGGCCCTGTGTGATGGTCTGTCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAATTTGGGAACACGGCCACCTGACCATCAGCAGGGTCGAAGCCG GGATGAGGCCGACTAT (SEQ ID NO: 9548)	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGAGCCTCTGGATTCACTTTAGTGTAT GCCATGAGTGGGTCCGACAGGCTCCAGGGAAGGGGCTGAGTGGGT CTCAGCTATTAGTGTGATGGTGGTGGCACATCTACGACGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC (SEQ ID NO: 9906)
		AA	ELMLTQPHSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVLVVYD DNDRPSGIPERFSGSNFGNTATLISRVEAGDEADYYCQVWDDSSDHVVF GGTKLTVL (SEQ ID NO: 9549)	EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCATG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9907)
18182-B7	18182-B7	NA	GAGCTCATGCTGACTCAGCCCACTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAGTGT GCAGTGGTACAGCAGAGCAGCCAGGCCCTGTGTGATGGTCTGTCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCTACCTGACCATCAGCAGGGTCGAAGCCG GGATGAGGCCGACTTT (SEQ ID NO: 9550)	GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGTGGGTCCGACAGGCTCCAGGGAAGGGGCTGAGTGGGT CTCAGCTATTAGTGTGATGGTGGTGGCACATCTACGACGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC (SEQ ID NO: 9908)
		AA	ELMLTQPHSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVLVVYD DNDRPSGIPERFSGSNFGNTATLISRVEAGDEADYYCQVWDDSSDHVVF GGTKLTVL (SEQ ID NO: 9551)	EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPQGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCATG KGVHLGFDHWGGTILVTYSS (SEQ ID NO: 9909)
18182-B7	18182-B7	NA	GAGCTCATGCTGACTCAGCCCACTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAGTGT GCAGTGGTACAGCAGAGCAGCCAGGCCCTGTGTGATGGTCTGTCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCTACCTGACCATCAGCAGGGTCGAAGCCG GGATGAGGCCGACTTT (SEQ ID NO: 9552)	EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPQGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNLSRAEDTAVYYCATG KGVHLGFDHWGGTILVTYSS (SEQ ID NO: 9910)

IPS:613543	18182-B10	NA	GAGCTCATGCTGACTAGCCCCACTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCCATGATACCAAGAACAGCCAGCCAGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCCGAAGCCG GGGATGAGGCCGCACTAT	(SEQ ID NO: 9553) ELMLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQAPVLMVYDD DNDRPSGIPERFSGNSGNTATLTSRVEAGDEADYYCQVWDDSSDHVVF GGGTKLTVL	(SEQ ID NO: 9553) EVQLLESGGDLVOPGGSLRLSCAASGFTFSYAMNWVRQAPGKGLEWVS AISGSGGTYYADSVKGRFTISRDNKNTLYLQMNSLRAREDYAVVYCATG KGVHLNFDYWGQGTLVTVSS	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAACCTGGGTCCGCGAGCTCCAGGGAAGGGCTGAGTGGGT CTCAGCTATTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGGCCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
IPS:613643	18182-C2	NA	GAGCTCGTGTGACGACGCCCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCAGTGTACCAAGAACAGCCAGCCAGCCCTGTGCTGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGGAACACGGCCACCCTGATTATCAGTAGGGTCCGAAGCCG GGATGAGGCCGCACTTT	(SEQ ID NO: 9554)	(SEQ ID NO: 9912)	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGCTCCAGGGAAGGGCTGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
IPS:613607	18182-C3	NA	GAGCTCGTGTGACGACGCCCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCATCGTACCAAGAACAGCCAGCCAGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCCGAAGCCG GGGATGAGGCCGCACTAT	(SEQ ID NO: 9556) ELVLTPPPSVSVAPGQTARITCGNNIGSKSVQWYQQKPGQAPVLMVYDD DNDRPSGIPERFSGNSGNTATLTSRVEAGDEADYYCQVWDDSSDHVVF GGGTKLTVL	(SEQ ID NO: 9914)	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCCAT GCCATGAGCTGGGTCCGCGAGCTCCAGGGAAGGGCTGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
IPS:613571	18182-C4	NA	GAGCTCATGCTGACTAGCCCCACTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCCATGATACCAAGAACAGCCAGCCAGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCCGAAGCCG GGGATGAGGCCGCACTAT	(SEQ ID NO: 9557) ELVLTPPPSVSVAPGQTARITCGNNIGSKSVHWYQQKPGQAPVLMVYDD DNDRPSGIPERFSGNSGNTATLTSRVEAGDEADYYCQVWDDSSDHVVF GGGTKLTVL	(SEQ ID NO: 9915)	GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGCTCCAGGGAAGGGCTGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC

iPS:613549	18182-D4	NA	GAGCTGCCCTGACTCAGCTGCTCCGCTCAGTGGCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCAGCCAGGCCCTGTGCTGGTCTGCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9567) ELALTPASASVAPGQTARITCGNNIGSKSVHWYQQKPGQAPLVVYD DNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYCQVWDSNDHVFVFG GGTKLTVL	(SEQ ID NO: 9568) GAGCTGCTGTGACACAGCTATCCTCGGTGTGAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCAGTGTACCAAGCAAGCAGCCAGTCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCGGCTC CAACTTGGGAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCGG GGGATGAGGCCGACTAT	GAGGTGCAGCTGCTCGAGTCCGGGGGAGACTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAGCTGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAACTATTAGTGGTAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9925) EVQLLESGGDLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWEVWS ITISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWQGTLVTYSS
		AA					(SEQ ID NO: 9926) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAGCTGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
iPS:613645	18182-D8	NA		(SEQ ID NO: 9569) ELVLTLSSVSAPGQTARITCGNNIGSKSVQWYQQKPGQSPVAVVYD DNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYCQVWDSNDHVFVFG GGTKLTVL	(SEQ ID NO: 9570) GAGCTGCTGCTGACTCAGGAGCCCTCGGTGTGAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCAGCCAGGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9927) EVQLLESGGGLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWQGTLVTYSS	(SEQ ID NO: 9928) GAGGTGCAGCTGCTCGAGTCCGGGGGAGACTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAGCTGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAACTATTAGTGGTAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGGGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA					(SEQ ID NO: 9929) EVQLLESGGDLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWEVWS ITISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWQGTLVTYSS
iPS:613537	18182-D9	NA		(SEQ ID NO: 9571) ELVVTQEPSVSAPGQTARITCGNNIGSKSVHWYQQKPGQAPVAVVYD DNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYCQVWDSNDHVFVFG GGTKLTVL	(SEQ ID NO: 9572) GAGCTCATGCTGACTCAGCCACCTCGGTGTGAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCAGCCAGGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9930) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAATGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9931) EVQLLESGGDLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWEVWS ITISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWQGTLVTYSS
		AA					(SEQ ID NO: 9932) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAATGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
iPS:613541	18182-D11	NA		(SEQ ID NO: 9573) ELVVTQEPSVSAPGQTARITCGNNIGSKSVHWYQQKPGQAPVAVVYD DNDRPSGIPERFSGSNFGNTATLIISRVEAGDEADYYCQVWDSNDHVFVFG GGTKLTVL	(SEQ ID NO: 9574) GAGCTCATGCTGACTCAGCCACCTCGGTGTGAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCAGCCAGGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAAGCCGG GGGATGAGGCCGACTAT	(SEQ ID NO: 9933) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAATGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9934) EVQLLESGGDLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWEVWS ITISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWQGTLVTYSS
		AA					(SEQ ID NO: 9935) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCCTCGGATTCACCTTTAGCAGCTAT GCCATGAATGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACAATACGACGACTCCGT GAAGGGCCGTTTCACTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC

IPS:613667	18182-E11	NA	GAGCTCATGCTGACTAGCCCACTCGGTGTCAGTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGTGACCAAGAACAGCCAGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	(SEQ ID NO: 9581) ELMLTQPHSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD DNDPSGIPERFSGNSGNTATLITSRVEAGDEADYYCQVWSSSDHVVFF GGTKLTVL	(SEQ ID NO: 9582) GAGCTCGTGTGACTCAGTCCCTCGGTGTCAGTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGTGACCAAGAACAGCCAGCCCTGTGCTGTCGTCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCTGATTATCAGTAGGGTCGAAGCCGG GGATGAGGCCGACTAT	GAGGTGCAGTCTCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTCTGTGACGCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC	(SEQ ID NO: 9939) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPQKGLEWVS AISGSGGTYYADSVKARFTISRDNKNTLYLQMNLSRAEDTAVVYCATG KGVHLGFDYWGQGLTVTVSS
	AA						(SEQ ID NO: 9940) GAGGTGCAGTCTCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTCTGTGACGCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCACATACTACGCAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC
IPS:613529	18182-F1	NA					(SEQ ID NO: 9941) EVQLLESGGDLVQPGGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCATG KGVHLNFDYWGQGLTVTVSS
	AA		ELVLTPSPSVVAPGQTARITCGNNIGSKSVHWYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLITSRVEAGDEADYYCQVWSSSDHVVFFGG GTKLTVL	(SEQ ID NO: 9583) ELVLTPSPSVVAPGQTARITCGNNIGSKSVHWYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLITSRVEAGDEADYYCQVWSSSDHVVFFGG GTKLTVL	(SEQ ID NO: 9584) GAGCTCGCCCTGACTCAGCTCCTCCTCGTGTCACTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGTGACCAAGAACAGCCAGCCAGCCCTGTCTGCTGCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	(SEQ ID NO: 9942) GAGGTGCAGTCTCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTCTGTGACGCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC	
IPS:613531	18182-F6	NA					(SEQ ID NO: 9943) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCATG KGVHLNFDYWGQGLTVTVSS
	AA		ELALTPPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLITSRVEAGDEADYYCQVWSSSDHVMFVG GGTKLTVL	(SEQ ID NO: 9585) ELALTPPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLITSRVEAGDEADYYCQVWSSSDHVMFVG GGTKLTVL	(SEQ ID NO: 9586) GAGCTCGTGTGACCGACCGCCCTCGGTGTCAGTGGCCCAAGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCATGTGACCAAGAACAGCCAGCCAGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	(SEQ ID NO: 9944) GAGGTGCAGTCTCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGACGCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC	
IPS:613623	18182-F8	NA					(SEQ ID NO: 9945) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVVYCATG KGVHLNFDYWGQGLTVTVSS

		AA	(SEQ ID NO: 9587) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD DNDPSPGIPERFSGNFGNTATLIISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9588) GAGCTCGTGTGACTCAGCCACCTCGGTGTGAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACCTGGCACAGCAAGCAGGACGCCCTGTGTGGTGTGCTTA TGATGATAACGACCGCCCTCAGGATCCCTGAGGATTTCTCTGGCTC CAACTTTGGGAACACGGCCACCTGATTATCAGTAGGTCGAAGCCCG GGATGAGGCCGACTAT	(SEQ ID NO: 9589) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVLYYDD DNDPSPGIPERFSGNFGNTATLIISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9590) GAGCTCGTGTGACTCAGCCACCTCGGTGTGAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACCTGGTACAGCAAGCAGGACGCCCTGTGTGGTGTGCTTA TGATGATAACGACCGCCCTCAGGATCCCTGAGGATTTCTCTGGCTC CAACTTTGGGAACACGGCCACCTGATTATCAGTAGGTCGAAGCCCG GGATGAGGCCGACTAT	(SEQ ID NO: 9591) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVLYYDD DNDPSPGIPERFSGNFGNTATLIISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9592) GAGCTCGTGTGACTCAGCCACCTCGGTGTGAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACCTGGTACAGCAAGCAGGACGCCCTGTGTGGTGTGCTTA TGATGATAACGACCGCCCTCAGGATCCCTGAGGATTTCTCTGGCTC CAACTTTGGGAACACGGCCACCTGATTATCAGTAGGTCGAAGCCCG GGATGAGGCCGACTAT	(SEQ ID NO: 9593) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD DNDPSPGIPERFSGNFGNTATLIISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9594) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD DNDPSPGIPERFSGNFGNTATLIISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9595) GAGCTCGTGTGACTCAGCCACCTCGGTGTGAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACCTGGTACAGCAAGCAGGACGCCCTGTGTGGTGTGCTTA TGATGATAACGACCGCCCTCAGGATCCCTGAGGATTTCTCTGGCTC CAACTTTGGGAACACGGCCACCTGATTATCAGTAGGTCGAAGCCCG GGATGAGGCCGACTAT	(SEQ ID NO: 9945) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS TISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9946) GAGGTGCACTGCTCGAGTCTGGGGGAGACTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGCACTGGTCCGCAAGCTCCGGGGAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGTGGCACATACGACGACTCCGT GAAGGCGCGTTCCACCTCTCCAGAGACAAATTCACAGAACACCTGTA TCTGCAAAATGAACAGC (SEQ ID NO: 9947) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9948) GAGGTGCACTGCTCGAGTCCGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGACTGGTCCGCAAGCTCCAGGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGTGGCACATTACTACGACGACTCCGT GAAGGCGCGTTCCACCTCTCCAGAGACAAATTCACAGAACACCTGTA TCTGCAAAATGAGCAGC (SEQ ID NO: 9949) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMTWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9950) GAGGTGCACTGCTCGAGTCCGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGTGGTCCGCAAGCTCCAGGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGTGGCACATACACGACGACTCCGT GAAGGCGCGTTCCACCTCTCCAGAGACAAATTCACAGAACACCTGTA TCTGCAAAATGAACAGC (SEQ ID NO: 9951) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAAYYCVTG KGVHLGFDYWGGTILVTYSS (SEQ ID NO: 9952) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLEWVS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAAYYCVTG KGVHLGFDYWGGTILVTYSS
IPS:613641	18182-G3	NA					
IPS:613527	18182-G4	NA					
IPS:613651	18182-G5	NA					

iPS:613625	18182-G9	NA	GAGCTGCCCTGACTAGCTTGCTCCGCTCAGTGGCCAGGACAG ACGCCAGGATTTCTGTGGGGAACAACATTGGAAGTAAAGGTGTG CAGTGTACCAAGCAAGCCAGCCAGCCCTGTACTGTGCTGTCTAT GATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTCC AACTTTGGAAACACGGCCACCCTGATTATCAGTAGGCTCGAAGCCGG GATGAGGCCGACTAT	(SEQ ID NO: 9595) ELALTPASASVAPGQTARISCGNNIGSKGVQWYQKPGQAPVLVYVD DNDPSGIPERFSGNSGNTATLISRVEAGDEADYYCQVWSSSDHVVF GGTKLTVL	(SEQ ID NO: 9593) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWQGQTLVTYSS	GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGTGGTCCGCAAGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGCACATACTACGCAGACTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAITTCAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA				
iPS:613589	18182-G11	NA	GAGCTGTGCTGACGACGGCCCTGGTGTCACTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCAGTGTACCAAGCAAGCCAGCCAGCCCTGTGTGCTGTCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGAAACACGGCCACCCTGATTATCAGTAGGCTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9596) GAGCTGTGCTGACGACGGCCCTGGTGTCACTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCAGTGTACCAAGCAAGCCAGCCAGCCCTGTGTGCTGTCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGAAACACGGCCACCCTGATTATCAGTAGGCTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9554) GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGTGGTCCGCAAGCTCCAGGAAGGGGCTAGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGCACATACTACGCAGACTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAITTCAGAACACGCTGTA TCTGCAAAATGAACAGC	
		AA		(SEQ ID NO: 9597) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVQWYQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLISRVEAGDEADYYCQVWSSSDHVVF GGTKLTVL	(SEQ ID NO: 9555) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWQGQTLVTYSS	
iPS:613587	18182-H5	NA	GAGCTCGTGGTGACTCAGGAGCCCTCGGTGTCACTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGCACCAAGCAAGCCAGCCAGCCCTGTGTGCTGTCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGAAACACGGCCACCCTGACCATCAGCAGGGTCTGAAGCCG GGGATGAGGCCGACTTT	(SEQ ID NO: 9598) GAGCTCGTGGTGACTCAGGAGCCCTCGGTGTCACTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGCACCAAGCAAGCCAGCCAGCCCTGTGTGCTGTCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGAAACACGGCCACCCTGACCATCAGCAGGGTCTGAAGCCG GGGATGAGGCCGACTTT	(SEQ ID NO: 9556) GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCCAT GCCATGAGTGGTCCGCAAGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGCACATACTACGCAGACTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAITTCAGAACACGCTGTA TCTGCAAAATGAACAGC	
		AA		(SEQ ID NO: 9599) ELVVTQPPSVSVAPGQTARITCGNNIGSKSVHWHQKPGQAPVLVYVD DNDPSGIPERFSGNSGNTATLISRVEAGDEADYYCQVWSSSDHVVF GGTKLTVL	(SEQ ID NO: 9557) EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAAYYCVTIG KGVHLGFDYWQGQTLVTYSS	
iPS:603153	18089-D12	NA	GAGCTGTGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGAG ACAGATCACCATCACTTCCGGGAGTCAAGGCAITTAAGCAATATT TAGCTGTGTATCAGCAGAAACAGGAAAGTTCCTAAGCTCTGATCT ATGCTGCATCCACTTTCGAATCAAGGGTCCCATCTCGGTTTCAGTGGA GTGGATCTGGACAGATTTCATCTCACCATCAGCAGGCTCGAGCCTG AAGATGTTGCAACT	(SEQ ID NO: 9600) GAGCTGTGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGAG ACAGATCACCATCACTTCCGGGAGTCAAGGCAITTAAGCAATATT TAGCTGTGTATCAGCAGAAACAGGAAAGTTCCTAAGCTCTGATCT ATGCTGCATCCACTTTCGAATCAAGGGTCCCATCTCGGTTTCAGTGGA GTGGATCTGGACAGATTTCATCTCACCATCAGCAGGCTCGAGCCTG AAGATGTTGCAACT	(SEQ ID NO: 9558) GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTTCAGCCTGGGAG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGTGGTCCGCAAGCTCCAGGAAGGGGCTGGAATGGGT GGCAGTTATATGATGAAGTAAATAAATATCTGAGACTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAITTCAGAACACGCTGTA TCTGCAAAATGAACAGC	
				(SEQ ID NO: 9601) GAGCTGTGATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGAG ACAGATCACCATCACTTCCGGGAGTCAAGGCAITTAAGCAATATT TAGCTGTGTATCAGCAGAAACAGGAAAGTTCCTAAGCTCTGATCT ATGCTGCATCCACTTTCGAATCAAGGGTCCCATCTCGGTTTCAGTGGA GTGGATCTGGACAGATTTCATCTCACCATCAGCAGGCTCGAGCCTG AAGATGTTGCAACT		

IPS-613717	18179-G12	AA	ELVMTQSPSSLSASVGRDVTITCRASQGISNYLAWYQKPKGVKPKLLISAA STLOSQVPSRFSGSGTDFLTITSLQPEDVATYYCQKYNAPFTFGPGTK VEIK (SEQ ID NO: 9602)	EVQLLESQGGVVPGRSLRSLSCASGFTFTYGMHWVRQAPGKGLEWVA VISYDSNKKYYADSVKGRFTISRDDSKNTLYLQMNLSRAEDTAVYYCAR GQLLTGYWQGQGLVTVSS (SEQ ID NO: 9960)
		NA	GAGCTCGTGATGACCCAGTCTCCATCTCCCTGTCGTGCACTCTGTAGGAG ACAGATCACCATCACTTGGCGGGAGTCAGGCAATTAGCAATATTT TAGCTGTGATACAGCAAAACAGGAAAGTTCTTAAGCTCTCTGATCT CTGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTGATGCGCAG TGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTGCGACCTGA AGATGTTGCAACT (SEQ ID NO: 9603)	GAGGTGCACTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCTGGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGTTACACTTTACCAGGAAT GGTCTCAGCTGGTGGCAGAGGCCCTGGACAAAGGGCTTGGTGGATG GGATGGATCAGCGGTTACAAATGGTGACAAAACTATGCACAGAGCTC CAGGGCAGAGCACCATGATCCACAGACATCCACGAGCACAGCCTA CATGGAGCTGAGGAGC (SEQ ID NO: 9961)
IPS-613759	18179-C1	AA	ELVMTQSPSSLSASVGRDVTITCRASQGISNYLAWYQKPKGVKPKLLISAA STLOSQVPSRFSGSGTDFLTITSLQPEDVATYYCQKYNAPFTFGPGTK LEIK (SEQ ID NO: 9604)	EVQLLESQGGVVPGRSLRSLSCASGFTFTYGMHWVRQAPGKGLEWVA VISYDSNKKYYADSVKGRFTISRDDSKNTLYLQMNLSRAEDTAVYYCAR RGRATFDYWQGQGLVTVSS (SEQ ID NO: 9962)
		NA	GAGCTCGTGATGACCCAGTCTCCATCTCCCTGTCGTGCACTCTGTAGGAG ACAGATCACCATCACTTGGCGGGAGTCAGGCAATTAGCAATATTT TAGCTGTGATACAGCAAAACAGGAAAGTTCTTAAGCTCTCTGATCT CTGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTGATGCGCAG TGGATCTGGACAGATTTCACTCTCACCATCAGCAGCTGCGACCTGA AGATGTTGCAACT (SEQ ID NO: 9605)	GAGGTGCACTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCTGGGGC CTCAGTGAAGGTCTCTGCAAGCTTCTGGTTACACTTTACCAGGAAT GGTCTCAGCTGGTGGCAGAGGCCCTGGACAAAGGGCTTGGTGGATG GGATGGATCAGCGGTTACAAATGGTGACAAAACTATGCACAGAGCTC CAGGGCAGAGCACCATGATCCACAGACATCCACGAGCACAGCCTA CATGGAGCTGAGGAGC (SEQ ID NO: 9963)
IPS-604976	18093-B11	AA	ELVMTQSPSSLSASVGRDVTITCRASQGISNYLAWYQKPKGVKPKLLISAA STLOSQVPSRFSGSGTDFLTITSLQPEDVATYYCQKYNAPFTFGPGTK VDIK (SEQ ID NO: 9606)	EVQLLESQGGVVPGRSLRSLSCASGFTFTYGMHWVRQAPGKGLEWVA VISYDSNKKYYADSVKGRFTISRDDSKNTLYLQMNLSRAEDTAVYYCAR RGRATFDYWQGQGLVTVSS (SEQ ID NO: 9964)
		NA	GAGCTCGTGCTGACTCAGCCGCCCTCGGTGTCAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAAACATGGAAGTAAAGTGT GCACTGGTACAGCAAGCAGCAGGCCCTGTGCTGTGCTGCTA TGATGATAGGACCGGCCCTCAGGATCCCTGAGGATTTCTTGGCTC CAACTCTGGAAACAGGCCACCCCTGACCATCAGCAGGGTCTGAAAGCCG GGGATGAGGCCGACTAT (SEQ ID NO: 9607)	GAGGTGCACTGCTCGAGTCTGGAGCAGAGGTGAAAAAGCTGGGGG GTCCCTGAGACTCTCTGTGAGCCCTCTGGATTCACCTTCAGTACTAC TACATGAGCTGGATCCGCAAGCTCCAGGGAAGGGCTGGAGTGGGTT TCATACATTAGTAAAGTGGTAGTACCATATCTACGAGACTCTGTG AAGGCCGATTCACCATCTCCAGGGGACAAACGCAAGAACTCACTGTAT CTGCAAAATGAACAGC (SEQ ID NO: 9965)
		AA	ELVLTQPPSVAPGQTARITCGNNIGSKSVHWYQKPGQAPLVVYDD SDRPSGIPERFSGSNSNTATLTISRVEAGDEADYYCQVWSSDHHVVFQ GGTKLTVL (SEQ ID NO: 9608)	EVQLLESQGGVLPKPGSLRSLSCASGFTFTYGMHWVRQAPGKGLEWVA ISKSGSTIYYADSVKGRFTISRDNKNSLYLQMNLSRAEDTAVYYCATYN YGHFDYWQGQGLVTVSS (SEQ ID NO: 9966)

IPS:613599	18182-B5	NA	GAGCTGCTGCTGACTCAGCACCCCTCGGTGTCAGTGGCCCCAGGACAG ACGCCAGGATAACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCAGCCAGGCCCTGTGCTGTCGTCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAAGCCGG GGATGAGGCCGACTAT	(SEQ ID NO: 9609) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVL VVYDD NDRPSGIPERFSGNSGNTATLTIISRVEAGDEADY YCQVWDSDDHVVFGG GTKLTVL	(SEQ ID NO: 967) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTA VVYCATG KGVHLFDYWQGQTLVTYSS	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCCTCTGGATTACCTTTAGCAGCCAT GCCATGAGCTGGTCCGCAAGCTCCAGGAAGGGGCTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCGT GAAGGGCCGTTTCAACCTCTCCAGAGACAAATTCGAAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA		(SEQ ID NO: 9610) GAGCTGCTGCTGACTCAGCACCCCTCGGTGTCAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCATGGCACCAAGCAAGCAGGCCAGGCCCTGTGTTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGACCATCAGCAGGGTCGAGGCCG GGGATGAGGCCGACTTT	(SEQ ID NO: 9669) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKARFTISRDNSKNTLYLQMNSLR AEDTA VVYCATG KGVHLFDYWQGQTLVTYSS	
IPS:613567	18182-H9	NA		(SEQ ID NO: 9611) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVL VVYDD NDRPSGIPERFSGNSGNTATLTIISRVEAGDEADY YCQVWDSDDHVVFGG GTKLTVL	(SEQ ID NO: 970) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKARFTISRDNSKNTLYLQMNSLR AEDTA VVYCATG KGVHLFDYWQGQTLVTYSS	
		AA		(SEQ ID NO: 9612) GAGCTGCTGCTGACTCAACCTCTCGGTGTCAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCAGGCCAGGCCCTGTGTTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGGAACACGGCCACCCCTGATTATCAGTAGGGTCGAGCCCG GGATGAGGCCGACTAT	(SEQ ID NO: 9971) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTA VVYCATG KGVHLFDYWQGQTLVTYSS	
IPS:613583	18182-E6	NA		(SEQ ID NO: 9613) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVL VVYDD NDRPSGIPERFSGNSGNTATLTIISRVEAGDEADY YCQVWDSDDHVVFGG GTKLTVL	(SEQ ID NO: 972) EVQLLESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPKGLWEVWS AISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTA VVYCATG KGVHLFDYWQGQTLVTYSS	
		AA		(SEQ ID NO: 9614) GAGCTGCTGCTGACTCAGCACCCCTCGGTGTCAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAAATAACATTGGAAGTAAAGTGT CACTGGCACCAAGCAAGCAGGCCAGTCCCTGTGTTGGTCACTAT GATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTTC AACTTGGGAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCCG GGATGAGGCCGACTAT		
IPS:613565	18182-G6	NA				
		AA				

		AA	(SEQ ID NO: 9615) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWHQKPGQSPVLVIYDD NDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSSDHVVF GGTKLTVL (SEQ ID NO: 9616) GAGCTGCTGCTGACTCAGCCACCTCGGTGTGTCAGTGGCCCCAGGACAG ACGCCAGGATAACCTGTGGGGAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAACAGAACAGGCCAGGCCCTGTGATGGTCGTCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCCGACTAT	(SEQ ID NO: 9973) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVS AISGSGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAA YYCVTG KGVHLGFDYWGQGTILVTSS (SEQ ID NO: 9974) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGCA GCCTCTGGATTCACTTTAGCAGCCAT GCCATGAGCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACAA CGCAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC	
PS:613647	18182-G2	NA		(SEQ ID NO: 9617) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWHYQKPGQAPVMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSSDHVVF GGTKLTVL (SEQ ID NO: 9618) GAGCTCATGCTGACTCAGCCCACTCGGTGTGTCAGTGGCCCCAGGACAG ACGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAAGAAAGCCAGGCCAGGCCCTGTGCTGGTCGTCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGGAACACGGCCACCTGATTATCAGTAGGGTCTGAAGCCGG GGATGAGGCCCGACTAT	(SEQ ID NO: 9975) EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGTYYNADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAA YYCVTG KGVHLGFDYWGQGTILVTSS (SEQ ID NO: 9976) GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCCTGTGCA GCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAACTATTAGTGGAA GTGGTGGCACATACTACGCAGACTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC
PS:613517	18182-H12	NA			(SEQ ID NO: 9977) EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVS TISGSGGTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGQGTILVTSS (SEQ ID NO: 9978) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTAAAGCTGGGG GTCCCTGAGACTCTCCTGTGCA GCCTCTGGATTCACTTTAGCAGCTAT GCCATGAACCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGG GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 9619) ELMLTQPHSVSVAPGQTARITCGGNNIGSKSVHWHYQKPGQAPVLVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9620) GAGCTGCTGCTGACTCAGCCACCTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATAACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAACAGAACAGGCCAGGCCCTGTGATGGTCGTCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCTGAAGCCG GGGATGAGGCCCGACTAT	(SEQ ID NO: 9979) EVQLLESGGGLVKPGGSLRLSCAASGFTFSYAMNVRQAPGKGLEWVS AISGSGGTYYADSGKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWGQGTILVTSS (SEQ ID NO: 9980) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTAAAGCTGGGG GTCCCTGAGACTCTCCTGTGCA GCCTCTGGATTCACTTTAGCAGCTAT GCCATGAACCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGG GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC	
PS:613523	18182-G8	NA		(SEQ ID NO: 9621) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWHYQKPGQAPVMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9622) GAGCTGCTGCTGACTCAGCCACCTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATAACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAACAGAACAGGCCAGGCCCTGTGATGGTCGTCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCTGAAGCCG GGGATGAGGCCCGACTAT	(SEQ ID NO: 9979) EVQLLESGGGLVKPGGSLRLSCAASGFTFSYAMNVRQAPGKGLEWVS AISGSGGTYYADSGKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWGQGTILVTSS (SEQ ID NO: 9980) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTAAAGCTGGGG GTCCCTGAGACTCTCCTGTGCA GCCTCTGGATTCACTTTAGCAGCTAT GCCATGAACCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGG GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA		(SEQ ID NO: 9621) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWHYQKPGQAPVMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSDHVVF GGTKLTVL (SEQ ID NO: 9622) GAGCTGCTGCTGACTCAGCCACCTCGGTGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATAACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAACAGAACAGGCCAGGCCCTGTGATGGTCGTCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCTGAAGCCG GGGATGAGGCCCGACTAT	(SEQ ID NO: 9979) EVQLLESGGGLVKPGGSLRLSCAASGFTFSYAMNVRQAPGKGLEWVS AISGSGGTYYADSGKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATG KGVHLNFDYWGQGTILVTSS (SEQ ID NO: 9980) GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTAAAGCTGGGG GTCCCTGAGACTCTCCTGTGCA GCCTCTGGATTCACTTTAGCAGCTAT GCCATGAACCTGGGTCCGCCAGGCTCCAGGAAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACTACGCAGACTCCGG GAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA TCTGCAAAATGAACAGC

IPS:613521	18182-E10	NA	GAGTCGCCCTGACTCAGCTGCTCCGCTCAGTGGCCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGCACCAAGCAAGCCAGCCAGCCCTGTGTTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGAAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTTT	GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCCAT GCCATGAGCTGGTCCGCAAGCTTCCAGGCAAGGCTTGGAGTGGGT CTCGTCTATTAGTGTAGCGGTGGTGGCACATACGACGCTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 9623) ELALTPASASVAPGQTARITCGNNIGSKSVHWHQKPGQAPVLVYDD DNDPSGIPERFSGNSGNTATLTISRVEAGDEADYCYQVWDSSDHVVF GGTKLTVL	(SEQ ID NO: 9981) EVQLLESGGGLVQPGSLRLSCAASGFTTSSHAMSWVRQAPQGLEWVS ISGSGGTYYAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGK GVHLNFDYWGQGITLVSS
IPS:613627	18182-B12	NA	GAGCTGCTGTGACGCAGCGCCCTCGGTGTCACTGGCCCGCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGCACCAAGCAAGCCAGCCAGCCCTGTGTTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGAAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTGGTCCGCAAGCTTCCAGGCAAGGCTTGGAGTGGGT CTCAGCTATTAGTGAAGTGGTGGCACATACGACGCTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 9625) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWHQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLTISRVEAGDEADYCYQVWDYSSDHVVF GGTKLTVL	(SEQ ID NO: 9983) EVQLLESGGGLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWVS AISGSGGTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGQGITLVSS
IPS:613525	18182-E5	NA	GAGCTGCTGCTGACTCAGCCACCTCGGTGTCACTGGCCCGCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGCACCAAGCAAGCCAGCCAGCCCTGTGTTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGAAACACGGCCACCCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGAGCTGGTCCGCAAGCTTCCAGGCAAGGCTTGGAGTGGGT CTCAACTATTAGTGAAGTGGTGGCACATACGACGACTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 9627) ELVLTQPPSVSVAPGQTARITCGNNIGSKSVHWHQKPGQAPVLVYDD NDRPSGIPERFSGNSGNTATLTISRVEAGDEADYCYQVWDYSSDHVVF GGTKLTVL	(SEQ ID NO: 9985) EVQLLESGGGLVQPGSLRLSCAASGFTTSSYAMSWVRQAPKGLWVS TISGSGGTYYADS VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGQGITLVSS
IPS:613555	18182-A4	NA	GAGCTGCTGCTGACTCAGCCACCTCGGTGTCACTGGCCCGCAGGACAG ACGCCAGGATTACCTGTGGGGAACAACATTGGAAGTAAAGTGT GCACTGGTACCAAGCAAGCCAGCCAGCCCTGTACTGGTCTGCTA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTTGGAAACACGGCCACCCCTGATTATCAGTAGGGTCGCGACCCG GGATGAGGCCGACTAT	GAGGTGCAGTCTCTGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCTGTGAGCCTCTGGATTACCTTTAGCAGCTAT GCCATGACTGGTCCGCAAGCTTCCAGGCAAGGCTTGGAGTGGGT CTCGTCTATTAGTGTAGCGGTGGTGGCACATACGACGCTCCGT GAAGGGCCGTTTACCATCTCCAGAGACAAATTCAGAACACGCTGTA TCTGCAAAATGAACAGC
			(SEQ ID NO: 9628)	(SEQ ID NO: 9986)

PS:603137	18089-D11	NA	GAGCTCGTGATGACCCAGTCTCCATCTCCCTGTCGTGCTAGGAG ACAGAGTCAACATCACTTGC CGGCAAGTCAGAGCAATTAGCAACTATT TCAATTGGTATCAGCAAGAACAGGAAAGCCCTAAGCTCTCTGATCT ATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTCAGTGGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9637) ELVMTQSPSSLSASVGDRLVTITCRASQSISSYLNWYQOKPKAPKLLIYAA SSLQSGVPSRFSGSGSDTFLTISSLQPEDFATYYCQSYSTPIPTFGGGTKL EIK	(SEQ ID NO: 9995) EVQLLESGPVLVKPTQILTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLLITKDTSKNQVVLTMTNMDPVDITATYYCAYR RYNWNVENWFDPPWGQGITLVTVSS
		AA	GAGCTCCAGATGACCCAGTCTCTTCTCCCTGCTGCATCTGTAGGAG ACAGAGTCAACATCACTTGC CGGCAAGTCAGTTATTAGCAGCTATT AAATTGGTATCAGCAAGAACAGGAAAGCCCTAAGCTCTCTGATCTA TGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTCAGTGGCCG TGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGA AGATTTTGCAACT	(SEQ ID NO: 9638)	(SEQ ID NO: 9996) GAGGTGCAGCTGCTCGAGTCTGGTCTACGCTGGAACCCACACACAG ACCTCAGCTGACCTGCACCTTCTCTGGTTTCTCATTTCACTTCAACCACTATA AAATGGGTGGACCTGGAATCCGTCAGCCCGCAGGAAAGGCCCTGGAGT GGCTTGCACTCATTTATTGGAAATGATGATAAGCGCTACAGCCCATCTCT GCAGAGTAGGCTCACCATCACCAGGACACCTTCCAAAAACCCAGGTGGT CCTCACAATGACC
PS:603187	18089-C9	NA			
		AA	ELQMTQSPSSLSASVGDRLVTITCRASQFISSYLNWYQOKPKAPKLLIYAA SSLQSGVPSRFSGRGSDTFLTISSLQPEDFATYYCQSYSTPIPTFGPGTK VEIK	(SEQ ID NO: 9639)	(SEQ ID NO: 9997) EVQLLESGPTLVKPTQILTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLLITKDTSKNQVVLTMTNMDPVDITATYYCAYR RYNWNVENWFDPPWGQGITLVTVSS
		NA	GAGCTCGTGATGACCCAGTCTCCAGACTCCCTGCTGCTGCATCTGTAGGA GACAGAGTCAACATCACTTGC CGGCAAGTCAGAGCAATTAGCAGCTAT TTAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCTCTGATC TATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTCAGTGGC AGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT GAAGATTTTGCAACT	(SEQ ID NO: 9640)	(SEQ ID NO: 9998) GAGGTGCAGCTGCTCGAGTCTGGTCTATGCTGGAACCCACACACAG ACCTCAGCTGACCTGCACCTTCTCTGGTTTCTCATTTCACTTCAACCACTATA AAATGGGTGGACCTGGAATCCGTCAGCCCGCAGGAAAGGCCCTGGAGT GGCTTGCACTCATTTATTGGAAATGATGATAAGCGCTACAGCCCATCTCT GCAGAGTAGGCTCACCATCACCAGGACACCTTCCAAAAACCCAGGTGGT CCTCACAATGACC
PS:603165	18089-D8	NA			
		AA	ELVMTQSPDSL SASVGDRLVTITCRASQSISSYLNWYQOKPKAPKLLIYAA SSLQSGVPSRFSGSGSDTFLTISSLQPEDFATYYCQSYSTPIPTFGQGTSL EIK	(SEQ ID NO: 9641)	(SEQ ID NO: 9999) EVQLLESGPMLVKPTQILTLCTFSGFSFTTHKMGVDWIRQPPGKALEWL ALIYWNDKRYSPSLQSRLLITKDTSKNQVVLTMTNMDPVDITATYYCAY RYNWNVENWFDPPWGQGITLVTVSS
		NA	GAGCTCAGATGACCCAGTCTCCATCTCCCTGCTGCTGCATCTGTAGGAG ACAGAGTCAACATCACTTGC CGGCAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCTCTGATCT ATGCTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTCAGTGGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 9642)	(SEQ ID NO: 10000) GAGGTGCAGCTGCTCGAGTCTGGTCTATGCTGGAACCCACACACAG ACCTCAGCTGACCTGCACCTTCTCTGGTTTCTCATTTCACTTCAACCACTATA AAATGGGTGGACCTGGAATCCGTCAGCCCGCAGGAAAGGCCCTGGAGT GGCTTGCACTCATTTATTGGAAATGATGATAAGCGCTACAGCCCATCTCT GCAGAGTAGGCTCACCATCACCAGGACACCTTCCAAAAACCCAGGTGGT CCTCACAATGACC
PS:601080	18081-F9	NA			

iPS:613743	18179-E1	NA	GAGCTCGTATGACCCAGTCTCCATCTCCCTGCTGCACTCTGAGGAG ACAGAGTCAACCATCACTTGC CGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAAAACAGGAGAGCCCTAAAGCTCTCTGATCT TTGCTGCATCCAGTTTGCAAGGTGGGTCGCCATCAAGGTTCAGTGCCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCTG AAGATTTGCAACT	(SEQ ID NO: 9651) ELVMTQSPSSLASVGDRTVTTCRTISQSISSYLNWYQQKPGKAPKLLIFAAS SLQGVPSRFSGSGTDFTLTISLQPEDFATYYCQQTYSMPFTFGPGTKV DIK	(SEQ ID NO: 10099) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVVG RIKNTYGGTIDYAAPVKGRFTISRDDSKNTLYLQMNLSLKIEDTAVYYCT TPSYSGSYNYFVSVMQVWVGQGTTTVTVSS	GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCCTGTGCAAGCCTCTGGATTCACTTTACAGTAACGCC TGAGTACGCTGGGTCCGCAAGCTCCAGGAAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGCAACACTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAAATG
		AA		(SEQ ID NO: 9652) GAGCTCAGATGACCCAGTCTCCATCTCCTGCTGCACTCTGAGGAG ACAGAGTCAACCATCACTTGC CGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTTTCAACAGAAACAGGAAAGCCCTAAAGCTCTGATCT TTGCTGCATCCAGTTTGCAAAGTGGGTCGCCATCAAGGTTCAGTGCCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTG AAGATTTGCAACT	(SEQ ID NO: 10010) GAGGTGCAGCTGCTCGAGTCTGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTTAGACTCTCCTGTGCAAGCCTCTGGATTCACTTTACAGTAACGCC TGAGTACGCTGGGTCCGCAAGCTCCAGGAAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGCAAAAACCTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAAATG	
iPS:613691	18179-H7	NA		(SEQ ID NO: 9653) ELQMTQSPSSLASVGDRTVTTCRTISQSISSYLNWYQQKPGKAPKLLIFAAS SLQSGVPSRFSGSGTDFTLTISLQPEDFATYYCQQSYSPFTFGPGTKV IK	(SEQ ID NO: 10011) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVVG RIKSKTYGGTIDYAAPVKGRFTISRDDSKNTLYLQMNLSLKIEDTAVYYCT TPSYSGSYNYFVSVMQVWVGQGTTTVTVSS	
		AA		(SEQ ID NO: 9654) GAGCTCGTATGACCCAGTCTCCATCTCCTGCTGCACTCTGAGGAG ACAGAGTCAACCATCACTTGC CGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTTTCAACAGAAACAGGAAAGCCCTAAAGCTCTGATCT TTGCTGCATCCAGTTTGCAAAGTGGGTCGCCATCAAGGTTCAGTGCCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCTG AAGATTTGCAACT	(SEQ ID NO: 10012) GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTTAGACTCTCCTGTGCAAGCCTCTGGATTCACTTTACAGTAACGCC TGAGTACGCTGGGTCCGCAAGCTCCAGGAAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGCAACAACCTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAAATG	
iPS:613785	18179-B12	NA		(SEQ ID NO: 9655) ELVMTQSPSSLASVGDRTVTTCRTISQSISSYLNWYQQKPGKAPKLLIFAAS SLQSGVPSRFSGSGTDFTLTISLQPEDFATYYCQQTYSMPFTFGPGTKV EIK	(SEQ ID NO: 10013) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVVG RIKNTYGGTIDYAAPVKGRFTISRDDSKNTLYLQMNLSLKIEDTAVYYCT TPSNSGSYNYFVSVMQVWVGQGTTTVTVSS	
		AA		(SEQ ID NO: 9656) GAGCTCAGATGACCCAGTCTCCATCTCCTGCTGCACTCTGAGGAG ACAGAGTCAACCATCACTTGC CGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAAAACAGGAGAGCCCTAAAGCTCTGATCT TTGCTGCATCCAGTTTGCAAAGTGGGTCGCCATCAAGGTTCAGTGCCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCTG AAGATTTGCAACT	(SEQ ID NO: 10014) GAGGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTAAAGCCTGGGGG GTCCCTTAGACTCTCCTGTGCAAGCCTCTGGATTCACTTTACAGTAACGCC TGAGTACGCTGGGTCCGCAAGCTCCAGGAAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGCAACAACCTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTATCTGCAAAATG	
iPS:613733	18179-D11	NA				

			(SEQ ID NO: 9657) ELQMTQSPSSLASVGDVITITCTQSISSYLNWYQQKPGRAPKLLIFAAS SLQGGVPSRFSGSGSGTDFLTISSLQPEDFATYYCQQTYSMPFTFGPGTKV DIK	(SEQ ID NO: 10015) EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVC RIKNTYGGTTDYAAPVKGRFTISRDKNTLFLQMNSLKLTEDTAVYYCT TPSYSGSYNYFVSVMQGVVTVSS
			(SEQ ID NO: 9658) GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCAACATCACTTCCGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACACGAGGAGGCCCTAAGCTCCTGCTGCT TTGCTGCATCCAGTTTGCAAGGTGGGTCCTCAATCAAGGTTCAAGTGCA GTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTCCAACCTG AAGAATTTGCAACT	(SEQ ID NO: 10016) GAGTGCAGTCTCTGAGTCCGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTCAGACTCTCTCTGTCAGCTCTGAGCTCTGATTCTTCACTTCAAGTAAACGCC TGATGAGTGGTCCGACAGCTCCAGGTCACAGGGAAGGGCTGGAGTGGGT TGCCGTATTAAAGCAACACTTATGCTGGGACAAACAGACTACGCTGC ACCGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAACAC GCTGTTCTGCAAAATG
			(SEQ ID NO: 9659) ELVMTQSPSSLASVGDVITITCTQSISSYLNWYQQKPGRAPKLLIFAAS SLQGGVPSRFSGSGSGTDFLTISSLQPEDFATYYCQQTYSMPFTFGPGTKV DIK	(SEQ ID NO: 10017) EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVC RIKNTYGGTTDYAAPVKGRFTISRDKNTLFLQMNSLKLTEDTAVYYCT TPSYSGSYNYFVSVMQGVVTVSS
			(SEQ ID NO: 9660) GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCAACATCACTTCCGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACACGAGGAGGCCCTAAGCTCCTGCTGATCT TTGCTGCATCCAGTTTGCAAGGTGGGTCCTCAATCAAGTTCAGTGGA GTGGATCTGGGACAGATTTCATCTCACCATCAGCAGTCTCCAACCTG AAGAATTTGCAACT	(SEQ ID NO: 10018) GAGTGCAGTCTCTGAGTCCGGGGAGGCTTGGTAAAGCCTGGGGG GTCCCTTAGACTCTCTGTGAGCCTCTGAGTCTGATTCTTCACTTCAAGTAAACGCC TGATGAGTGGTCCGACAGCTCCAGGTCACAGGGAAGGGCTGGAGTGGGT TGCCGTATTAAAGCAACACTTATGCTGGGACAAACAGACTACGCTGC ACCGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAACAC GCTGTTCTGCAAAATG
			(SEQ ID NO: 9661) ELVMTQSPSSLASVGDVITITCTQSISSYLNWYQQKPGRAPKLLIFAAS SLQGGVPSRFSGSGSGTDFLTISSLQPEDFATYYCQQTYSMPFTFGPGTKV DIK	(SEQ ID NO: 10019) EVQLLESGGGLVKPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVC RIKNTYGGTTDYAAPVKGRFTISRDKNTLFLQMNSLKLTEDTAVYYCT TPSYSGSYNYFVSVMQGVVTVSS
			(SEQ ID NO: 9662) GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGCCCTCACCCCTGGA GAGCGGCTCCTCATCTCCTGAGGTAGTCAGAGCCTCCTGCTGATAGA AATGGATACAACTATTGGATTGATCCTGCAGAACCCAGGGCAGTCT CCACAGCTCCTGATCTATTGGTCTTAATCGGGCTCCGGGCTCCCTG ACAGGTTCACTGGCAGTGGATCAGGCACAGATTTCAACGCTGAAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 10020) GAGTGCAGTCTCTGAGTCCGGGGAGGCTTGGTAAAGCCTTACAG ACCTGTCCCTCACCTGCAGTCTCTGCTGAGTCTTCCATCAGCAGTAATC CTTACTAGTGGAGTGGATCCGCCAGCAGCAGGGAAGGGCTGGAGT GGATTGGGTACATCTCTTACAGTGGGATCACCACTACACCCCTCCCT CAAGAGTCACTGATCCCATGTCAGTGGACAGCTCAAGAACCAAGCTTCTC CCTGAAGCTGAGC
			(SEQ ID NO: 9663) ELVMTQTPSLPLPVTPEPASISCRSSQLLHRNGYNLYDWYLKPGQSPQL LIYLGSRASGVDPDRFSGSGSGTDFLTKSRVEAGDVGYVYCMQALQTPW TFGGTKVEIK	(SEQ ID NO: 10021) EVQLLESGGLVKPSQSLSLTCTVSGDSSISNPYYWSWRQHPGKGLEWIG YISYSGITNYPNLSKSRVTMSVDISKQSLKLTSLTAADTAVYYCAREK MWFGVLYNYGMDVWQGVVTVSS
			(SEQ ID NO: 9664)	(SEQ ID NO: 10022)

IPS:615266	18181-G10	NA	GAGCTCGTGAATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAG AGCCGGCTCCATCTCTGCAGGTCTAGTCAGAGCCTCTCTGCATAGTA CTGGATACAACTATGTGGATTGGTACCTCAGAGCCAGGCGAGTCTC CACAGCTCTGATCTATTTGGGTCTTAATCGGGCTCCGGGTCCTCTGA CAGGTTCAAGTCGGCAGTGGATCAGGCACAGATTTTACACTAAAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 9665) ELVMTQSPSLSPVTPGEPASISCRSSQSLHSTGYNYVDWYLQKPGQSPQL LIYLGSRNRASGVDPDRFSGSGGTDFTLKISRVEAEDVGFYYCMQALQTPRT FQGGTKVEIK	(SEQ ID NO: 10023) EVQLLESGPGLVKPSQTLSTLTCTVSGDSISSNPYYWSWIRQLPGKGLEWIG YISYSGSTFPYNPSLKSRTVITSDISKQFSLNLTSTVTAADTAVYYCARDRL WFGVLYNYYYGMDVWVWGLGTTVTIVSS	GAGGTGCAGTCTGCTCGAGTCGGGCGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCAGCTGTCTCTGTGACTCCATCAGCAGTAATC CTTACTTGAGCTGGATCCGCGCAGCTCCCGGGAAGGGCTGGAGTGGAT GGATTGGGTACATCTTACAGTGGGACACCTTCTACAACCCCTCCCT CAAGAGTCGAGTTACCATATCATAGTACAGACAGCTCTAAGAACCAAGTCTC CCTGAATCTGACC
		AA		(SEQ ID NO: 9666) GAGCTCGTGAATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGAG ACAGAGTCACCATCACTTCCGGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGGAAGCCCTAAACTCTCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCAAGTGGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 10024) GAGGTGCAGTCTGCTCGAGTCGGGGGAGGCTTGGTACAGCCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACITTCAGTAACGCC TGGATGAGCTGGTCCGCGCAGGCTCCAGGGAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGGCAACACTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTCTGCAAAATG	
IPS:615250	18181-C8	NA		(SEQ ID NO: 9667) ELVMTQSPSSLSASVGDRTVITCRISQSISSYLNWYQQKPGKAPKLLIYAA SSLQSGVPSRFSGSGGTDFTLTITSLQPEDFATYYCQQYISMPFTFGGGTK VEIK	(SEQ ID NO: 10025) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVROAPGKGLEWVG RIKGNITYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKIEDTAVYYCT TPSNSGSYNYFVSVMVWQGGTIVTVSS	
		AA		(SEQ ID NO: 9668) GAGCTCGTGAATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGAG ACAGAGTCACCATCACTTCCGGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGGAAGCCCTAAAGCTCTCTGATCT TTGCTGCATCCAGTTGCAAGTGGGTCCCATCAAGGTTCAAGTGGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 10026) GAGGTGCAGTCTGCTCGAGTCGGGGGAGGCTTGGTGCAGCCTGGGGG GTCCCTTAGACTCTCTGTGCAGCCTCTGGATTCACITTCAGTAACGCC TGGATGAGCTGGTCCGCGCAGGCTCCAGGGAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGGCAACACTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTCTGCAAAATG	
IPS:615194	18181-F3	NA		(SEQ ID NO: 9669) ELVMTQSPSSLSASVGDRTVITCRISQSISSYLNWYQQKPGKAPKLLIFAAAS SLQGGVPSRFSGSGGTDFTLTITSLQPEDFATYYCQSYSPFTFGPGTKV EIK	(SEQ ID NO: 10027) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVROAPGKGLEWVG RIKGNITYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKIEDTAVYYCT TPSYSGSYNYFVSVMVWQGGTIVTVSS	
		AA		(SEQ ID NO: 9670) GAGCTCGTGAATGACCCAGTCTCCATCTCCCTGTCTGCACTGTAGGAG ACAGAGTCACCATCACTTCCGGGACAAGTCAGAGCAATTAGCAGCTATT TAAATTGGTATCAGCAGAAACAGGGAAGCCCTAAAGCTCTCTGATCT TTGCTGCATCCAGTTGCAAGTGGGTCCCATCAAGGTTCAAGTGGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCTG AAGATTTTGCAACT	(SEQ ID NO: 10028) GAGGTGCAGTCTGCTCGAGTCGGGGGAGGCTTGGTAAAGCCTGGGGG GTCCCTTAGACTCTCTGTGCAGCCTCTGGATTCACITTCAGTAACGCC TGGATGAGCTGGTCCGCGCAGGCTCCAAGGGAAGGGGCTGGAGTGGGT TGGCCGTATTAAAGGCAACACTTATGGTGGGACAACAGACTACGCTGC ACCCGTGAAGGAGGATTCACCATCTCAAGAGATGATTCAAAAAACAC GCTGTTTCTGCAAAATG	
IPS:615180	18181-F1	NA				

			(SEQ ID NO: 9671) ELVMTQSPSSLSASVGDRTVITICRTSQSISSVYLNWYQQKPGRAPKLLIFAA SLQGGVPSRFSGSGSDTFLTISSLQPEDFATYYCQQTYSPFTFGPGTKLH IK	(SEQ ID NO: 10029) EVQLLESGGGLVKPSGSLRLSCAASGFTFSNAWMSVVRQAPGKGLEWVC RIKGNITYGGITDYAAPVKGRFTISRDISKNTLFLQMNSLKLTEDTAVYYCT TPSYSGSYNYFVSVMQVWVGQGTITVYSS
18181-E2	NA		(SEQ ID NO: 9672) GAGCTCGTGATGACCCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCGGCTCCATCTCCTCGAGGTCTAGTCAGAGCCTCCTGCAATAGT AGTGGATACAACTATTGGATTGGTACTCTGCAGAACCCAGGGCAGTCT CCACAGCTCCTGATCTATTGGGTCTTAATCGGGCTCCGGGTCCTCG ACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCA GCAAGTGGAGGCT	(SEQ ID NO: 10030) GAGGTGCAGTGTCTGAGTCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATC CTTACTACTGGAGTGGATCCGCCAGCACCAGGGAAGGGCCCTGGAGT GGATTGGGTACATCTCTCACAGTGGAGCACTTATTACAATCCCGTCCCT CAAGAGTCGAGTAACCATATCATGATAGACACGCTAAGAAATCATGTTCTC CCTGAATCTGACC
	AA		(SEQ ID NO: 9673) ELVMTQSPSLPVPVTPGEPASISCRSSQSLHSSGVNVDWYLLKPGQSPQLI IYLGSRASGVDPDRFSGSGSDTFLTKISKVEAEADVGVYCMQALQTPFTF GQGTKVDIK	(SEQ ID NO: 10031) EVQLLESGPGLVKPSQTLSLTCTVSGDSISSNPYYWSWIRQHPGKGLEWIG YISHSGSYNPSLKSRTVTSVDTSKNQSLNLTSTVTAADTAVYYCARDRL WFGVLYYYGMDVWVGLTITVYSS
18181-C9	NA		(SEQ ID NO: 9674) GAGCTCGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAG AGCCGGCTCCATCTCTCGAGGTCTAGTCAGAGCCTCTCTGCACAGAA ATGGATACAACTATTGGATTGGTACCTGCAGAACCCAGGGCAGTCTC CACAGTCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCGA CAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAG CAGAGTGGAGGCT	(SEQ ID NO: 10032) GAGGTGCAGTGTCTGAGTCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTAATC CTTACTACTGGAGTGGATCCGCCAGTCCCGGGAAGGGCCCTGGAGT GGATTGGGTACATCTCTTACAGTGGAGCACTTCTACAACCCCGTCCCT CAAGAGTCGAGTACCATATCATGATAGACACGCTAAGAACCACTGTTCTC CCTGAATCTGACC
	AA		(SEQ ID NO: 9675) ELVLTQSPSLPVPVTPGEPASISCRSSQSLHNRNGYNVDWYLLKPGQSPQLI IYLGSRASGVDPDRFSGSGSDTFLTKISRVEAEADVGVYCMQGLQTPFTF GPGTKVEIK	(SEQ ID NO: 10033) EVQLLESGPGLVKPSQTLSLTCTVSGDSISSNPYYWSWIRQLPGKGLEWIG YISYSGSYNPSLKSRTVTSVDTSKNQSLNLTSTVTAADTAVYYCARDRL WFGVLYYYGMDVWVGLTITVYSS
18181-B8	NA		(SEQ ID NO: 9676) GAGCTCGTGATGACTCAGACTCCACTCTCCCTGCCCGTCAACCCCTGGA GAGCGGCTCCATCTCCTCGAGGTCTAGTCAGAGCCTCCTGCAATAGA AATGGATACAACTATTGGATTGGTACTCTGCAGAACCCAGGGCAGTCT CCACAGCTCCTGATCTATTGGGTCTAATCGGGCTCCGGGTCCTCG ACAGGTTCACTGGCAGTGGTCAAGGCACAGATTTTACACTGGAATCA GCAGAGTGGAGGCT	(SEQ ID NO: 10034) GAGGTGCAGTGTCTGAGTCGGGCCAGGACTGGTGAAGCCTTCACAG ACCTGTCCCTCACCTGCACTGTCTCTGGTGACTCCATCAGCAGTGGTG GTTACTACTGGAGTGGATCCGCCAGCACCAGGGAAGGGCCCTGGAGT GGATTGGGTACATCTCTCACAGTGGAGCACTTATTACAATCCCGTCCCT CAAGAGTCGAGTAACCATATCATGATAGACACGCTAAGAAATCATGTTCTC CCTGAATCTGACC
	AA		(SEQ ID NO: 9677) ELVMTQTPSLPVPVTPGEPASISCRSSQSLHNRNGYNVDWYLLKPGQSPQL LIYLGSRASGVDPDRFSGSGSDTFLTKISRVEAEADVGVYCMQALQTPSF GQGTKVEIK	(SEQ ID NO: 10035) EVQLLESGPGLVKPSQTLSLTCTVSGDSISSGYYWSWIRQHPGKGLEWIG YISHSGSYNPSLKSRTVTSVDTSKNQSLNLTSTVTAADTAVYYCAREKM WFGVLYYYGMDVWVGQGTITVYSS
			(SEQ ID NO: 9678)	(SEQ ID NO: 10036)

iPS:615222	18181-A6	NA	GAGTCGTGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGAG ACAGATCACCATCACTTCGCGGCAAGTCAGAGATTAGCAGCTATT TAAATTGGTATCAGCAAAACAGGAGAGCCCTAAAGTCTCTGATCT TTGCTGCATCCAGTTTGCAAGGTGGGTCGCCATCAAGGTTCAGTGGCA GTGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTCCAACCTG AAGATTTCGCAATG		
			(SEQ ID NO: 9679) ELVMTQSPSSLSASVGDRTVITTCRASQSISSYLWYQKPKGRAPKLLIFAA SLQGGVPSRFSGSGTGDTFLTISSLQPEDFATYYCQQTYSMPFTFGPGTKL EIK	(SEQ ID NO: 10037) EVQLLESGGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV RIKGNITYGGITTDYAAPVKGRFTISRDTSKNTLYLQMNSLKTEDTAVYYCT TPSYSGSYNYFVSVMQVWVGQGTITVTVSS	
iPS:1855072	18403-F12-AS	NA	(SEQ ID NO: 9680) <i>No data seq available</i>	(SEQ ID NO: 10038) <i>No data seq available</i>	
		AA	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPKGPQAPVMVYD DNDRPSGIPERFSGNSGNTATLIISRVAAAGDEADYYCQVWDYRYSQVF GGGTKLTVL	(SEQ ID NO: 10039) <i>No data seq available</i>	EVQLLESGGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVS AISGSGGTYYAASVKGRFTISRDNSKNTLYLQMSLSRAEDTAVYYCVTG KGVHLGFDYWGGTILTVSS
iPS:1855074	18403-G10-AS	NA	(SEQ ID NO: 9681) <i>No data seq available</i>	(SEQ ID NO: 10040) <i>No data seq available</i>	
		AA	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPKGPQAPVMVYD DNDRPSGIPERFSGNSGNTATLIISRVAAAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 10040) <i>No data seq available</i>	EVQLLESGGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVS AISGSGGTYYAASVKGRFTISRDNSKNTLYLQMSLSRAEDTAVYYCATG KGVHLGFDYWGGTILTVSS
iPS:1855054	02-C1-86-A4-N-F5_final	NA	(SEQ ID NO: 9682) <i>No data seq available</i>	(SEQ ID NO: 10041) <i>No data seq available</i>	
		AA	DIQMTQSPSSLSASVGDRTVITTCRASQGSNLYAWYQKPKGVPKLLIYAA STLQSGVPSRFSGSGTGDTFLTISSLQPEDVATYYCQKYNAPFTFGPGTK VEIK	(SEQ ID NO: 10041) <i>No data seq available</i>	QVQLVESGGGVVQPGGSLRLSCAASGFTSTYGMHWVRQAPGKGLEWV AVISYDAETVKYAESVKGRFTISRDNSKNTLYLQMSLSRAEDTAVYYCAR GQLLTGYWGGTILTVSS
iPS:1855068	03-F3-88-B3-F9_final	NA	(SEQ ID NO: 9683) <i>No data seq available</i>	(SEQ ID NO: 10042) <i>No data seq available</i>	
		AA	SYVLTQPPSVSVAPGQTARITCGNNIGSKSVHWYQKPKGPQAPVLVYD DADRPSPGIPERFSGNSGNTATLIISRVAAAGDEADYYCQVWDASAGYGVV FGGTKLTVL	(SEQ ID NO: 10042) <i>No data seq available</i>	QVQLVESGGGLVKPGGSLRLSCAASGFTSDYYSWVRQAPGKGLEWVS YISKSSYTVTYADAVKGRFTISRDNAKNSLYLQMSLSRAEDTAVYYCATY NYGHFDYWGGTILTVSS
iPS:1855106	81-H7-SG-F28_final	NA	(SEQ ID NO: 9684) <i>No data seq available</i>	(SEQ ID NO: 10043) <i>No data seq available</i>	
		AA	DIVMTQTPSLPLPVTPGEPASISCRSSQSLHRSYGNLYLDWYLOKPGQSPQL LIYLSGNRASGVDPDRFSGSGTGDTFLTKISRVAAAGDVGYVYCMQALQTPW TFGGQTKVEIK	(SEQ ID NO: 10043) <i>No data seq available</i>	QVQLQESGPGLVKPSQTLSTCTVSGDSISNPYYWSWIRQHPGKGLEWIG YISYSGITNYPNPSLRSRVTMSSVDTSKQFSLKLTSLTAADTAVYYCAREK MWFGVLYNYGYGMDVWVGQGTITVTVSS
iPS:1891845	18081-B9_final	NA	(SEQ ID NO: 9685) <i>No data seq available</i>	(SEQ ID NO: 10044) <i>No data seq available</i>	
		AA	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNLYAWYQKPKGQPP KLLIYWASTRESGVDPDRFSGSGTGDTFLTISSLQAEADVAVYYCQFYSTPI TFGGQTRLEIK	(SEQ ID NO: 10044) <i>No data seq available</i>	QVQLQESGPGLVKPSQTLSTCTVSGDSISNPYYWSWIRQHPGKGLEWIG SIYYSYSTYNNPSLRSRVTMSSVDTSKQFSLKLTSLTAADTAVYYCARGIFG VITYFDYWGGTILTVSS
iPS:1891847	18398-C7_final	NA	(SEQ ID NO: 9686) <i>No data seq available</i>	(SEQ ID NO: 10044) <i>No data seq available</i>	

		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYRILDSV GGGTIKLTVL (SEQ ID NO: 9687) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS ISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGGTLVTSS (SEQ ID NO: 10045) <i>No data seq available</i>
iPS:1891849	18403-D8_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYRILDSV GGGTIKLTVL (SEQ ID NO: 9688) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS ITSGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10046) <i>No data seq available</i>
iPS:1855064	18403-D8_AS_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYRILDSV GGGTIKLTVL (SEQ ID NO: 9689) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS ITSGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10047) <i>No data seq available</i>
iPS:1855066	18403-E11_AS_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYRILDSV GGGTIKLTVL (SEQ ID NO: 9690) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVTG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10048) <i>No data seq available</i>
iPS:1891851	18403-F12_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVAAGDEADYYCQVWDYRILDSV GGGTIKLTVL (SEQ ID NO: 9691) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVTG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10049) <i>No data seq available</i>
iPS:1855072	18403-F12-AS_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVAAGDEADYYCQVWDYRILDSV GGGTIKLTVL (SEQ ID NO: 9692) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVTG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10050) <i>No data seq available</i>
iPS:1891853	18403-G10_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTIKLTVL (SEQ ID NO: 9693) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10051) <i>No data seq available</i>
iPS:1855074	18403-G10-AS_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVYD DNDPSPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTIKLTVL (SEQ ID NO: 9694) <i>No data seq available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVLGFDYWGGGTLVTSS (SEQ ID NO: 10052) <i>No data seq available</i>
iPS:1891855	18409-E2_final	NA		

IPS:1891857	18409-F12_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV EIK (SEQ ID NO: 9695) <i>No info. seq. available</i>	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRISKTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVWVGQGTITVTSS (SEQ ID NO: 10053) <i>No info. seq. available</i>
		NA		
IPS:1891859	18409-G10_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SSLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV VEIK (SEQ ID NO: 9696) <i>No info. seq. available</i>	QITLKESGPALVKPTQILTLCTFSGHSFTTHKMGVDVWIRQPPGKALEWLA LIYWDDKRYSPSLQSRLLITKDTSKNQVVLTMNTNMDPVDATATYYCAYR RYNWNENWFDPWGQGTITVTSS (SEQ ID NO: 10054) <i>No info. seq. available</i>
		NA		
IPS:1891861	18409-H7_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SSLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV EIK (SEQ ID NO: 9697) <i>No info. seq. available</i>	QITLKESGPALVKPTQILTLCTFSGHSFTTHKMGVDVWIRQPPGKALEWLA GHYDDKRYSPSLQSRLLITKDTSKNQVVLTMNTNMDPVDATATYYCAYR RYNWNENWFDPWGQGTITVTSS (SEQ ID NO: 10055) <i>No info. seq. available</i>
		NA		
IPS:1891863	18409-H10_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SSLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV VEIK (SEQ ID NO: 9698) <i>No info. seq. available</i>	QITLKESGPALVKPTQILTLCTFSGHSFTTHKMGVDVWIRQPPGKALEWLA LIYWDDKRYSPSLQSRLLITKDTSKNQVVLTMNTNMDPVDATATYYCAYR RYNWNENWFDPWGQGTITVTSS (SEQ ID NO: 10056) <i>No info. seq. available</i>
		NA		
IPS:1891865	18410-B5_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SSLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV VEIK (SEQ ID NO: 9699) <i>No info. seq. available</i>	QITLKESGPALVKPTQILTLCTFSGHSFTTHKMGVDVWIRQPPGKALEWLA LIYWDDKRYSPSLQSRLLITKDTSKNQVVLTMNTNMDPVDATATYYCAYR RYNWNENWFDPWGQGTITVTSS (SEQ ID NO: 10057) <i>No info. seq. available</i>
		NA		
IPS:1891867	18410-B6_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV VEIK (SEQ ID NO: 9700) <i>No info. seq. available</i>	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRISRSYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVWVGQGTITVTSS (SEQ ID NO: 10058) <i>No info. seq. available</i>
		NA		
IPS:1891869	18410-D3_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV IK (SEQ ID NO: 9701) <i>No info. seq. available</i>	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRISKTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVWVGQGTITVTSS (SEQ ID NO: 10059) <i>No info. seq. available</i>
		NA		
IPS:1891871	18410-D6_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV DIK (SEQ ID NO: 9702) <i>No info. seq. available</i>	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRITSSRYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVWVGQGTITVTSS (SEQ ID NO: 10060) <i>No info. seq. available</i>
		NA		
IPS:1891873	18410-D9_final	AA	DIQMTQSPSLSASVGDRTVTTCRTSQSISSYLNWYQOKPGRAPKLLIFAAS SLQGGVPSRFSGSGTDFLTISSLQPEDFATYYCQOSYTPFTFGPGTKV DIK (SEQ ID NO: 9703) <i>No info. seq. available</i>	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRILNNAYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVWVGQGTITVTSS (SEQ ID NO: 10061) <i>No info. seq. available</i>
		NA		

iPS:1891873	18410-G10_final	NA	(SEQ ID NO: 9703) <i>No. nuc. seq. available</i>	(SEQ ID NO: 10061) <i>No. nuc. seq. available</i>
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVD DNDPSPGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYVAPRHVF GGGTIKLTVL (SEQ ID NO: 9704) <i>No. nuc. seq. available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGTYNADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGGQTLVTVSS (SEQ ID NO: 10062) <i>No. nuc. seq. available</i>
iPS:1855092	18410-G10_AS_final	NA		
		AA	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQOKPGQAPVMVVD DNDPSPGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDYVAPRHVF GGGTIKLTVL (SEQ ID NO: 9705) <i>No. nuc. seq. available</i>	EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGTYNADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGGQTLVTVSS (SEQ ID NO: 10063) <i>No. nuc. seq. available</i>
iPS:1891875	18410-H1_final	NA		
		AA	DIQMTQSPSSLSASVGDRTVTITCRISQISSYLNWYQOKPGRAPKLLIFAAS SLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQTYSMPFTFGPGTKV DIK (SEQ ID NO: 9706) <i>No. nuc. seq. available</i>	EVQLVESGGGLVQPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRITSGYGGTIDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVDVWGQGTITVTVSS (SEQ ID NO: 10064) <i>No. nuc. seq. available</i>
iPS:1891877	18410-H3_final	NA		
		AA	DIQMTQSPSSLSASVGDRTVTITCRISQISSYLNWYQOKPGRAPKLLIFAAS SLQGGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQTYSMPFTFGPGTKLH IK (SEQ ID NO: 9707) <i>No. nuc. seq. available</i>	EVQLVESGGGLVQPGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWV GRIRSRPYGGTIDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYC ITPSYSGSYNYFVSVMVDVWGQGTITVTVSS (SEQ ID NO: 10065) <i>No. nuc. seq. available</i>
iPS:1891879	18486-A4_final	NA		
		AA	DIQMTQSPSSLSASVGDRTVTITCRASQISNYLAWYQOKPKVPKLLIYAA STLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQKYNAPFTFGPGTK VEIK (SEQ ID NO: 9708) <i>No. nuc. seq. available</i>	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSYGMHWVRQAPGKGLEWV AVISYDASNKYYAESVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAR GQLLTGYWGQGTITVTVSS (SEQ ID NO: 10066) <i>No. nuc. seq. available</i>

Table 2
4th Variable Region Primers Alignment
CDRs defined by Kabat
Alignment numbering defined by Angen Reference (4b)

Variable Region	Sequence	K1	K2	K3	K4	K5	K6	K7	K8	K9	K10	K11	K12	K13	K14	K15	K16	K17	K18	K19	K20	K21	K22	K23	K24	K25	K26	K27	K28	K29	K30	K31	K32	K33	K34	K35	K36	K37	K38	K39	K40	K41	K42	K43	K44	K45	K46	K47	K48	K49	K50	K51	K52	K53	K54	K55	K56	K57	K58	K59	K60	K61	K62	K63	K64	K65	K66	K67	K68	K69	K70	K71	K72	K73	K74	K75	K76	K77	K78	K79	K80	K81	K82	K83	K84	K85	K86	K87	K88	K89	K90	K91	K92	K93	K94	K95	K96	K97	K98	K99	K100	K101	K102	K103	K104	K105	K106	K107	K108	K109	K110	K111	K112	K113	K114	K115	K116	K117	K118	K119	K120	K121	K122	K123	K124	K125	K126	K127	K128	K129	K130	K131	K132	K133	K134	K135	K136	K137	K138	K139	K140	K141	K142	K143	K144	K145	K146	K147	K148	K149	K150	K151	K152	K153	K154	K155	K156	K157	K158	K159	K160	K161	K162	K163	K164	K165	K166	K167	K168	K169	K170	K171	K172	K173	K174	K175	K176	K177	K178	K179	K180	K181	K182	K183	K184	K185	K186	K187	K188	K189	K190	K191	K192	K193	K194	K195	K196	K197	K198	K199	K200	K201	K202	K203	K204	K205	K206	K207	K208	K209	K210	K211	K212	K213	K214	K215	K216	K217	K218	K219	K220	K221	K222	K223	K224	K225	K226	K227	K228	K229	K230	K231	K232	K233	K234	K235	K236	K237	K238	K239	K240	K241	K242	K243	K244	K245	K246	K247	K248	K249	K250	K251	K252	K253	K254	K255	K256	K257	K258	K259	K260	K261	K262	K263	K264	K265	K266	K267	K268	K269	K270	K271	K272	K273	K274	K275	K276	K277	K278	K279	K280	K281	K282	K283	K284	K285	K286	K287	K288	K289	K290	K291	K292	K293	K294	K295	K296	K297	K298	K299	K300	K301	K302	K303	K304	K305	K306	K307	K308	K309	K310	K311	K312	K313	K314	K315	K316	K317	K318	K319	K320	K321	K322	K323	K324	K325	K326	K327	K328	K329	K330	K331	K332	K333	K334	K335	K336	K337	K338	K339	K340	K341	K342	K343	K344	K345	K346	K347	K348	K349	K350	K351	K352	K353	K354	K355	K356	K357	K358	K359	K360	K361	K362	K363	K364	K365	K366	K367	K368	K369	K370	K371	K372	K373	K374	K375	K376	K377	K378	K379	K380	K381	K382	K383	K384	K385	K386	K387	K388	K389	K390	K391	K392	K393	K394	K395	K396	K397	K398	K399	K400	K401	K402	K403	K404	K405	K406	K407	K408	K409	K410	K411	K412	K413	K414	K415	K416	K417	K418	K419	K420	K421	K422	K423	K424	K425	K426	K427	K428	K429	K430	K431	K432	K433	K434	K435	K436	K437	K438	K439	K440	K441	K442	K443	K444	K445	K446	K447	K448	K449	K450	K451	K452	K453	K454	K455	K456	K457	K458	K459	K460	K461	K462	K463	K464	K465	K466	K467	K468	K469	K470	K471	K472	K473	K474	K475	K476	K477	K478	K479	K480	K481	K482	K483	K484	K485	K486	K487	K488	K489	K490	K491	K492	K493	K494	K495	K496	K497	K498	K499	K500	K501	K502	K503	K504	K505	K506	K507	K508	K509	K510	K511	K512	K513	K514	K515	K516	K517	K518	K519	K520	K521	K522	K523	K524	K525	K526	K527	K528	K529	K530	K531	K532	K533	K534	K535	K536	K537	K538	K539	K540	K541	K542	K543	K544	K545	K546	K547	K548	K549	K550	K551	K552	K553	K554	K555	K556	K557	K558	K559	K560	K561	K562	K563	K564	K565	K566	K567	K568	K569	K570	K571	K572	K573	K574	K575	K576	K577	K578	K579	K580	K581	K582	K583	K584	K585	K586	K587	K588	K589	K590	K591	K592	K593	K594	K595	K596	K597	K598	K599	K600	K601	K602	K603	K604	K605	K606	K607	K608	K609	K610	K611	K612	K613	K614	K615	K616	K617	K618	K619	K620	K621	K622	K623	K624	K625	K626	K627	K628	K629	K630	K631	K632	K633	K634	K635	K636	K637	K638	K639	K640	K641	K642	K643	K644	K645	K646	K647	K648	K649	K650	K651	K652	K653	K654	K655	K656	K657	K658	K659	K660	K661	K662	K663	K664	K665	K666	K667	K668	K669	K670	K671	K672	K673	K674	K675	K676	K677	K678	K679	K680	K681	K682	K683	K684	K685	K686	K687	K688	K689	K690	K691	K692	K693	K694	K695	K696	K697	K698	K699	K700	K701	K702	K703	K704	K705	K706	K707	K708	K709	K710	K711	K712	K713	K714	K715	K716	K717	K718	K719	K720	K721	K722	K723	K724	K725	K726	K727	K728	K729	K730	K731	K732	K733	K734	K735	K736	K737	K738	K739	K740	K741	K742	K743	K744	K745	K746	K747	K748	K749	K750	K751	K752	K753	K754	K755	K756	K757	K758	K759	K760	K761	K762	K763	K764	K765	K766	K767	K768	K769	K770	K771	K772	K773	K774	K775	K776	K777	K778	K779	K780	K781	K782	K783	K784	K785	K786	K787	K788	K789	K790	K791	K792	K793	K794	K795	K796	K797	K798	K799	K800	K801	K802	K803	K804	K805	K806	K807	K808	K809	K810	K811	K812	K813	K814	K815	K816	K817	K818	K819	K820	K821	K822	K823	K824	K825	K826	K827	K828	K829	K830	K831	K832	K833	K834	K835	K836	K837	K838	K839	K840	K841	K842	K843	K844	K845	K846	K847	K848	K849	K850	K851	K852	K853	K854	K855	K856	K857	K858	K859	K860	K861	K862	K863	K864	K865	K866	K867	K868	K869	K870	K871	K872	K873	K874	K875	K876	K877	K878	K879	K880	K881	K882	K883	K884	K885	K886	K887	K888	K889	K890	K891	K892	K893	K894	K895	K896	K897	K898	K899	K900	K901	K902	K903	K904	K905	K906	K907	K908	K909	K910	K911	K912	K913	K914	K915	K916	K917	K918	K919	K920	K921	K922	K923	K924	K925	K926	K927	K928	K929	K930	K931	K932	K933	K934	K935	K936	K937	K938	K939	K940	K941	K942	K943	K944	K945	K946	K947	K948	K949	K950	K951	K952	K953	K954	K955	K956	K957	K958	K959	K960	K961	K962	K963	K964	K965	K966	K967	K968	K969	K970	K971	K972	K973	K974	K975	K976	K977	K978	K979	K980	K981	K982	K983	K984	K985	K986	K987	K988	K989	K990	K991	K992	K993	K994	K995	K996	K997	K998	K999	K1000	K1001	K1002	K1003	K1004	K1005	K1006	K1007	K1008	K1009	K1010	K1011	K1012	K1013	K1014	K1015	K1016	K1017	K1018	K1019	K1020	K1021	K1022	K1023	K1024	K1025	K1026	K1027	K1028	K1029	K1030	K1031	K1032	K1033	K1034	K1035	K1036	K1037	K1038	K1039	K1040	K1041	K1042	K1043	K1044	K1045	K1046	K1047	K1048	K1049	K1050	K1051	K1052	K1053	K1054	K1055	K1056	K1057	K1058	K1059	K1060	K1061	K1062	K1063	K1064	K1065	K1066	K1067	K1068	K1069	K1070	K1071	K1072	K1073	K1074	K1075	K1076	K1077	K1078	K1079	K1080	K1081	K1082	K1083	K1084	K1085	K1086	K1087	K1088	K1089	K1090	K1091	K1092	K1093	K1094	K1095	K1096	K1097	K1098	K1099	K1100	K1101	K1102	K1103	K1104	K1105	K1106	K1107	K1108	K1109	K1110	K1111	K1112	K1113	K1114	K1115	K1116	K1117	K1118	K1119	K1120	K1121	K1122	K1123	K1124	K1125	K1126	K1127	K1128	K1129	K1130	K1131	K1132	K1133	K1134	K1135	K1136	K1137	K1138	K1139	K1140	K1141	K1142	K1143	K1144	K1145	K1146	K1147	K1148	K1149	K1150	K1151	K1152	K1153	K1154	K1155	K1156	K1157	K1158	K1159	K1160	K1161	K1162	K1163	K1164	K1165	K1166	K1167	K1168	K1169	K1170	K1171	K1172	K1173	K1174	K1175	K1176	K1177	K1178	K1179	K1180	K1181	K1182	K1183	K1184	K1185	K1186	K1187	K1188	K1189	K1190	K1191	K1192	K1193	K1194	K1195	K1196	K1197	K1198	K1199	K1200	K1201	K1202	K1203	K1204	K1205	K1206	K1207	K1208	K1209	K1210	K1211	K1212	K1213	K1214	K1215	K1216	K1217	K1218	K1219	K1220	K1221	K1222	K1223	K1224	K1225	K1226	K1227	K1228	K1229	K1230	K1231	K1232	K1233	K1234	K1235	K1236	K1237	K1238	K1239	K1240	K1241	K1242	K1243	K1244	K1245	K1246	K1247	K1248	K1249	K1250	K1251	K1252	K1253	K1254	K1255	K1256	K1257	K1258	K1259	K1260	K1261	K1262	K1263	K1264	K1265	K1266	K1267	K1268	K1269	K1270	K1271	K1272	K1273	K1274	K1275	K1276	K1277	K1278	K1279	K1280	K1281	K1282	K1283	K1284	K1285	K1286	K1287	K1288	K1289	K1290	K1291	K1292	K1293	K1294	K1295	K1296	K1297	K1298	K1299	K1300	K1301	K1302	K1303	K1304	K1305	K1306	K1307	K1308	K1309	K1310	K1311	K1312	K1313	K1314	K1315	K1316	K1317	K1318	K1319	K1320	K1321	K1322	K1323	K1324	K1325	K1326	K1327	K1328	K1329	K1330	K1331	K1332	K1333	K1334	K1335	K1336	K1337	K1338	K1339	K1340	K1341	K1342	K1343	K1344	K1345	K1346	K1347	K1348	K1349	K1350	K1351	K1352	K1353	K1354	K1355	K1356	K1357	K1358	K1359	K1360	K1361	K1362	K1363	K1364	K1365	K1366	K1367	K1368	K1369	K1370	K1371	K1372	K1373	K1374	K1375	K1376	K1377	K1378	K1379	K1380	K1381	K1382	K1383	K1384	K1385	K1386	K1387	K1388	K1389	K1390	K1391	K1392	K1393	K1394	K1395	K1396	K1397	K1398	K1399	K1400	K1401	K1402	K1403	K1404	K1405	K1406	K1407	K1408	K1409	K1410	K1411	K1412	K1413	K1414	K1415	K1416	K1417	K1418	K1419	K1420	K1421	K1422	K1423	K1424	K1425	K1426	K1427	K1428	K1429	K1430	K1431	K1432	K1433	K1434	K1435	K1436	K1437	K1438	K1439	K1440	K1441	K1442	K1443	K1444	K1445	K1446	K1447	K1448	K1449	K1450	K1451	K1452	K1453	K1454	K1455	K1456	K1457	K1458	K1459	K1460	K1461	K1462	K1463	K1464	K1465	K1466	K1467	K1468	K1469	K1470	K1471	K1472	K1473	K1474	K1475
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TABLE 10
UNITARY VARIABLE

UNITARY VARIABLE	SEQ ID NO.	L_1	L_2	L_3	L_4	L_5	L_6	L_7	L_8	L_9	L_10	L_11	L_12	L_13	L_14	L_15	L_16	L_17	L_18	L_19	L_20	L_21	L_22	L_23	L_24	L_25	L_26	L_27	L_28	L_29	L_30	L_31	L_32	L_33	L_34	L_35	L_36	L_37	L_38	L_39	L_40	L_41	L_42	L_43	L_44	L_45	L_46	L_47	L_48	L_49	L_50	L_51	L_52	L_53	L_54	L_55	L_56	L_57	L_58	L_59	L_60	L_61	L_62	L_63	L_64	L_65	L_66	L_67	L_68	L_69	L_70	L_71	L_72	L_73	L_74	L_75	L_76	L_77	L_78	L_79	L_80	L_81	L_82	L_83	L_84	L_85	L_86	L_87	L_88	L_89	L_90	L_91	L_92	L_93	L_94	L_95	L_96	L_97	L_98	L_99	L_100	L_101	L_102	L_103	L_104	L_105	L_106	L_107	L_108	L_109	L_110	L_111	L_112	L_113	L_114	L_115	L_116	L_117	L_118	L_119	L_120	L_121	L_122	L_123	L_124	L_125	L_126	L_127	L_128	L_129	L_130	L_131	L_132	L_133	L_134	L_135	L_136	L_137	L_138	L_139	L_140	L_141	L_142	L_143	L_144	L_145	L_146	L_147	L_148	L_149	L_150	L_151	L_152	L_153	L_154	L_155	L_156	L_157	L_158	L_159	L_160	L_161	L_162	L_163	L_164	L_165	L_166	L_167	L_168	L_169	L_170	L_171	L_172	L_173	L_174	L_175	L_176	L_177	L_178	L_179	L_180	L_181	L_182	L_183	L_184	L_185	L_186	L_187	L_188	L_189	L_190	L_191	L_192	L_193	L_194	L_195	L_196	L_197	L_198	L_199	L_200	L_201	L_202	L_203	L_204	L_205	L_206	L_207	L_208	L_209	L_210	L_211	L_212	L_213	L_214	L_215	L_216	L_217	L_218	L_219	L_220	L_221	L_222	L_223	L_224	L_225	L_226	L_227	L_228	L_229	L_230	L_231	L_232	L_233	L_234	L_235	L_236	L_237	L_238	L_239	L_240	L_241	L_242	L_243	L_244	L_245	L_246	L_247	L_248	L_249	L_250	L_251	L_252	L_253	L_254	L_255	L_256	L_257	L_258	L_259	L_260	L_261	L_262	L_263	L_264	L_265	L_266	L_267	L_268	L_269	L_270	L_271	L_272	L_273	L_274	L_275	L_276	L_277	L_278	L_279	L_280	L_281	L_282	L_283	L_284	L_285	L_286	L_287	L_288	L_289	L_290	L_291	L_292	L_293	L_294	L_295	L_296	L_297	L_298	L_299	L_300	L_301	L_302	L_303	L_304	L_305	L_306	L_307	L_308	L_309	L_310	L_311	L_312	L_313	L_314	L_315	L_316	L_317	L_318	L_319	L_320	L_321	L_322	L_323	L_324	L_325	L_326	L_327	L_328	L_329	L_330	L_331	L_332	L_333	L_334	L_335	L_336	L_337	L_338	L_339	L_340	L_341	L_342	L_343	L_344	L_345	L_346	L_347	L_348	L_349	L_350	L_351	L_352	L_353	L_354	L_355	L_356	L_357	L_358	L_359	L_360	L_361	L_362	L_363	L_364	L_365	L_366	L_367	L_368	L_369	L_370	L_371	L_372	L_373	L_374	L_375	L_376	L_377	L_378	L_379	L_380	L_381	L_382	L_383	L_384	L_385	L_386	L_387	L_388	L_389	L_390	L_391	L_392	L_393	L_394	L_395	L_396	L_397	L_398	L_399	L_400	L_401	L_402	L_403	L_404	L_405	L_406	L_407	L_408	L_409	L_410	L_411	L_412	L_413	L_414	L_415	L_416	L_417	L_418	L_419	L_420	L_421	L_422	L_423	L_424	L_425	L_426	L_427	L_428	L_429	L_430	L_431	L_432	L_433	L_434	L_435	L_436	L_437	L_438	L_439	L_440	L_441	L_442	L_443	L_444	L_445	L_446	L_447	L_448	L_449	L_450	L_451	L_452	L_453	L_454	L_455	L_456	L_457	L_458	L_459	L_460	L_461	L_462	L_463	L_464	L_465	L_466	L_467	L_468	L_469	L_470	L_471	L_472	L_473	L_474	L_475	L_476	L_477	L_478	L_479	L_480	L_481	L_482	L_483	L_484	L_485	L_486	L_487	L_488	L_489	L_490	L_491	L_492	L_493	L_494	L_495	L_496	L_497	L_498	L_499	L_500	L_501	L_502	L_503	L_504	L_505	L_506	L_507	L_508	L_509	L_510	L_511	L_512	L_513	L_514	L_515	L_516	L_517	L_518	L_519	L_520	L_521	L_522	L_523	L_524	L_525	L_526	L_527	L_528	L_529	L_530	L_531	L_532	L_533	L_534	L_535	L_536	L_537	L_538	L_539	L_540	L_541	L_542	L_543	L_544	L_545	L_546	L_547	L_548	L_549	L_550	L_551	L_552	L_553	L_554	L_555	L_556	L_557	L_558	L_559	L_560	L_561	L_562	L_563	L_564	L_565	L_566	L_567	L_568	L_569	L_570	L_571	L_572	L_573	L_574	L_575	L_576	L_577	L_578	L_579	L_580	L_581	L_582	L_583	L_584	L_585	L_586	L_587	L_588	L_589	L_590	L_591	L_592	L_593	L_594	L_595	L_596	L_597	L_598	L_599	L_600	L_601	L_602	L_603	L_604	L_605	L_606	L_607	L_608	L_609	L_610	L_611	L_612	L_613	L_614	L_615	L_616	L_617	L_618	L_619	L_620	L_621	L_622	L_623	L_624	L_625	L_626	L_627	L_628	L_629	L_630	L_631	L_632	L_633	L_634	L_635	L_636	L_637	L_638	L_639	L_640	L_641	L_642	L_643	L_644	L_645	L_646	L_647	L_648	L_649	L_650	L_651	L_652	L_653	L_654	L_655	L_656	L_657	L_658	L_659	L_660	L_661	L_662	L_663	L_664	L_665	L_666	L_667	L_668	L_669	L_670	L_671	L_672	L_673	L_674	L_675	L_676	L_677	L_678	L_679	L_680	L_681	L_682	L_683	L_684	L_685	L_686	L_687	L_688	L_689	L_690	L_691	L_692	L_693	L_694	L_695	L_696	L_697	L_698	L_699	L_700	L_701	L_702	L_703	L_704	L_705	L_706	L_707	L_708	L_709	L_710	L_711	L_712	L_713	L_714	L_715	L_716	L_717	L_718	L_719	L_720	L_721	L_722	L_723	L_724	L_725	L_726	L_727	L_728	L_729	L_730	L_731	L_732	L_733	L_734	L_735	L_736	L_737	L_738	L_739	L_740	L_741	L_742	L_743	L_744	L_745	L_746	L_747	L_748	L_749	L_750	L_751	L_752	L_753	L_754	L_755	L_756	L_757	L_758	L_759	L_760	L_761	L_762	L_763	L_764	L_765	L_766	L_767	L_768	L_769	L_770	L_771	L_772	L_773	L_774	L_775	L_776	L_777	L_778	L_779	L_780	L_781	L_782	L_783	L_784	L_785	L_786	L_787	L_788	L_789	L_790	L_791	L_792	L_793	L_794	L_795	L_796	L_797	L_798	L_799	L_800	L_801	L_802	L_803	L_804	L_805	L_806	L_807	L_808	L_809	L_810	L_811	L_812	L_813	L_814	L_815	L_816	L_817	L_818	L_819	L_820	L_821	L_822	L_823	L_824	L_825	L_826	L_827	L_828	L_829	L_830	L_831	L_832	L_833	L_834	L_835	L_836	L_837	L_838	L_839	L_840	L_841	L_842	L_843	L_844	L_845	L_846	L_847	L_848	L_849	L_850	L_851	L_852	L_853	L_854	L_855	L_856	L_857	L_858	L_859	L_860	L_861	L_862	L_863	L_864	L_865	L_866	L_867	L_868	L_869	L_870	L_871	L_872	L_873	L_874	L_875	L_876	L_877	L_878	L_879	L_880	L_881	L_882	L_883	L_884	L_885	L_886	L_887	L_888	L_889	L_890	L_891	L_892	L_893	L_894	L_895	L_896	L_897	L_898	L_899	L_900	L_901	L_902	L_903	L_904	L_905	L_906	L_907	L_908	L_909	L_910	L_911	L_912	L_913	L_914	L_915	L_916	L_917	L_918	L_919	L_920	L_921	L_922	L_923	L_924	L_925	L_926	L_927	L_928	L_929	L_930	L_931	L_932	L_933	L_934	L_935	L_936	L_937	L_938	L_939	L_940	L_941	L_942	L_943	L_944	L_945	L_946	L_947	L_948	L_949	L_950	L_951	L_952	L_953	L_954	L_955	L_956	L_957	L_958	L_959	L_960	L_961	L_962	L_963	L_964	L_965	L_966	L_967	L_968	L_969	L_970	L_971	L_972	L_973	L_974	L_975	L_976	L_977	L_978	L_979	L_980	L_981	L_982	L_983	L_984	L_985	L_986	L_987	L_988	L_989	L_990	L_991	L_992	L_993	L_994	L_995	L_996	L_997	L_998	L_999	L_1000	L_1001	L_1002	L_1003	L_1004	L_1005	L_1006	L_1007	L_1008	L_1009	L_1010	L_1011	L_1012	L_1013	L_1014	L_1015	L_1016	L_1017	L_1018	L_1019	L_1020	L_1021	L_1022	L_1023	L_1024	L_1025	L_1026	L_1027	L_1028	L_1029	L_1030	L_1031	L_1032	L_1033	L_1034	L_1035	L_1036	L_1037	L_1038	L_1039	L_1040	L_1041	L_1042	L_1043	L_1044	L_1045	L_1046	L_1047	L_1048	L_1049	L_1050	L_1051	L_1052	L_1053	L_1054	L_1055	L_1056	L_1057	L_1058	L_1059	L_1060	L_1061	L_1062	L_1063	L_1064	L_1065	L_1066	L_1067	L_1068	L_1069	L_1070	L_1071	L_1072	L_1073	L_1074	L_1075	L_1076	L_1077	L_1078	L_1079	L_1080	L_1081	L_1082	L_1083	L_1084	L_1085	L_1086	L_1087	L_1088	L_1089	L_1090	L_1091	L_1092	L_1093	L_1094	L_1095	L_1096	L_1097	L_1098	L_1099	L_1100	L_1101	L_1102	L_1103	L_1104	L_1105	L_1106	L_1107	L_1108	L_1109	L_1110	L_1111	L_1112	L_1113	L_1114	L_1115	L_1116	L_1117	L_1118	L_1119	L_1120	L_1121	L_1122	L_1123	L_1124	L_1125	L_1126	L_1127	L_1128	L_1129	L_1130	L_1131	L_1132	L_1133	L_1134	L_1135	L_1136	L_1137	L_1138	L_1139	L_1140	L_1141	L_1142	L_1143	L_1144	L_1145	L_1146	L_1147	L_1148	L_1149	L_1150	L_1151	L_1152	L_1153	L_1154	L_1155	L_1156	L_1157	L_1158	L_1159	L_1160	L_1161	L_1162	L_1163	L_1164	L_1165	L_1166	L_1167	L_1168	L_1169	L_1170	L_1171	L_1172	L_1173	L_1174	L_1175	L_1176	L_1177	L_1178	L_1179	L_1180	L_1181	L_1182	L_1183	L_1184	L_1185	L_1186	L_1187	L_1188	L_1189	L_1190	L_1191	L_1192	L_1193	L_1194	L_1195	L_1196	L_1197	L_1198	L_1199	L_1200	L_1201	L_1202	L_1203	L_1204	L_1205	L_1206	L_1207	L_1208	L_1209	L_1210	L_1211	L_1212	L_1213	L_1214	L_1215	L_1216	L_1217	L_1218	L_1219	L_1220	L_1221	L_1222	L_1223	L_1224	L_1225	L_1226	L_1227	L_1228	L_1229	L_1230	L_1231	L_1232	L_1233	L_1234	L_1235	L_1236	L_1237	L_1238	L_1239	L_1240	L_1241	L_1242	L_1243	L_1244	L_1245	L_1246	L_1247	L_1248	L_1249	L_1250	L_1251	L_1252	L_1253	L_1254	L_1255	L_1256	L_1257	L_1258	L_1259	L_1260	L_1261	L_1262	L_1263	L_1264	L_1265	L_1266	L_1267	L_1268	L_1269	L_1270	L_1271	L_1272	L_1273	L_1274	L_1275	L_1276	L_1277	L_1278	L_1279	L_1280	L_1281	L_1282	L_1283	L_1284	L_1285	L_1286	L_1287	L_1288	L_1289	L_1290	L_1291	L_1292	L_1293	L_1294	L_1295	L_1296	L_1297	L_1298	L_1299	L_1300	L_1301	L_1302	L_1303	L_1304	L_1305	L_1306	L_1307	L_1308	L_1309	L_1310	L_1311	L_1312	L_1313	L_1314	L_1315	L_1316	L_1317	L_1318	L_1319	L_1320	L_1321	L_1322	L_1323	L_1324	L_1325	L_1326	L_1327	L_1328	L_1329	L_1330
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[illegible]
$$f_{\alpha}(\mathbf{z}) = \frac{1}{2} \mathbf{z}^T \mathbf{A} \mathbf{z} + \mathbf{b}^T \mathbf{z} + c, \quad \mathbf{z} \in \mathbb{R}^n, \quad \mathbf{A} \in \mathbb{R}^{n \times n}, \quad \mathbf{b} \in \mathbb{R}^n, \quad c \in \mathbb{R}.$$

[illegible]

[illegible]

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[illegible]

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PS-61325	18182-ES	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18182	S-.....TAMG	18566	WFGARSGELAWG	11414	T1858--GSGTVAASVG	11872	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12130	GGVH-.....LGRDY	12791	WQGTUJPTBS	13149
PS-61325	18182-A4	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18182	S-.....TAMT	18567	WFGARSGELAWG	11415	T1858--GSGTVAASVG	11873	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12131	GGVH-.....LGRDY	12792	WQGTUJPTBS	13150
PS-61345	18182-E1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18180	S-.....TAMG	18568	WFGARSGELAWG	11416	T1858--GSGTVAASVG	11874	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12132	GGVH-.....LGRDY	12793	WQGTUJPTBS	13151
PS-185817	18183-F12-AS	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18581	S-.....TAMG	18569	WFGARSGELAWG	11417	T1858--GSGTVAASVG	11875	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12133	GGVH-.....LGRDY	12794	WQGTUJPTBS	13152
PS-185819	18183-GH-AS	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18582	S-.....TAMG	18569	WFGARSGELAWG	11418	T1858--GSGTVAASVG	11876	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12134	GGVH-.....LGRDY	12795	WQGTUJPTBS	13153
PS-189184	18188-CJ- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18583	S-.....TAMG	18561	WFGARSGELAWG	11419	T1858--GSGTVAASVG	11877	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12135	GGVH-.....LGRDY	12796	WQGTUJPTBS	13154
PS-185866	18183-B9-AS- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18584	S-.....TAMG	18562	WFGARSGELAWG	11420	T1858--GSGTVAASVG	11878	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12136	GGVH-.....LGRDY	12797	WQGTUJPTBS	13155
PS-185866	18183-E11-AS- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18585	S-.....TAMG	18563	WFGARSGELAWG	11421	T1858--GSGTVAASVG	11879	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12137	GGVH-.....LGRDY	12798	WQGTUJPTBS	13156
PS-189185	18183-F12- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18586	S-.....TAMG	18564	WFGARSGELAWG	11422	T1858--GSGTVAASVG	11880	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12138	GGVH-.....LGRDY	12799	WQGTUJPTBS	13157
PS-189185	18183-F12-AS- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18587	S-.....TAMG	18565	WFGARSGELAWG	11423	T1858--GSGTVAASVG	11881	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12139	GGVH-.....LGRDY	12800	WQGTUJPTBS	13158
PS-189185	18183-GH- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18588	S-.....TAMG	18566	WFGARSGELAWG	11424	T1858--GSGTVAASVG	11882	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12140	GGVH-.....LGRDY	12801	WQGTUJPTBS	13159
PS-189185	18183-GH- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18589	S-.....TAMG	18567	WFGARSGELAWG	11425	T1858--GSGTVAASVG	11883	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12141	GGVH-.....LGRDY	12802	WQGTUJPTBS	13160
PS-185819	18183-GH-AS- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18590	S-.....TAMG	18568	WFGARSGELAWG	11426	T1858--GSGTVAASVG	11884	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12142	GGVH-.....LGRDY	12803	WQGTUJPTBS	13161
PS-189187	18189-GH- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18591	S-.....TAMG	18569	WFGARSGELAWG	11427	T1858--GSGTVAASVG	11885	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12143	GGVH-.....LGRDY	12804	WQGTUJPTBS	13162
PS-185897	18189-GH-AS- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18592	S-.....TAMG	18570	WFGARSGELAWG	11428	T1858--GSGTVAASVG	11886	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12144	GGVH-.....LGRDY	12805	WQGTUJPTBS	13163
PS-185897	18189-GH-AS- final	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18593	S-.....TAMG	18571	WFGARSGELAWG	11429	T1858--GSGTVAASVG	11887	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12145	GGVH-.....LGRDY	12806	WQGTUJPTBS	13164
PS-61345	18182-B1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18594	S-.....TAMG	18572	WFGARSGELAWG	11430	T1858--GSGTVAASVG	11888	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12146	GGVH-.....LGRDY	12807	WQGTUJPTBS	13165
PS-61345	18182-B1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18595	S-.....TAMG	18573	WFGARSGELAWG	11431	T1858--GSGTVAASVG	11889	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12147	GGVH-.....LGRDY	12808	WQGTUJPTBS	13166
PS-61345	18182-B1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18596	S-.....TAMG	18574	WFGARSGELAWG	11432	T1858--GSGTVAASVG	11890	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12148	GGVH-.....LGRDY	12809	WQGTUJPTBS	13167
PS-185894	18183-B1-1HR72JH4	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18597	S-.....TAMG	18575	WFGARSGELAWG	11433	T1858--GSGTVAASVG	11891	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12149	GGVH-.....LGRDY	12810	WQGTUJPTBS	13168
PS-185894	18183-B1-1HR72JH4	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18598	S-.....TAMG	18576	WFGARSGELAWG	11434	T1858--GSGTVAASVG	11892	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12150	GGVH-.....LGRDY	12811	WQGTUJPTBS	13169
PS-185894	18183-B1-1HR72JH4	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18599	S-.....TAMG	18577	WFGARSGELAWG	11435	T1858--GSGTVAASVG	11893	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12151	GGVH-.....LGRDY	12812	WQGTUJPTBS	13170
PS-61317	18179-G12	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18600	S-.....TAMG	18578	WFGARSGELAWG	11436	T1858--GSGTVAASVG	11894	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12152	GGVH-.....LGRDY	12813	WQGTUJPTBS	13171
PS-61317	18179-G1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18601	S-.....TAMG	18579	WFGARSGELAWG	11437	T1858--GSGTVAASVG	11895	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12153	GGVH-.....LGRDY	12814	WQGTUJPTBS	13172
PS-61317	18179-G1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18602	S-.....TAMG	18580	WFGARSGELAWG	11438	T1858--GSGTVAASVG	11896	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12154	GGVH-.....LGRDY	12815	WQGTUJPTBS	13173
PS-61317	18179-G1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18603	S-.....TAMG	18581	WFGARSGELAWG	11439	T1858--GSGTVAASVG	11897	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12155	GGVH-.....LGRDY	12816	WQGTUJPTBS	13174
PS-61317	18179-G1	VH13-21D06-1HR72JH4	VOULLES-OSGLVQSGELAFCHASG-PTFS	18604	S-.....TAMG	18582	WFGARSGELAWG	11440	T1858--GSGTVAASVG	11898	BP11BBSBSBSBT1ZAMNBSLBSBSBSVTCAT	12156	GGVH-.....LGRDY	12817	WQGTUJPTBS	13175

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PS-59382	17784-B9	VN1A19JN1	EL	N	FRI	13127	B.....Y.B	13785		14243		14701	A.....	15159	..37.....T.P.	15617		16078
PS-59386	17777-B1	VN2A19JN4	EL	N	FRI	13129	Y.....	13787		14245		14703		15161		15619		16082
PS-59394	17777-C3	VN2A19JN4	EL	L	B.....	13132	Y.....	13788		14246		14704		15162		15620	D.....	16084
PS-59392	17783-C11	VN2A19JN4	EL	L		13131	Y.....	13789		14247		14705		15163		15621	L.....	16082
PS-597154	17813-F1	VN2A19JN4	EL	B.....	13132			13790		14248		14706		15164		15622		16083
PS-613797	18179-A9	VN2A19JN4	EL		13133			13791		14249		14707		15165		15623		16084
PS-597471	17784-C9	VN2O1JN2	EL	N	FRI	13135	Y.B-YN-Y	13793		14251		14709		15167		15625		16086
PS-613799	18179-B6	VN2O1JN2	EL		13136			13794		14252		14710		15168		15626	G.....	16087
PS-59398	17779-B11	VN1O1JN1	EL	N	FRI	13138		13796		14254		14712		15170		15628		16089
PS-610198	18081-D12	VN1O1JN1	EL		13139			13797		14255		14713		15171		15629		16090
PS-60469	18093-E2	VN1O1JN1	EL		13140			13798		14256		14714		15172		15630	D.....	16091
PS-60466	18093-F5	VN1O1JN1	EL		13141			13799		14257		14715		15173		15631	D.....	16092
PS-1891857	18099-F12_Final	VN1O1JN1	EL		13142			13800		14258		14716		15174		15632	P.....	16093
PS-1891861	18099-H7_Final	VN1O1JN1	EL		13143			13801		14259		14717		15175		15633	P.....	16094
PS-1891863	18099-H10_Final	VN1O1JN1	EL		13144			13802		14260		14718		15176		15634	P.....	16095
PS-597857	17780-D12	VN2O1JN3	EL	N	FRI	13146	Y.B-YN-Y	13804		14262		14720		15178		15636		16097
PS-59385	17784-C9	VN2O1JN3	EL		13147			13805		14263		14721		15179		15637		16098
PS-59389	17781-B1	VN2A19JN1	EL	N	FRI	13149	Y.....	13807		14265		14723		15181		15639	D.....	16100
PS-597845	17781-D12	VN2A19JN1	EL	B.....	13150			13808		14266		14724		15182		15640	D.....	16101
PS-593018	17784-B5	VN2A19JN1	EL	L		13151	Y.....	13809		14267		14725		15183		15641	P.....	16102
PS-601108	18089-C5	VN2A19JN1	EL	L		13152		13810		14268		14726		15184		15642	R.....	16103
PS-613715	18179-F6	VN2A19JN1	EL		13153			13811		14269		14727		15185		15643		16104
PS-613881	18179-C8	VN2A19JN1	EL		13154			13812		14270		14728		15186		15644	R.....	16105
PS-613528	18181-H10	VN2A19JN1	EL		13155			13813		14271		14729		15187		15645	D.....	16106
PS-613266	18181-C10	VN2A19JN1	EL		13156			13814		14272		14730		15188		15646	R.....	16107
PS-613184	18181-E2	VN2A19JN1	EL		13157			13815		14273		14731		15189		15647	D.....	16108
PS-59384	17784-C7	VN1A30JN3	EL	N	FRI	13163		13821		14279		14737		15195		15653	B.....	16114
PS-601191	18089-H9	VN1A30JN3	EL		13164			13822		14280		14738		15196		15654		16115
PS-601153	18089-D12	VN1A30JN3	EL		13165			13823		14281		14739		15197		15655	B.....	16116
PS-613759	18179-C1	VN1A30JN3	EL		13166			13824		14282		14740		15198		15656		16117
PS-1855954	02-C186-A4-N-F5_Final	VN1A30JN3	EL		13167			13825		14283		14741		15199		15657	B.....	16118
PS-18918739	18086-A4_Final	VN1A30JN3	EL		13168			13826		14284		14742		15200		15658	B.....	16119
PS-593942	17784-C11	VN2O1JN3	EL	N	FRI	13170	Y.B-YN-Y	13828		14286		14744		15202		15660	B.....	16121
PS-597136	17813-D8	VN1A30JN1	EL	N	FRI	13172		13830		14288		14746		15204		15662		16123
PS-597150	17814-D9	VN2A19JN3	EL	N	FRI	13174	Y.B-YN-D	13832		14290		14748		15206		15664		16125
PS-601181	18071-C4	VN1B1JN1	EL		13176			13834		14292		14750		15208		15666		16127
PS-601123	18071-D4	VN1B1JN1	EL		13177			13835		14293		14751		15209		15667		16128
PS-601159	18086-H4	VN1B1JN1	EL		13178			13836		14294		14752		15210		15668	D.....	16129
PS-601201	18074-D12	VN1O1JN1	EL	N	FRI	13180		13838		14296		14754		15212		15670		16131

[illegible]

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TABLE 1

PS-61327	18082-812	V130H-012	EL	Q	Q	13489	13947	H	V	14405	D	H	14863	15321	Y	15779	16240
PS-61328	18082-82	V130H-012	EL	Q	Q	13490	13948	H	V	14406	D	H	14864	15322	Y	15780	16241
PS-61355	18082-84	V130H-012	EL	Q	Q	13491	13949	H	V	14407	D	H	14865	15323	Y	15781	16242
PS-61354	18082-81	V130H-012	EL	Q	Q	13492	13950	H	V	14408	D	H	14866	15324	Y	15782	16243
PS-185072	18083-712-AS	V130H-012	EL	Q	Q	13493	13951	H	V	14409	D	H	14867	15325	Y	15783	16244
PS-185074	18083-G10-AS	V130H-012	EL	Q	Q	13494	13952	H	V	14410	D	H	14868	15326	Y	15784	16245
PS-185068	18083-813-9-AS	V130H-012	EL	Q	Q	13495	13953	H	V	14411	D	H	14869	15327	Y	15785	16246
PS-1891847	18083-C7_Final	V130H-012	EL	Q	Q	13496	13954	H	V	14412	D	H	14870	15328	Y	15786	16247
PS-185066	18083-811-AS_Final	V130H-012	EL	Q	Q	13497	13955	H	V	14413	D	H	14871	15329	Y	15787	16248
PS-1891851	18083-712_Final	V130H-012	EL	Q	Q	13498	13956	H	V	14414	D	H	14872	15330	Y	15788	16249
PS-185072	18083-712-AS_Final	V130H-012	EL	Q	Q	13499	13957	H	V	14415	D	H	14873	15331	Y	15789	16250
PS-1891853	18083-G10_Final	V130H-012	EL	Q	Q	13500	13958	H	V	14416	D	H	14874	15332	Y	15790	16251
PS-185074	18083-G10-AS_Final	V130H-012	EL	Q	Q	13501	13959	H	V	14417	D	H	14875	15333	Y	15791	16252
PS-1891873	18083-G10_Final	V130H-012	EL	Q	Q	13502	13960	H	V	14418	D	H	14876	15334	Y	15792	16253
PS-185092	18083-G10-AS_Final	V130H-012	EL	Q	Q	13503	13961	H	V	14419	D	H	14877	15335	Y	15793	16254
PS-1891848	18083-D8_Final	V130H-012	EL	Q	Q	13504	13962	H	V	14420	D	H	14878	15336	Y	15794	16255
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13505	13963	H	V	14421	D	H	14879	15337	Y	15795	16256
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13506	13964	H	V	14422	D	H	14880	15338	Y	15796	16257
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13507	13965	H	V	14423	D	H	14881	15339	Y	15797	16258
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13508	13966	H	V	14424	D	H	14882	15340	Y	15798	16259
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13509	13967	H	V	14425	D	H	14883	15341	Y	15799	16260
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13510	13968	H	V	14426	D	H	14884	15342	Y	15800	16261
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13511	13969	H	V	14427	D	H	14885	15343	Y	15801	16262
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13512	13970	H	V	14428	D	H	14886	15344	Y	15802	16263
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13513	13971	H	V	14429	D	H	14887	15345	Y	15803	16264
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13514	13972	H	V	14430	D	H	14888	15346	Y	15804	16265
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13515	13973	H	V	14431	D	H	14889	15347	Y	15805	16266
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13516	13974	H	V	14432	D	H	14890	15348	Y	15806	16267
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13517	13975	H	V	14433	D	H	14891	15349	Y	15807	16268
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13518	13976	H	V	14434	D	H	14892	15350	Y	15808	16269
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13519	13977	H	V	14435	D	H	14893	15351	Y	15809	16270
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13520	13978	H	V	14436	D	H	14894	15352	Y	15810	16271
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13521	13979	H	V	14437	D	H	14895	15353	Y	15811	16272
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13522	13980	H	V	14438	D	H	14896	15354	Y	15812	16273
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13523	13981	H	V	14439	D	H	14897	15355	Y	15813	16274
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13524	13982	H	V	14440	D	H	14898	15356	Y	15814	16275
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13525	13983	H	V	14441	D	H	14899	15357	Y	15815	16276
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13526	13984	H	V	14442	D	H	14900	15358	Y	15816	16277
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13527	13985	H	V	14443	D	H	14901	15359	Y	15817	16278
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13528	13986	H	V	14444	D	H	14902	15360	Y	15818	16279
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13529	13987	H	V	14445	D	H	14903	15361	Y	15819	16280
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13530	13988	H	V	14446	D	H	14904	15362	Y	15820	16281
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13531	13989	H	V	14447	D	H	14905	15363	Y	15821	16282
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13532	13990	H	V	14448	D	H	14906	15364	Y	15822	16283
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13533	13991	H	V	14449	D	H	14907	15365	Y	15823	16284
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13534	13992	H	V	14450	D	H	14908	15366	Y	15824	16285
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13535	13993	H	V	14451	D	H	14909	15367	Y	15825	16286
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13536	13994	H	V	14452	D	H	14910	15368	Y	15826	16287
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13537	13995	H	V	14453	D	H	14911	15369	Y	15827	16288
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13538	13996	H	V	14454	D	H	14912	15370	Y	15828	16289
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13539	13997	H	V	14455	D	H	14913	15371	Y	15829	16290
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13540	13998	H	V	14456	D	H	14914	15372	Y	15830	16291
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13541	13999	H	V	14457	D	H	14915	15373	Y	15831	16292
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13542	14000	H	V	14458	D	H	14916	15374	Y	15832	16293
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13543	14001	H	V	14459	D	H	14917	15375	Y	15833	16294
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13544	14002	H	V	14460	D	H	14918	15376	Y	15834	16295
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13545	14003	H	V	14461	D	H	14919	15377	Y	15835	16296
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13546	14004	H	V	14462	D	H	14920	15378	Y	15836	16297
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13547	14005	H	V	14463	D	H	14921	15379	Y	15837	16298
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13548	14006	H	V	14464	D	H	14922	15380	Y	15838	16299
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13549	14007	H	V	14465	D	H	14923	15381	Y	15839	16300
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13550	14008	H	V	14466	D	H	14924	15382	Y	15840	16301
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13551	14009	H	V	14467	D	H	14925	15383	Y	15841	16302
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13552	14010	H	V	14468	D	H	14926	15384	Y	15842	16303
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13553	14011	H	V	14469	D	H	14927	15385	Y	15843	16304
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13554	14012	H	V	14470	D	H	14928	15386	Y	15844	16305
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13555	14013	H	V	14471	D	H	14929	15387	Y	15845	16306
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13556	14014	H	V	14472	D	H	14930	15388	Y	15846	16307
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13557	14015	H	V	14473	D	H	14931	15389	Y	15847	16308
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13558	14016	H	V	14474	D	H	14932	15390	Y	15848	16309
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13559	14017	H	V	14475	D	H	14933	15391	Y	15849	16310
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13560	14018	H	V	14476	D	H	14934	15392	Y	15850	16311
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13561	14019	H	V	14477	D	H	14935	15393	Y	15851	16312
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13562	14020	H	V	14478	D	H	14936	15394	Y	15852	16313
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13563	14021	H	V	14479	D	H	14937	15395	Y	15853	16314
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13564	14022	H	V	14480	D	H	14938	15396	Y	15854	16315
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13565	14023	H	V	14481	D	H	14939	15397	Y	15855	16316
PS-185094	18083-D8-AS_Final	V130H-012	EL	Q	Q	13566	14024	H	V	14482	D	H	14940	15398	Y	15	

PS-97906	1778-F1	VH04-30J035-10R7J016	B...L...	13542	14000	M	14058		14916		15374	D.....	15833		16333
PS-97901	1778-B8	VH04-30J035-10R7J016	B...L...	13543	14001		14059	R.....	14917	A.....	15375	D.....	15834		16334
PS-97900	1779-E1	VH04-30J035-10R7J016	B...L...	13544	14002		14060		14918		15376	D.....	15835		16335
PS-97902	1778-C11	VH04-30J035-10R7J016	B...L...	13545	14003		14061		14919		15377	D.....	15836		16336
PS-97918	1778-A5	VH04-30J035-10R7J016	B...L...	13546	14004		14062		14920	P.....	15378	D.....	15837		16337
PS-97903	1778-D12	VH04-30J035-10R7J016	B...L...	13547	14005	M	14063		14921		15379	D.....	15838		16338
PS-97916	1783-E5	VH04-30J035-10R7J016	B...L...	13548	14006		14064		14922		15380	D.....	15839		16339
PS-93189	1808-B4	VH04-30J035-10R7J016	B...L...	13549	14007		14065		14923		15381	D.....	15840		16340
PS-97902	1771-B2	VH04-30J035-10R7J016	B...L...	13550	14008		14066		14924		15382	D.....	15841		16341
PS-93201	1807-A12	VH04-30J035-10R7J016	B...L...	13551	14009		14067		14925		15383	D.....	15842		16342
PS-93205	1809-D12	VH04-30J035-10R7J016	B...L...	13552	14010		14068		14926		15384	D.....	15843		16343
PS-93206	1809-E2	VH04-30J035-10R7J016	B...L...	13553	14011		14069		14927		15385	D.....	15844		16344
PS-93195	1808-B2	VH04-30J035-10R7J016	B...L...	13554	14012		14070		14928		15386	D.....	15845		16345
PS-97902	1778-B9	VH04-30J035-10R7J016	B...L...	13555	14013		14071		14929		15387	D.....	15846		16346
PS-93204	1784-C7	VH04-30J035-10R7J016	B...L...	13556	14014		14072		14930		15388	D.....	15847		16347
PS-93199	1809-B9	VH04-30J035-10R7J016	B...L...	13557	14015		14073		14931		15389	D.....	15848		16348
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13558	14016		14074		14932		15390	D.....	15849		16349
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13559	14017		14075		14933		15391	D.....	15850		16350
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13560	14018		14076		14934		15392	D.....	15851		16351
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13561	14019		14077		14935		15393	D.....	15852		16352
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13562	14020		14078		14936		15394	D.....	15853		16353
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13563	14021		14079		14937		15395	D.....	15854		16354
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13564	14022		14080		14938		15396	D.....	15855		16355
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13565	14023		14081		14939		15397	D.....	15856		16356
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13566	14024		14082		14940		15398	D.....	15857		16357
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13567	14025		14083		14941		15399	D.....	15858		16358
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13568	14026		14084		14942		15400	D.....	15859		16359
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13569	14027		14085		14943		15401	D.....	15860		16360
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13570	14028		14086		14944		15402	D.....	15861		16361
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13571	14029		14087		14945		15403	D.....	15862		16362
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13572	14030		14088		14946		15404	D.....	15863		16363
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13573	14031		14089		14947		15405	D.....	15864		16364
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13574	14032		14090		14948		15406	D.....	15865		16365
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13575	14033		14091		14949		15407	D.....	15866		16366
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13576	14034		14092		14950		15408	D.....	15867		16367
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13577	14035		14093		14951		15409	D.....	15868		16368
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13578	14036		14094		14952		15410	D.....	15869		16369
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13579	14037		14095		14953		15411	D.....	15870		16370
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13580	14038		14096		14954		15412	D.....	15871		16371
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13581	14039		14097		14955		15413	D.....	15872		16372
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13582	14040		14098		14956		15414	D.....	15873		16373
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13583	14041		14099		14957		15415	D.....	15874		16374
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13584	14042		14100		14958		15416	D.....	15875		16375
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13585	14043		14101		14959		15417	D.....	15876		16376
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13586	14044		14102		14960		15418	D.....	15877		16377
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13587	14045		14103		14961		15419	D.....	15878		16378
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13588	14046		14104		14962		15420	D.....	15879		16379
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13589	14047		14105		14963		15421	D.....	15880		16380
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13590	14048		14106		14964		15422	D.....	15881		16381
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13591	14049		14107		14965		15423	D.....	15882		16382
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13592	14050		14108		14966		15424	D.....	15883		16383
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13593	14051		14109		14967		15425	D.....	15884		16384
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13594	14052		14110		14968		15426	D.....	15885		16385
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13595	14053		14111		14969		15427	D.....	15886		16386
PS-93197	1817-A5	VH04-30J035-10R7J016	B...L...	13596	14054		14112		14970		15428	D.....	15887		16387

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TABLE 1 (continued)

PS-613222	18181-A6	YH3-10103-10R2J06	...L.....Q.....	13452	14110	14568	...OH...Y.....	15026		15484	PS-6087.....R.FW...	15945		16410
PS-1891855	18189-F2 [final]	YH3-10103-10R2J06	...Q.....Q.....	13453	14111	14569	...Y.....	15027	F.....	15485	PS-6087.....R.FW...	15946		16411
PS-1891861	18191-B6 [final]	YH3-10103-10R2J06	...Q.....Q.....	13454	14112	14570	...R.FW...Y.....	15028	P.....	15486	PS-6087.....R.FW...	15947		16412
PS-1891867	18191-B6 [final]	YH3-10103-10R2J06	...Q.....Q.....	13455	14113	14571	...Y.....Y.....	15029		15487	PS-6087.....R.FW...	15948		16413
PS-1891869	18191-B1 [final]	YH3-10103-10R2J06	...Q.....Q.....	13456	14114	14572	...T.HH...Y.....	15030	F.....	15488	PS-6087.....R.FW...	15949		16414
PS-1891871	18191-B6 [final]	YH3-10103-10R2J06	...Q.....Q.....	13457	14115	14573	...1000...Y.....	15031		15489	PS-6087.....R.FW...	15950		16415
PS-1891875	18191-H1 [final]	YH3-10103-10R2J06	...Q.....Q.....	13458	14116	14574	...T.G1...Y.....	15032		15490	PS-6087.....R.FW...	15951		16416
PS-1891877	18191-H1 [final]	YH3-10103-10R2J06	...Q.....Q.....	13459	14117	14575	...R.FW...Y.....	15033		15491	PS-6087.....R.FW...	15952		16417
Continued														
PS-613879	18179-F3	YH4-50103-10R2J06	...L.....T.....	13461	14119	14577	...H.....H.....	15035		15493	PS-6087.....R.FW...	15954		16419
PS-613731	18179-F10	YH4-50103-10R2J06	...L.....T.....	13462	14120	14578	...R.....H.....	15036	T.L.....	15494	PS-6087.....R.FW...	15955		16420
PS-613586	18181-H10	YH4-50103-10R2J06	...L.....N.....	13463	14121	14579	...H.....F.....	15037	T.L.....	15495	PS-6087.....R.FW...	15956		16421
Continued														
PS-613561	18182-A3	YH3-21006-10R2J04	...D.....D.....	13465	14123	14581	...G.....G.....	15039		15497	PS-6087.....R.FW...	15958		16423
PS-613551	18182-A5	YH3-21006-10R2J04	...D.....D.....	13466	14124	14582	...G.....G.....	15040		15498	PS-6087.....R.FW...	15959		16424
PS-613591	18182-A6	YH3-21006-10R2J04	...D.....D.....	13467	14125	14583	...T.....G.....	15041		15499	PS-6087.....R.FW...	15960		16425
PS-613819	18182-A7	YH3-21006-10R2J04	...D.....D.....	13468	14126	14584	...G.....G.....	15042		15500	PS-6087.....R.FW...	15961		16426
PS-613573	18182-A8	YH3-21006-10R2J04	...D.....D.....	13469	14127	14585	...G.N.....G.....	15043	A.VT.....	15501	PS-6087.....R.FW...	15962		16427
PS-613513	18182-A11	YH3-21006-10R2J04	...D.....D.....	13470	14128	14586	...G.....G.....	15044		15502	PS-6087.....R.FW...	15963		16428
PS-613529	18182-B1	YH3-21006-10R2J04	...D.....D.....	13471	14129	14587	...G.N.....G.....	15045		15503	PS-6087.....R.FW...	15964		16429
PS-613503	18182-B4	YH3-21006-10R2J04	...D.....D.....	13472	14130	14588	...G.....A.....	15046		15504	PS-6087.....R.FW...	15965		16430
PS-613817	18182-B6	YH3-21006-10R2J04	...D.....D.....	13473	14131	14589	...G.....G.....	15047		15505	PS-6087.....R.FW...	15966		16431
PS-613843	18182-C2	YH3-21006-10R2J04	...D.....D.....	13474	14132	14590	...G.....G.....	15048		15506	PS-6087.....R.FW...	15967		16432
PS-613897	18182-C3	YH3-21006-10R2J04	...D.....D.....	13475	14133	14591	...G.....G.....	15049		15507	PS-6087.....R.FW...	15968		16433
PS-613571	18182-C4	YH3-21006-10R2J04	...D.....D.....	13476	14134	14592	...G.....G.....	15050		15508	PS-6087.....R.FW...	15969		16434
PS-613521	18182-C5	YH3-21006-10R2J04	...D.....D.....	13477	14135	14593	...G.....G.....	15051		15509	PS-6087.....R.FW...	15970		16435
PS-613521	18182-C10	YH3-21006-10R2J04	...D.....D.....	13478	14136	14594	...G.....G.....	15052		15510	PS-6087.....R.FW...	15971		16436
PS-613529	18182-C12	YH3-21006-10R2J04	...D.....D.....	13479	14137	14595	...G.....G.....	15053		15511	PS-6087.....R.FW...	15972		16437
PS-613529	18182-C12	YH3-21006-10R2J04	...D.....D.....	13480	14138	14596	...G.....G.....	15054		15512	PS-6087.....R.FW...	15973		16438
PS-613549	18182-D4	YH3-21006-10R2J04	...D.....D.....	13481	14139	14597	...G.....G.....	15055		15513	PS-6087.....R.FW...	15974		16439
PS-613445	18182-D8	YH3-21006-10R2J04	...D.....D.....	13482	14140	14598	...G.....G.....	15056		15514	PS-6087.....R.FW...	15975		16440
PS-613537	18182-D9	YH3-21006-10R2J04	...D.....D.....	13483	14141	14599	...G.....G.....	15057		15515	PS-6087.....R.FW...	15976		16441
PS-613541	18182-D11	YH3-21006-10R2J04	...D.....D.....	13484	14142	14600	...G.....G.....	15058		15516	PS-6087.....R.FW...	15977		16442
PS-613857	18182-E2	YH3-21006-10R2J04	...D.....D.....	13485	14143	14601	...G.....G.....	15059		15517	PS-6087.....R.FW...	15978		16443
PS-613519	18182-E3	YH3-21006-10R2J04	...D.....D.....	13486	14144	14602	...G.....G.....	15060		15518	PS-6087.....R.FW...	15979		16444
PS-613596	18182-E8	YH3-21006-10R2J04	...D.....D.....	13487	14145	14603	...G.....G.....	15061		15519	PS-6087.....R.FW...	15980		16445
PS-613567	18182-E11	YH3-21006-10R2J04	...D.....D.....	13488	14146	14604	...G.....A.....	15062		15520	PS-6087.....R.FW...	15981		16446
PS-613529	18182-F1	YH3-21006-10R2J04	...D.....D.....	13489	14147	14605	...G.....G.....	15063		15521	PS-6087.....R.FW...	15982		16447
PS-613531	18182-F6	YH3-21006-10R2J04	...D.....D.....	13490	14148	14606	...G.....G.....	15064		15522	PS-6087.....R.FW...	15983		16448
PS-613523	18182-F8	YH3-21006-10R2J04	...D.....D.....	13491	14149	14607	...G.....G.....	15065		15523	PS-6087.....R.FW...	15984		16449
PS-613841	18182-G3	YH3-21006-10R2J04	...D.....D.....	13492	14150	14608	...G.....G.....	15066		15524	PS-6087.....R.FW...	15985		16450
PS-613527	18182-G4	YH3-21006-10R2J04	...D.....D.....	13493	14151	14609	...G.....G.....	15067		15525	PS-6087.....R.FW...	15986		16451
PS-613551	18182-G5	YH3-21006-10R2J04	...D.....D.....	13494	14152	14610	...G.N.....G.....	15068	A.VT.....	15526	PS-6087.....R.FW...	15987		16452
PS-613525	18182-G9	YH3-21006-10R2J04	...D.....D.....	13495	14153	14611	...G.....G.....	15069		15527	PS-6087.....R.FW...	15988		16453
PS-613589	18182-G11	YH3-21006-10R2J04	...D.....D.....	13496	14154	14612	...G.....G.....	15070		15528	PS-6087.....R.FW...	15989		16454
PS-613887	18182-H5	YH3-21006-10R2J04	...D.....D.....	13497	14155	14613	...G.N.....G.....	15071	A.VT.....	15529	PS-6087.....R.FW...	15990		16455
PS-613599	18182-H8	YH3-21006-10R2J04	...D.....D.....	13498	14156	14614	...G.....G.....	15072		15530	PS-6087.....R.FW...	15991		16456
PS-613567	18182-H9	YH3-21006-10R2J04	...D.....D.....	13499	14157	14615	...G.....G.....	15073		15531	PS-6087.....R.FW...	15992		16457
PS-613583	18182-J6	YH3-21006-10R2J04	...D.....D.....	13500	14158	14616	...G.....G.....	15074		15532	PS-6087.....R.FW...	15993		16458
PS-613566	18182-J8	YH3-21006-10R2J04	...D.....D.....	13501	14159	14617	...G.....G.....	15075	A.VT.....	15533	PS-6087.....R.FW...	15994		16459
PS-613847	18182-K2	YH3-21006-10R2J04	...D.....D.....	13502	14160	14618	...G.N.....G.....	15076		15534	PS-6087.....R.FW...	15995		16460
PS-613817	18182-K12	YH3-21006-10R2J04	...D.....D.....	13503	14161	14619	...G.....G.....	15077		15535	PS-6087.....R.FW...	15996		16461
PS-613523	18182-L8	YH3-21006-10R2J04	...D.....D.....	13504	14162	14620	...G.....G.....	15078		15536	PS-6087.....R.FW...	15997		16462
PS-613521	18182-E10	YH3-21006-10R2J04	...D.....D.....	13505	14163	14621	...G.....A.....	15079		15537	PS-6087.....R.FW...	15998		16463
PS-613527	18182-B12	YH3-21006-10R2J04	...D.....D.....	13506	14164	14622	...G.....G.....	15080		15538	PS-6087.....R.FW...	15999		16464

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Table 64
scFv Full Sequences

iPS#	Ab	Type	scFv
iPS:1262018 18398-C7		NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCCGGATTCACTTTAGCAGCCATG CCATGAGCTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCT CGTCTATTAGTGGTAGCGGTGGTGGCACATACTACGCAGCCTCCCGTGAA GGCCCGTTCAACCATCTCCAGAGACAAATTCCAAGAACACGCTGTATCTG CAAATGAACAGC
		AA	(SEQ ID NO: 16485) EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSSI SGSGGGTYAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTTLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMMVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWDYSPLRHVFVGGGKLTIVL
			(SEQ ID NO: 16486)

iPS:1262596 18403-D1		NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTGACTACTA CATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTC ATACATTAGTAAAGTGGTAGTACCATATATACTACGCAGACTCTGTGAAG GGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 16487) EVQLLESGGGLVKPGGSLRLSCAASGFTTFSDYYMSWIRQAPGKGLEWVSYI SKSGSTIYYADSVKGRFTISRDNNAKNSLYLQMNSLRAEDTAVYYCATYNY GHFDYWGGQGLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQTAR ITCGGNNIGSKSVHWYQQKPGQAPVLYVYDDSDRPSGIPERFSGNSGNTA TLTISRVEAGDEADYYCQVVDSSLSYGTVFGGGTKLTVL (SEQ ID NO: 16488)

iPS:1262762	18403-D8	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AACTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAAATCCAAAGAACACGGCTGTATCTG CAATGAACAGC
		AA	(SEQ ID NO: 16489) EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSTI SGSGGGTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNFG NTATLIISRVEAGDEADYYCQVWDYRITLDWVFGGGTKLTVL (SEQ ID NO: 16490)

iPS:1262774 18403-E11		NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGACATACAACGCAGACTCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
		AA	(SEQ ID NO: 16491) EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCVTGK GVHLGFDYW'GQGTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNIGSKSVHWYQQKPGQAPV'MVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVWDYYSNRAVFGGGTKLTVL (SEQ ID NO: 16492)

iPS:1262602	18403-F3	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGTTAAAGCCTGGGGGG TCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTGACTACTA CATGAGCTGGATCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTC ATACATTAGTAAAGTAGCTACACCGTCACGTACGCAGACTCTGTGAAG GGCCGATTCACCATCTCCAGGGACAACGCCAAGAACTCACTGTATCTGC AAATGAACAGC
		AA	(SEQ ID NO: 16493) EVQLLESGGGLVKPGGSLRLSCAASGFTFSDDYYMSWIRQAPGKGLEWVSYI SKSSYTVTYADSVKGRFTISRDNAKNSLYLQMNSLR AEDTAVYYCATYNY GHFDYWGGQGLTVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQTAR ITCGGNNIGSKSVHWYQQKPGQAPVLYVYDDSDRPSGIPERFSGNSGNTA TLTISRVEAGDEADYYCQVVDASAGYGVVFGGGTKLTVL (SEQ ID NO: 16494)

iPS:1262788 18403-G10		NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGAAGTGGTGGTGGCACATACTACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAGCAGC
		AA	(SEQ ID NO: 16495) EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSA ISGSGGGTYADSVKGRFTISRDN SKNTLYLQMSSLRAEDTAVYYCATGKG VHLGFDYWGGTLLVTVSSGGGGGGGGGGSELVLTQPPSVSVAPGQT ARITCGGNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNSG NTATLTISRVEAGDEADYYCQVWVDYSGQRQVFGGTKLTVL (SEQ ID NO: 16496)

iPS:1270705	18409-E2	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTTAGACTCTCTGTGTGCAAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGG CCGTATTAAAGCAAACTTATGGTGGGACAACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAAACACGCT GTTTCTGCAATG
		AA	(SEQ ID NO: 16497) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIKSKTYGGTTDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCTT PSYSGSYNYFVMDVWVGQTTTVSSGGGGGGGGGGGGSELVMTQS PSSLASVGDRTITCRTSQSSSYLNWYQQKPGRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQSYSSPFTFGPGTKVEIK (SEQ ID NO: 16498)

iPS:1270679	18409-F12	NA	GAGGTGCAGCTGCTCGAGTCTGGTCTGCGCTGGTGAACCCACACAG ACCTCAGCTGACCTGACCTTCTCTGGTTCTCATTCACCACTCATAA AATGGGTGTGACTGGATCCGTAGCCCCCAGGAAAGGCCCTGGAGTG GCTTGCACTCATTATTGGAATGATGATAAGCGCTACAGCCCATCTCTG CAGAGTAGGCTCACCATCACCAGGACACCTCCAAAAAACCAAGGTGGTC CTCACAATGACC
		AA	(SEQ ID NO: 16499) EVQLLESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRR YNWNYENWFDPPWGQGLTVVSSGGGGGGGGGGSELQMTQSPSSLS ASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYAASLQSGVPSRFS GRSGTDFTLTISLQPEDFATYYCQQSYYYPTLFGPGTKVEIK (SEQ ID NO: 16500)

iPS:1270671 18409-G10		NA	GAGGTGCAGCTGCTCGAGTCTGGTCTACGCTGGTGAACCCACACAG ACCCTCAGCGTGACCTGCACCTTCTCTGGTTTCTCATTCACCACTCATAA AATGGGTGTGGAAGTGGATCCGTCAGCCCCCAGGAAAGGCCCTGGAGTG GCTTGCAGGGATCCACATCTACGATGATAAGCGCTACAGCCCCATCTCTG CAGAGTAGGCTCACCATCACCAGGACACCTCCAAAAAACCAAGGTGGTC CTCACAATGACC
		AA	(SEQ ID NO: 16501) EVQLLESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA GIHIYDDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRRY NWNYENWFDPPW/GQGTLVTVSSGGGGGGGGGGSELQMTQSPSSLSA SVGDRVTITCQASQDISNYFNWYQQKPKAPKLLIYAASLQSGVPSRFSGS GSGTDFTLTISSLQPEDFATYYCQQSYITPFTFGPGTKVEIK (SEQ ID NO: 16502)

iPS:1270663 18409-H7		NA	GAGGTGCAGCTGCTCGAGTCTGGTCTCTGCGCTGGTGAACCCACACAG ACCTCAGCTGACCTGACCTTCTCTGGTTTCTCATTCACCACTCATAA AATGGGTGTGACTGGATCCGTAGCCCCCAGGAAAGGCCCTGGAGTG GCTTGCACTCATTATTGGAATGATGATAAGCGCTACAGCCCATCTCTG CAGAGTAGGCTCACCATCACCAAGGACACCTCCAAAAAACCAAGGTGGTC CTCACAATGACC
		AA	(SEQ ID NO: 16503) EVQLLESGPALVKPTQTTLTCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDDKRYSPSLQSRLTITKDTSKNQVVLMTNMDPVDATYYCAYRR YNWNYENWFDPWGQGLTVSSGGGGGGGGGGSELQMTQSPSSL ASVGDRTITCQASQDISNYLNWYQQKPGKAPKLLIYAASLQSGVPSRFS GSGGTDFTLTISLQPEDFATYYCQQSYFPVVEFGPGTKVEIK (SEQ ID NO: 16504)

iPS:1270745	18410-G10	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCCATGC CATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTGGCACATACAACGCAGACTCCCGTGAA GGCCCGGTTCAACCATCTCCAGAGACAATTCCAAGAACACGGCTGTATCTG CAATGAACAGC
		AA	(SEQ ID NO: 16505) EVQLLESGGGLVQPGGSLRLSCAASGFTTSSHAMSWVRQAPGKGLEWVSA ISGSGGGTYNADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGGQTLVTVSSGGGGGGGGGGSEL VLTQPPSVSVAPGQ TARITCGGNNIGSKSVHWYQQKPGQAPVMVYDDNDRPSGIPERFSGSNS GNTATLTISRVEAGDEADYYCQVWDYVAPRHVFGGGTKLTVL (SEQ ID NO: 16506)

iPS:1270743 18410-H1	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTTAGACTCTCTGTGTGAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCGCCAGGCTCCAGGGAAGGGTTGGAGTGGGTTGG CCGCATTACGTCCGGCATCTATGGTGGGACAAACAGACTACGCTGCACCC GTGAAAGGCAGATTCACCCATCTCAAGAGATGATTCAAAAAACACGCTG TATCTGCAAAATG
		(SEQ ID NO: 16507)
	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPKGLEWVG RITSGIYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYNFSVMDVWGQGTTVTVSSGGGGGGGGGGSELVMTQS PSSLASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQSGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQTYSMPTFTFGPGTKVDIK
		(SEQ ID NO: 16508)

iPS:1270739 18410-H3	NA	GAGGTGCAGCTGCTCGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGG TCCCTGAGACTCTCTGTGCAGCCTCTGGATTCACTTTCAGTAACGCCTG GATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGG CCGATTAGGAGCAGGCCCTATGGTGGGACAACAGACTACGCTGCACC CGTGAAAGGCAGATTCAACCATCTCAAGAGATGATTCAAAAAACACGCT GTATCTGCAATG
		(SEQ ID NO: 16509)
	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RIRSRPYGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT PSYSGSYNYFSVMDVWQGTTTVSSGGGGGGGGGGSELQMTQS PSSLASVGDRTITCRTSQSISSYLNWYQQKPKRAPKLLIFAASSLQGGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQTYSSPFTFGPGTKLEIK
		(SEQ ID NO: 16510)

Table 65
scFv VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:1262018 18398-C7		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTG CAC (SEQ ID NO: 16511)	GATGATAACGACCGGCCCTCA (SEQ ID NO: 16563)	CAGGTGTGGGATTATAGCCCCCTTGAGGCACG TA (SEQ ID NO: 16615)
		AA	GGNIGSKSVH (SEQ ID NO: 16512)	DDNDRPS (SEQ ID NO: 16564)	QVWDYSPRHV (SEQ ID NO: 16616)
		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTG CAC (SEQ ID NO: 16513)	GATGATACGACCGGCCCTCA (SEQ ID NO: 16565)	CAGGTGTGGGACTCTAGTCTGTCTACGGGA CGTA (SEQ ID NO: 16617)
IPS:1262596 18403-D1		AA	GGNIGSKSVH (SEQ ID NO: 16514)	DDSDRPS (SEQ ID NO: 16566)	QVWDSSLSYGV (SEQ ID NO: 16618)
		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTG CAC (SEQ ID NO: 16515)	GATGATAACGACCGGCCCTCA (SEQ ID NO: 16567)	CAGGTGTGGGATTATCGCACGCTCGACTGGG TA (SEQ ID NO: 16619)
		AA	GGNIGSKSVH (SEQ ID NO: 16516)	DDNDRPS (SEQ ID NO: 16568)	QVWDYRTLDWV (SEQ ID NO: 16620)
IPS:1262774 18403-E11		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTG CAC (SEQ ID NO: 16517)	GATGATAACGACCGGCCCTCA (SEQ ID NO: 16569)	CAGGTGTGGGATTATTACTCCACAGGGCCG TA (SEQ ID NO: 16621)
		AA	GGNIGSKSVH (SEQ ID NO: 16518)	DDNDRPS (SEQ ID NO: 16570)	QVWDYYSNRAV (SEQ ID NO: 16622)
		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTG CAC (SEQ ID NO: 16519)	GATGATACGACCGGCCCTCA (SEQ ID NO: 16571)	CAGGTGTGGGACGCTAGTGGGGGTACGGG GTCGTA (SEQ ID NO: 16623)
IPS:1262602 18403-F3		AA	GGNIGSKSVH (SEQ ID NO: 16520)	DDSDRPS (SEQ ID NO: 16572)	QVWDASAGYGV (SEQ ID NO: 16624)
		NA	GGGGAAACAACATTGGAAAGTAAAAAGTGTG CAC (SEQ ID NO: 16521)	GATGATAACGACCGGCCCTCA (SEQ ID NO: 16573)	CAGGTGTGGGATTATTCGGGGCAGAGCAG GTA (SEQ ID NO: 16625)
		AA	GGNIGSKSVH (SEQ ID NO: 16522)	DDNDRPS (SEQ ID NO: 16574)	QVWDYSGQRQV (SEQ ID NO: 16626)
IPS:1270705 18409-E2		NA	CGGACAAGTCAGAGCATTAGCAGCTATTTA AAT (SEQ ID NO: 16523)	GCTGCATCCAGTTTGCAAGGT (SEQ ID NO: 16575)	CAACAGAGTTACAGTAGTCCATTCACT (SEQ ID NO: 16627)
		AA	RTSQSISSYLN (SEQ ID NO: 16524)	AASSLOG (SEQ ID NO: 16576)	QQSYSSPFT (SEQ ID NO: 16628)
		NA	CAGCGAGTCAGGACATTAGCAACTATTTA AAT (SEQ ID NO: 16525)	GCTGCATCCAGTTTGCAAGGT (SEQ ID NO: 16577)	CAACAGAGTTACTACTCCACCACCTC (SEQ ID NO: 16629)
IPS:1270679 18409-F12		AA	QASQDISNYLN (SEQ ID NO: 16526)	AASSLOS (SEQ ID NO: 16578)	QQSYYYPTL (SEQ ID NO: 16630)
		NA	CAGCGAGTCAGGACATTAGCAACTATTTA AT (SEQ ID NO: 16527)	GCTGCATCCAGTTTGCAAGGT (SEQ ID NO: 16579)	CAACAGAGTTACATTACCCTCGTTCACT (SEQ ID NO: 16631)
		AA	QASQDISNYFN (SEQ ID NO: 16528)	AASSLOS (SEQ ID NO: 16580)	QQSYITPFT (SEQ ID NO: 16632)

iPS:1270663	18409-H7	NA	CAGGCGAGTCAGGACATTAGCAACTATTTA AAT (SEQ ID NO: 16529)	GCTGCATCCAGTTTGCAAAGT (SEQ ID NO: 16581)	CAACAGAGTTACTTCCCGTCGTCGAG (SEQ ID NO: 16633)
		AA	QASQDISNYLN (SEQ ID NO: 16530)	AASSLQS (SEQ ID NO: 16582)	QOSYFPVVE (SEQ ID NO: 16634)
iPS:1270745	18410-G10	NA	GGGGAAACAACATTTGGAAGTAAAGTGTG CAC (SEQ ID NO: 16531)	GATGATAACGACCGGCCCTCA (SEQ ID NO: 16583)	CAGGTGTGGGATTATGTGGCGCCGAGGCAC GTA (SEQ ID NO: 16635)
		AA	GNNIGSKSVH (SEQ ID NO: 16532)	DDNDRPS (SEQ ID NO: 16584)	QVWDYVAPRHV (SEQ ID NO: 16636)
iPS:1270743	18410-H1	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT (SEQ ID NO: 16533)	GCTGCATCCAGTTTGCAAAGT (SEQ ID NO: 16585)	CAACAGACTTACAGTATGCCAATCACT (SEQ ID NO: 16637)
		AA	RTSQSISSYLN (SEQ ID NO: 16534)	AASSLQS (SEQ ID NO: 16586)	QQTYSPFT (SEQ ID NO: 16638)
iPS:1270739	18410-H3	NA	CGGACAAAGTCAGAGCATTAGCAGCTATTTA AAT (SEQ ID NO: 16535)	GCTGCATCCAGTTTGCAAAGT (SEQ ID NO: 16587)	CAACAGACTTACAGTATGCCAATCACT (SEQ ID NO: 16639)
		AA	RTSQSISSYLN (SEQ ID NO: 16536)	AASSLQS (SEQ ID NO: 16588)	QQTYSPFT (SEQ ID NO: 16640)

Table 66
scFv VH CDRs

iPS#	Ab	Type	CDR1	CDR2	CDR3
iPS:1262018	18398-C7	NA	AGCCATGCATGAGC (SEQ ID NO: 16537)	TCTATTAGTGTAGCGGTGGGCACATATCT ACGCAGCCTCCGTGAAGGGC (SEQ ID NO: 16589)	GGAAAGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 16641)
		AA	SHAMS (SEQ ID NO: 16538)	SISGGGTYYAASVKG (SEQ ID NO: 16590)	GKGVHLGFDY (SEQ ID NO: 16642)
iPS:1262596	18403-D1	NA	GACTACTACATGAGC (SEQ ID NO: 16539)	TACATTAGTAAAGTGGTAGTACCATATATCT ACGCAGACTCTGTGAAGGGC (SEQ ID NO: 16591)	TACAACTATGGTCACTTTGACTAC (SEQ ID NO: 16643)
		AA	DYYMS (SEQ ID NO: 16540)	YISKSGSTIYADSVKG (SEQ ID NO: 16592)	YNYGHFDY (SEQ ID NO: 16644)
iPS:1262762	18403-D8	NA	AGCCATGCATGAGC (SEQ ID NO: 16541)	ACTATTAGTGAAGTGGTGGGCACATATCT ACGCAGACTCCGTGAAGGGC (SEQ ID NO: 16593)	GGAAAGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 16645)
		AA	SHAMS (SEQ ID NO: 16542)	TISGGGTYYADSVKG (SEQ ID NO: 16594)	GKGVHLGFDY (SEQ ID NO: 16646)
iPS:1262774	18403-E11	NA	AGCCATGCATGAGC (SEQ ID NO: 16543)	GCTATTAGTGAAGTGGTGGGCACATAC ACGCAGACTCCGTGAAGGGC (SEQ ID NO: 16595)	GGAAAGGAGTACATCTGGGCTTTGACTAC (SEQ ID NO: 16647)
		AA	SHAMS (SEQ ID NO: 16544)	AISGGGTYYNADSVKG (SEQ ID NO: 16596)	GKGVHLGFDY (SEQ ID NO: 16648)
iPS:1262602	18403-F3	NA	GACTACTACATGAGC (SEQ ID NO: 16545)	TACATTAGTAAAGTAGTACACCGTCACGT ACGCAGACTCTGTGAAGGGC (SEQ ID NO: 16597)	TACAACTATGGTCACTTTGACTAC (SEQ ID NO: 16649)
		AA	DYYMS (SEQ ID NO: 16546)	YISKSYTYIYADSVKG (SEQ ID NO: 16598)	YNYGHFDY (SEQ ID NO: 16650)

IPS:1262788	18403-G10	NA	AGCTATGCCATGAGC	GCTATTAGTGGAAAGTGGTGGTGCCACATAC	GGAAAGGAGTACATCTGGGCTTTGACTAC
		AA	(SEQ ID NO: 16547)	ACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 16651)
		NA	SYAMS	(SEQ ID NO: 16599)	GKGVHLGFDY
IPS:1270705	18409-E2	AA	(SEQ ID NO: 16548)	AISGSGGTYADSVK	(SEQ ID NO: 16652)
		NA	AACGCCTGGATGAGC	CGTATTAAAGCAAACTTATGGTGGACA	CCTTCGTATAGTGGAGCTATTATAATTACT
		NA	ACAGACTAGCTGCAACCCGTGAAAGGC	ACAGACTAGCTGCAACCCGTGAAAGGC	TCTCCGTTATGGACGTC
IPS:1270679	18409-F12	AA	(SEQ ID NO: 16549)	(SEQ ID NO: 16601)	(SEQ ID NO: 16653)
		AA	NAWMS	RIKSKTYGGTIDYAAPVK	PSYSGSYNYFVSMDV
		NA	(SEQ ID NO: 16550)	(SEQ ID NO: 16602)	(SEQ ID NO: 16654)
IPS:1270671	18409-G10	AA	ACTCATAAAATGGGTGTGGAC	CTCATTATTGGAATGATGATAAGCGCTACA	AGACGGTATAACTGGAACTAGGAGAACTGG
		NA	THKMGVD	GCCCATCTCTGCAGAGT	ITCGACCCC
		AA	(SEQ ID NO: 16551)	(SEQ ID NO: 16603)	(SEQ ID NO: 16655)
IPS:1270663	18410-H7	AA	THKMGVD	LIYWDDDKRYSPSLQS	RRYNNWNYENWFD
		NA	(SEQ ID NO: 16552)	(SEQ ID NO: 16604)	(SEQ ID NO: 16656)
		AA	ACTCATAAAATGGGTGTGGAC	GGGATCCACATCTACGATGATAAGCGCTAC	AGACGGTATAACTGGAACTAGGAGAACTGG
IPS:1270745	18410-G10	AA	THKMGVD	AGCCCATCTCTGCAGAGT	ITCGACCCC
		NA	(SEQ ID NO: 16553)	(SEQ ID NO: 16605)	(SEQ ID NO: 16657)
		AA	THKMGVD	GHYDDDKRYSPSLQS	RRYNNWNYENWFD
IPS:1270743	18410-H1	AA	(SEQ ID NO: 16554)	(SEQ ID NO: 16606)	(SEQ ID NO: 16658)
		NA	ACTCATAAAATGGGTGTGGAC	CTCATTATTGGAATGATGATAAGCGCTACA	AGACGGTATAACTGGAACTAGGAGAACTGG
		AA	THKMGVD	GCCCATCTCTGCAGAGT	ITCGACCCC
IPS:1270739	18410-H3	AA	(SEQ ID NO: 16555)	(SEQ ID NO: 16607)	(SEQ ID NO: 16659)
		NA	THKMGVD	LIYWDDDKRYSPSLQS	RRYNNWNYENWFD
		AA	(SEQ ID NO: 16556)	(SEQ ID NO: 16608)	(SEQ ID NO: 16660)
IPS:1270743	18410-H1	AA	AGCCATGCCATGAGC	GCTATTAGTGGTGGTGGTGCCACATACA	GGAAAGGAGTACATCTGGGCTTTGACTAC
		NA	(SEQ ID NO: 16557)	ACGCAGACTCCGTGAAGGGC	(SEQ ID NO: 16661)
		AA	SHAMS	AISGSGGTYNADSVK	GKGVHLGFDY
IPS:1270743	18410-H1	AA	(SEQ ID NO: 16558)	(SEQ ID NO: 16610)	(SEQ ID NO: 16662)
		NA	AACGCCTGGATGAGC	CGCATTAGTCCGCATCTATGGTGGACA	CCTTCGTATAGTGGAGCTATTATAATTACT
		NA	ACAGACTAGCTGCAACCCGTGAAAGGC	CAGACTAGCTGCAACCCGTGAAAGGC	TCTCCGTTATGGACGTC
IPS:1270739	18410-H3	AA	(SEQ ID NO: 16559)	(SEQ ID NO: 16611)	(SEQ ID NO: 16663)
		AA	NAWMS	RITSGIYGGTIDYAAPVK	PSYSGSYNYFVSMDV
		NA	(SEQ ID NO: 16560)	(SEQ ID NO: 16612)	(SEQ ID NO: 16664)
IPS:1270739	18410-H3	AA	AACGCCTGGATGAGC	CGGATTAGGAGCAGCGCTATGGTGGACA	CCTTCGTATAGTGGAGCTATTATAATTACT
		NA	ACAGACTAGCTGCAACCCGTGAAAGGC	ACAGACTAGCTGCAACCCGTGAAAGGC	TCTCCGTTATGGACGTC
		AA	(SEQ ID NO: 16561)	(SEQ ID NO: 16613)	(SEQ ID NO: 16665)
IPS:1270739	18410-H3	AA	NAWMS	RIRSRPYGGTIDYAAPVK	PSYSGSYNYFVSMDV
		NA	(SEQ ID NO: 16562)	(SEQ ID NO: 16614)	(SEQ ID NO: 16666)

Table 67
scFv Variable Region Sequences

IPS#	Ab	Type	LC V-region	HC V-region
IPS:1262018 18398-C7		NA	GAGCTGCTGCTGACTCAGCCACCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAACAGAAGCAGGCCAGGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	GAGGTGCAGCTGCTGAGTCCGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCCGGATTACCTTTAGCAGCCAT GCCATGAGTGGTCCGCGAGCTCCAGGAAAGGGCTGGAGTGGGT CTCGTCTATTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGGCCGGTTCACCATCTCCAGAGACAAATTCGAAGAACACCTGT TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 16667) ELVLTPPPSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSLRHVF GGGTKLTVL	(SEQ ID NO: 16693) EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWSVRQAPKGLWVVS ISGSGGTYYAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGK GVHLGFDYWGQGTILVTSS
IPS:1262596 18403-D1		NA	GAGCTGCTGCTGACTCAGCCGCCCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAACAAGCAGGCCAGGCCCTGTGATGGTCTGCTA TGATGATAGGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	GAGGTGCAGCTGCTGAGTCCGGGGAGGCTTGGTAAAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCCGGATTACCTTTAGCAGTAC TACATGAGTGGTCCGCGAGCTCCAGGAAAGGGCTGGAGTGGGT TCATACATTAGTAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT AAGGGCCGATTACCATCTCCAGGACAAACGCAAGAACTCACTGTAT CTGCAAAATGAACAGC
		AA	(SEQ ID NO: 16669) ELVLTPPPSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSLSYGTVFG GGTKLTVL	(SEQ ID NO: 16695) EVQLLESGGGLVQPGSLRLSCAASGFTFSYIMSWIRQAPKGLWVVS ISKSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCATYN YGHFDYWGQGTILVTSS
IPS:1262762 18403-D8		NA	GAGCTGCTGCTGACTCAGCCACCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAGTGT GCACTGGTACCAACAAGCAGGCCAGGCCCTGTGATGGTCTGCTA TGATGATAACGACCGGCCCTCAGGATCCCTGAGCGATTCTCTGGCTC CAACTTTGGGAACACGGCCACCTGATTATCAGTAGGGTCGAAGCCCG GGATGAGGCCGACTAT	GAGGTGCAGCTGCTGAGTCCGGGGAGGCTTGGTACAGCCTGGGG GTCCCTGAGACTCTCTGTGAGCCTCCGGATTACCTTTAGCAGCCAT GCCATGAGTGGTCCGCGAGCTCCAGGAAAGGGCTGGAGTGGGT CTCAACTATTAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT GAAGGGCCGGTTCACCATCTCCAGAGACAAATTCGAAGAACACCTGT TCTGCAAAATGAACAGC
		AA	(SEQ ID NO: 16671) ELVLTPPPSVAPGQTARITCGNNIGSKSVHWYQKPGQAPVMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYRILDWVF GGGTKLTVL	(SEQ ID NO: 16697) EVQLLESGGGLVQPGSLRLSCAASGFTFSHAMSWSVRQAPKGLWVS ITISGSGGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATG KGVHLGFDYWGQGTILVTSS
			(SEQ ID NO: 16672)	(SEQ ID NO: 16698)

PS:1262774 18403-E11	NA	GAGCTCGTCTGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATAAACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACTGGTACCAACAGAAAGCCAGCCAGCCCTGTGATGTCTGCTCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCTCGAAGCCG GGGATGAGGCCCGACTAT	(SEQ ID NO: 16673 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYYSNRAVF GGGTKLTVL	(SEQ ID NO: 16674 GAGCTCGTCTGACTCAGCCGCCCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATTACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAAGAACAGCCAGCCAGCCCTGTGCTGTGCTGCTA TGATGATAGCAGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCTCGAAGCCG GGGATGAGGCCCGACTAT	(SEQ ID NO: 16675 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVLMVYDD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDASAGYGVVF GGGTKLTVL	(SEQ ID NO: 16676 GAGCTCGTGTGACGCAAGCCGCCCTCGGTGTCAGTGGCCCCAGGACAG ACGGCCAGGATAAACCTGTGGGGAAACAACATTGGAAGTAAAAGTGT GCACCTGGTACCAAGAACAGCCAGCCAGCCCTGTGATGGTCTGCTA TGATGATAACGACCGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCTCGAAGCCG GGGATGAGGCCCGACTAT																																																																														
	AA		(SEQ ID NO: 16677 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16678 GAGCTCGTGTATGACCCAGCTCCATCTCCCTGCTGCTGCTGATCTGAGGAG ACAGAGTCACCATCACTTGGCGGACAAGTCAGAGCAATTAGAGCTATT TAAATTGGTATCAGCAGAAACAGGGAGAGCCCTAAGCTCTGTGATCT TTGCTGATCAGTTTGCAAGGTGGGGTCCCATCAAGGTTTCAGTGGCA GTGGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCACT	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL																																																																														
	NA		(SEQ ID NO: 16678 GAGCTCGTGTATGACCCAGCTCCATCTCCCTGCTGCTGCTGATCTGAGGAG ACAGAGTCACCATCACTTGGCGGACAAGTCAGAGCAATTAGAGCTATT TAAATTGGTATCAGCAGAAACAGGGAGAGCCCTAAGCTCTGTGATCT TTGCTGATCAGTTTGCAAGGTGGGGTCCCATCAAGGTTTCAGTGGCA GTGGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCACT	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL																																																																														
	AA		(SEQ ID NO: 16677 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16678 GAGCTCGTGTATGACCCAGCTCCATCTCCCTGCTGCTGCTGATCTGAGGAG ACAGAGTCACCATCACTTGGCGGACAAGTCAGAGCAATTAGAGCTATT TAAATTGGTATCAGCAGAAACAGGGAGAGCCCTAAGCTCTGTGATCT TTGCTGATCAGTTTGCAAGGTGGGGTCCCATCAAGGTTTCAGTGGCA GTGGATCTGGGACAGATTTCATCTCTCACCATCAGCAGTCTGCAACCTG AAGATTTTGCACT	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL	(SEQ ID NO: 16679 ELVLTOPPSVSAPGQTARITCGGNNIGSKSVHWHYQQRKPGQAPVMMVYD SDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVF GGGTKLTVL																																																																													
PS:1262788 18403-G10	NA	GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCCAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATYN YGHFDYWQQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 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CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATTAGTGGAAAGTGGTGGCGACATACACCGAGACTCTCGT GAAGGCGCGGTTCACCATCTCCAGAGACAATTCGAAGAACACGCTGTA TCTGCAATGAGCAGC	(SEQ ID NO: 16703 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPQKGLEWVS AISGSGGTYYADSVKGRFTISRDNKSNLYLQMNSLR AEDTAVYYCATG KGVHLGFDYWGQGITLVTS	(SEQ ID NO: 16702 GAGTGCAGCTGCTCGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTGCAGCCTCTGGATTCACTTTAGCAGCTAT GCCATGAGCTGGGTCCGCGAGGCTCCAGGGAAGGGCTGGAGTGGGT CTCAGCTATT

PS:12/7067918409-F12	AA	ELVMTQSPSSLASVGDRLVITTCRTSOSISSYLNWYQOKPGRAPKLLIFAA SLOGGVPSRFSGSGTDFLTISSLQPEDFATYYCQSYSSPFTFGPGTKV EIK	(SEQ ID NO: 16680)	GAGCTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCAGGCGAGTCAGGACATTAGCAACTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCACTGGCC GTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTG AAGAATTTGCAACT	(SEQ ID NO: 16706)	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSVVRQAPGKGLEWVG RUKSKTYGGTIDYAAPVKGRFTISRDDSKNTLFLQMNSLKTEDTAVYYCT TPSYSGSYNYSFVMDVWVGQGTITVTSS	
	NA					GAGGTGCAGCTGCTCGAGTCTGGTCTCGCTGGTGAAACCCACACAG ACCTCAGCTGACCTGCACCTTCTCTGGTTTCTCATTCACCACTCAT AAATTGGGTGTGAGCTGATCGGTACAGCCCGCAGAAAGCCCTGGAGT GGCTTGCACTCAATTTATTTGGAATGATGATAAGCGCTACAGCCCATCTCT GCAGATAGCTCACCATCACCACCAAGGACACCTCCAAAAACCAAGGTGGT CCTCACAAATGACC	
PS:12/7067118409-G10	AA	ELQMTQSPSSLASVGDRLVITTCQASQDISNLYNWYQOKPGRAPKLLIYAA SSLQSGVPSRFSGRSGTDFLTISSLQPEDFATYYCQSYYPYPTLFGPGTK VEIK	(SEQ ID NO: 16681)	GAGTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCAGGCGAGTCAGGACATTAGCAACTATT TCAATTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCACTGGCA GTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTG AAGAATTTGCAACT	(SEQ ID NO: 16707)	EVQLLESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLLITTKDTSKNQVVLTMTNMDPVDITATYYCAYR RYNWNENWFDPPWVGQGTILVTSS	
	NA					(SEQ ID NO: 16708)	GAGGTGCAGCTGCTCGAGTCTGGTCTACGCTGGTGAAACCCACACAG ACCTCAGCTGACCTGCAGCTGCACCTTCTCTGGTTTCTCATTCACCACTCAT AAATTGGGTGTGAGCTGATCGGTACAGCCCGCAGAAAGCCCTGGAGT GGCTTGCAAGGATCCACATCTACGATGATAAGCGCTACAGCCCATCTC TGCAGATGAGCTCACCATCACCACCAAGGACACCTCCCAAAAAACCAAGGTGG TCCTCACAAATGACC
PS:12/7066318409-H7	AA	ELQMTQSPSSLASVGDRLVITTCQASQDISNLYNWYQOKPGRAPKLLIYAA SSLQSGVPSRFSGSGTDFLTISSLQPEDFATYYCQSYPTPFTFGPGTKV EIK	(SEQ ID NO: 16683)	GAGTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCAGGCGAGTCAGGACATTAGCAACTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCACTGGCA GTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTG AAGAATTTGCAACT	(SEQ ID NO: 16709)	EVQLLESGPTLVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA GHIHYDDKRYSPSLQSRLLITTKDTSKNQVVLTMTNMDPVDITATYYCAYRR YNWNENWFDPPWVGQGTILVTSS	
	NA					(SEQ ID NO: 16710)	GAGGTGCAGCTGCTCGAGTCTGGTCTCGCTGGTGAAACCCACACAG ACCTCAGCTGACCTGCAGCTGCACCTTCTCTGGTTTCTCATTCACCACTCAT AAATTGGGTGTGAGCTGATCGGTACAGCCCGCAGAAAGCCCTGGAGT GGCTTGCACTCAATTTATTTGGAATGATGATAAGCGCTACAGCCCATCTCT GCAGATAGCTCACCATCACCACCAAGGACACCTCCAAAAACCAAGGTGGT CCTCACAAATGACC
	AA	ELQMTQSPSSLASVGDRLVITTCQASQDISNLYNWYQOKPGRAPKLLIYAA SSLQSGVPSRFSGSGTDFLTISSLQPEDFATYYCQSYFPVVEFGPGTK VEIK	(SEQ ID NO: 16685)	GAGTCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAG ACAGAGTCACCATCACTTGCAGGCGAGTCAGGACATTAGCAACTATT TAAATTGGTATCAGCAGAAACAGGAAAGCCCTAAGCTCCTGATCT ATGCTGCATCCAGTTTGCAAAGTGGGTCCCATCAAGGTTCACTGGCA GTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAGTCTGCAACCTG AAGAATTTGCAACT	(SEQ ID NO: 16711)	EVQLLESGPALVKPTQTLTLCTFSGFSFTTHKMGVDWIRQPPGKALEWLA LIYWNDKRYSPSLQSRLLITTKDTSKNQVVLTMTNMDPVDITATYYCAYR RYNWNENWFDPPWVGQGTILVTSS	
						(SEQ ID NO: 16712)	

iPS:1270745 18410-G10	NA	GAGCTCGTGTGACGCAGCCGCCCTCGGTGTCAAGTGGCCCGACGACAG ACGCCAGGATTACCTCTGGGGAACAACATTGGAACTAAAGTGT GCATGTGATCAACAAGACGAGCCAGCCCTGTGATGGTCTGCTCA TGATGATAACGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTC CAACTCTGGGAACACGGCCACCCTGACCATCAGCAGGGTCGAAGCCG GGGATGAGGCCGACTAT	(SEQ ID NO: 16687) ELVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVMVVYD DNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQWVDYVAPRHVF GGGTKLTVL	(SEQ ID NO: 16713) EVQLLESGGGLVQPGGSLRLSCAASGFTFSHAMSWVRQAPGKGLEWVS AISGSGGTYNADSVKGRFTISRDNKNILYLQMSLRAEDTAVYYCATG KGVHLGFDYWQGQTLVTSS	GAGGTGCAGCTCTCTGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTGAGACTCTCTCTGTCAGCCCTCGGATTCACCTTAGCAGCCAT GCCATGAGCTGGGTCCGCAAGGCTCCAGGGAAGGGCTTGGAGTGGGT CTCAGCTATTAGTGGTAGTGGTGGCACATACAAACGACAGCTCCGT GAAGGCCGGTTCACCATCTCCAGAGACAAATTCGAAGAACACGCTGTGA TCTGCAATGAACAGC
	AA				
		NA	GAGCTCGTGTGACCCAGTCTCCATCTCCCTGTCTGCACTCTGTAGGAG ACAGAGTCACCATCACTTCCGGAACAAGTCAGAGCAITTAGCAGCTATT TAAATTGGTATCAGCAGAAACGAGGAGAGCCCTAAGCTCTCTGATCT TTGCTGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGTTTCAGTGGCA GTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACTG AAGATTTTGCACCT	(SEQ ID NO: 16688)	(SEQ ID NO: 16714) GAGGTGCAGCTCTCTGAGTCCGGGGAGGCTTGGTACAGCTGGGGG GTCCCTTAGACTCTCTCTGTCAGCCCTCGGATTCACCTTAGTAACGCC TGGATGAGCTGGGTCCGCAAGGCTCCAGGGAAGGGTTCGAGTGGGT GGCCGATTAACGTCCGGCATCTATGTGGGACAAACAGACTACGCTGCA CCCGTGAAGGACAGATTCACCATCTCAAGAGATGATTCAAAAAACACG CTGTATCTGCAAAATG
iPS:1270743 18410-H1	AA	ELVMTQSPSSLASVGDVVTITRTSQSISSYLNWYQKPGRAPKLLIFAA SLQSGVPSRFSGSGSDFTLTISLQPEDFATYYCQTYSPMPTFGPTKVI DIK	(SEQ ID NO: 16689)	(SEQ ID NO: 16715) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVG RITSGYGGTTDYAAPVKGRFTISRDDSKNLTLYQMSLKTEDTAVYYCTT PSYSGSYNYFVSVMVDVWQGQTLTVSS	
	NA				
iPS:1270739 18410-H3	AA	ELQMTQSPSSLASVGDVVTITRTSQSISSYLNWYQKPGRAPKLLIFAA SLQGGVPSRFSGSGSDFTLTISLQPEDFATYYCQTYSPPTFGPTKLH IK	(SEQ ID NO: 16691)	(SEQ ID NO: 16717) EVQLLESGGGLVQPGGSLRLSCAASGFTFSNAWMSWVRQAPGKLEWVC RIRSRPYGGTTDYAAPVKGRFTISRDDSKNLTLYQMSLKTEDTAVYYCT TPSYSGSYNYFVSVMVDVWQGQTLTVSS	

Table 65
4th Variable Region Primers Alignment
CDRs defined by Kabat
Alignment numbering defined by Angen References (Ato)

KAPPA VARIABLE									
GENOTYPE	K. FRI	SEQ ID NO.	K. CDR1	SEQ ID NO.	K. FRS	SEQ ID NO.	K. CDR2	SEQ ID NO.	K. FPM
PS-127903 18409-E2	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-127903 18409-G10	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-127912 18410-H1	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-127907 18409-F12	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-127963 18409-H7	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-127912 18410-H3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK

TABLE 66

KAPPA VARIABLE									
GENOTYPE	L. FRI	SEQ ID NO.	L. CDR1	SEQ ID NO.	L. FRS	SEQ ID NO.	L. CDR2	SEQ ID NO.	L. FPM
PS-126918 18408-C7	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-D1	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-E11	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-F3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-G10	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-H3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK

TABLE 70

KAPPA VARIABLE									
GENOTYPE	H. FRI	SEQ ID NO.	H. CDR1	SEQ ID NO.	H. FRS	SEQ ID NO.	H. CDR2	SEQ ID NO.	H. FPM
PS-126918 18408-C7	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-D1	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-E11	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-F3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-G10	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-H3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK

TABLE 71

KAPPA VARIABLE									
GENOTYPE	L. FRI	SEQ ID NO.	L. CDR1	SEQ ID NO.	L. FRS	SEQ ID NO.	L. CDR2	SEQ ID NO.	L. FPM
PS-126918 18408-C7	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-D1	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-E11	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-F3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-G10	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK
PS-126918 18408-H3	BLMTGSPGSIAGAGVGGVITTC	16733	QAS--QD18-----STDM	16792	WTQGFQDAKALLAF	16796	A-----ASLADP	16848	PGAGTATVTLK

[illegible]592

Table 78

scFv Full Sequences

iPS#	Ab	Type	SCFV
iPS:598065	I2E	NA	<i>No nuc. seq available</i>
			(SEQ ID NO: ***)
		AA	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNNLKTEDTAV YYCARAGNFGSSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTITCGSSTGAVTSGNYPNWVQKKPGQAPRGLIG GTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWV FGSGTKLTVL
			(SEQ ID NO: 17223)

Table 79

scFv VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:598065 12E		NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17224)	GTKFLAP (SEQ ID NO: 17226)	VLWYSNRWV (SEQ ID NO: 17228)

scFv VH CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:598065 12E		NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
		AA	KYAIN (SEQ ID NO: 17225)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 17227)	AGNFGSSYISYWAY (SEQ ID NO: 17229)

Table 80
scFv Variable Region Sequences

IPS#	Ab	Type	LC V-region	HC V-region
IPS:598065 12E		NA	<i>Sequence not available</i>	<i>Sequence not available</i>
		AA	QTVVITQEPSLTVSPGGTIVITTCGSSITGAVTSGNYPNWVQKPGQAPRGII	EVQLVESGGGLVQPGGSLKLSCAAASGFTFNKYAINWVRQAPGKGLEWV
			IGGTFKLAPGTPARFSGLSGGKAALTLGVPQPEDEAEYYCVLWYSNRWV	ARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYVYLMNNILKTEDTAVY
			VFGSGTKLTIVL	YCARAGNFGSSYISYWAYWGQGILVTYSS
			(SEQ ID NO: 17230)	(SEQ ID NO: 17231)

Table S1
Hypervariable Region Protein Alignment
CDRs defined by Kabat
Alignment numbering defined by Angen Reference (A16)

LIGHT VARIABLE									
	Germline	L FR1	L CDR1	L FR2	L CDR2	L FR3	L CDR3	L FR4	SEQ ID NO.
PS:59866	VL774L36	QTVVTQE-PLTVSEPGTVETTC	SSST-QAVTSQ---NIPR	WQKRFQAPRGLIG	Q-----TRGLAP	TFARFESFASG--GRAAATLSGQFQDGAETC	VIANKS-----	FQSTFETVTL	17256
12E	VL774L36	QTVVTQE-PLTVSEPGTVETTC	SSST-QAVTSQ---NIPR	WQKRFQAPRGLIG	Q-----TRGLAP	TFARFESFASG--GRAAATLSGQFQDGAETC	VIANKS-----	FQSTFETVTL	17257
HEAVY VARIABLE									
	Germline	H FR1	H CDR1	H FR2	H CDR2	H FR3	H CDR3	H FR4	SEQ ID NO.
PS:59866	VH33-73/D21-21/RF2JH4	YQQRFS-GRATVQFQSHVAFSGGSG-FTT	E-----TALN	WQKAPFQILAEVYA	RTERT-NTATATTAGAVND	FTTSGDSSTVTLQNNILKSTQNTATTCAR	AMVYSS-----TLEWAT	WQQLVLTVES	17258
12E	VH33-73/D21-21/RF2JH4	YQQRFS-GRATVQFQSHVAFSGGSG-FTT	E-----TALN	WQKAPFQILAEVYA	RTERT-NTATATTAGAVND	FTTSGDSSTVTLQNNILKSTQNTATTCAR	AMVYSS-----TLEWAT	WQQLVLTVES	17259

Table 62
Table 62: Variable Region Consensus Protein Alignment
CDRs defined by Kabat
Alignment numbering defined by Angen Reference (A16)

LAMBDA VARIABLE									
	Germline	L FR1	SEQ ID NO.	L CDR1	SEQ ID NO.	L FR2	SEQ ID NO.	L CDR2	SEQ ID NO.
PS:598065	VL779L3b	E.....	17261	G.....N.....	17265	V.K.....G.G	17269	G.....KELAP	17273
12E									
HEAVY VARIABLE									
	Germline	H FR1	SEQ ID NO.	H CDR1	SEQ ID NO.	H FR2	SEQ ID NO.	H CDR2	SEQ ID NO.
PS:598065	VH33-73/D21-21/HP2JH4		17283	K.....L.N	17287	P.....A	17291	T.N.....T.Ga.TD	17295
12E									
LAMBDA VARIABLE									
	Germline	L FR1	SEQ ID NO.	L CDR1	SEQ ID NO.	L FR2	SEQ ID NO.	L CDR2	SEQ ID NO.
PS:598065	VL779L3b	E.....	17261	G.....N.....	17265	V.K.....G.G	17269	G.....KELAP	17273
12E									
HEAVY VARIABLE									
	Germline	H FR1	SEQ ID NO.	H CDR1	SEQ ID NO.	H FR2	SEQ ID NO.	H CDR2	SEQ ID NO.
PS:598065	VH33-73/D21-21/HP2JH4		17283	K.....L.N	17287	P.....A	17291	T.N.....T.Ga.TD	17295
12E									

Table 83
scFv scFc Full Sequences

iPS#	Ab	Type	SCFV SCFC
		NA	<i>No data was available</i>
iPS:281203 8	12E_x_scFc_variant__	AA	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWY ARIRSKYNNYATYYADA VKDRFTISRDDSKNTVYLQMNLLKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTSSGGGSGGGSGGGGSSQT VVTOEPSLTVSPGGTVTITCGSTGAVTSGNYPNWVQKKPGQAPRGLIG GTKFLAPGTPARFSGSLSGKKAALTLGVPQPEDEAEYYCVLWYSNRWV FGSGTKLTVLGGGDKTHTCPCPAPELLGGPSVFLPPPKPKDLYITRE PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYCKVSNKALPAPIEKTKSKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPGKG GGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG VFLPPPKPKDLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEAL HNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 17288) <i>No data was available</i>
iPS:280817 3	12E_x_scFc__	AA	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWY ARIRSKYNNYATYYADA VKDRFTISRDDSKNTVYLQMNLLKTEDTAV YYCARAGNFGSSYISYWAYWGQGTILVTSSGGGSGGGSGGGGSSQT VVTOEPSLTVSPGGTVTITCGSTGAVTSGNYPNWVQKKPGQAPRGLIG GTKFLAPGTPARFSGSLSGKKAALTLGVPQPEDEAEYYCVLWYSNRWV FGSGTKLTVLGGGDKTHTCPCPAPELLGGPSVFLPPPKPKDLYITRE PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCV SVLTVLHQDWLNGKEYCKVSNKALPAPIEKTKSKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSKLTVDKSRWQQGNVFSVSMHEALHNHYTQKSLSLSPGKG GGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG VFLPPPKPKDLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSVSMHEAL HNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 17289) <i>No data was available</i>

Table 84

scFv scFc VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:281203 8	12E_x_scFc_variant__	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17290)	GTKFLAP (SEQ ID NO: 17294)	VLWYSNRWV (SEQ ID NO: 17298)
IPS:280817 3	12E_x_scFc__	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17291)	GTKFLAP (SEQ ID NO: 17295)	VLWYSNRWV (SEQ ID NO: 17299)

scFv scFc VH CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:281203 8	12E_x_scFc_variant__	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KYAIN (SEQ ID NO: 17292)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 17296)	AGNFGSSYISYWAY (SEQ ID NO: 17300)
IPS:280817 3	12E_x_scFc__	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	KYAIN (SEQ ID NO: 17293)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 17297)	AGNFGSSYISYWAY (SEQ ID NO: 17301)

Table 85
scFv scFc Variable Region Sequences

IPS#	Ab	Type	LC V-region	HC V-region
IPS:281203 8	12E_x_scFc_variant__	NA	No seq. seq. available	No seq. seq. available
		AA	QIVVITQEPSSLTVSPGGTIVTITCGSSITGAVTSGNYPNWVQKKPGQAPRGII IGGTFKLAPGTPARFSGLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRW VFGSGTKLTVL (SEQ ID NO: 17302)	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYVYLMNNILKTEDTAVY YCARAGNFGSSYSYWAYWVGQGITLVTVSS (SEQ ID NO: 17304)
		NA	No seq. seq. available	No seq. seq. available
IPS:280817 3	12E_x_scFc__	AA	QIVVITQEPSSLTVSPGGTIVTITCGSSITGAVTSGNYPNWVQKKPGQAPRGII IGGTFKLAPGTPARFSGLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRW VFGSGTKLTVL (SEQ ID NO: 17303)	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYVYLMNNILKTEDTAVY YCARAGNFGSSYSYWAYWVGQGITLVTVSS (SEQ ID NO: 17305)

Table S6
CDRs Variable Region Protein Alignment
CDRs defined by Kabat
Alignment numbering defined by Angen Reference (A16)

LIGHT VARIABLE									
	Sequence	L_FBI	SEQ ID NO.	L_CDR1	SEQ ID NO.	L_CDR2	SEQ ID NO.	L_FBI	SEQ ID NO.
PS-28130	VL77aJL3b	QTVVQGF-PGLTVSGPQVTVTC	17307	SSST-QAVTSQ---NTPR	17313	WQKRFQAPRGLIG	17319	FPAPFSSLSGG-GRAAATLSGQVQDGRATC	17331
PS-28687	VL77aJL3b	QTVVQGF-PGLTVSGPQVTVTC	17308	SSST-QAVTSQ---NTPR	17314	WQKRFQAPRGLIG	17320	FPAPFSSLSGG-GRAAATLSGQVQDGRATC	17332
3									
HEAVY VARIABLE									
	Sequence	H_FBI	SEQ ID NO.	H_CDR1	SEQ ID NO.	H_CDR2	SEQ ID NO.	H_FBI	SEQ ID NO.
PS-28130	VL77aJL3b	WQKRFQAPRGLIG	17310	K-----IAIN	17316	RIKENT-NHATVYAGAVND	17322	FTTSSGDSNATVYLGNNILKTSQAVTCAR	17334
PS-28687	VL77aJL3b	WQKRFQAPRGLIG	17311	K-----IAIN	17317	RIKENT-NHATVYAGAVND	17323	FTTSSGDSNATVYLGNNILKTSQAVTCAR	17335
3									
LIGHT VARIABLE									
	Sequence	L_FBI	SEQ ID NO.	L_CDR1	SEQ ID NO.	L_CDR2	SEQ ID NO.	L_FBI	SEQ ID NO.
PS-28130	VL77aJL3b	QTVVQGF-PGLTVSGPQVTVTC	17307	SSST-QAVTSQ---NTPR	17313	WQKRFQAPRGLIG	17319	FPAPFSSLSGG-GRAAATLSGQVQDGRATC	17331
PS-28687	VL77aJL3b	QTVVQGF-PGLTVSGPQVTVTC	17308	SSST-QAVTSQ---NTPR	17314	WQKRFQAPRGLIG	17320	FPAPFSSLSGG-GRAAATLSGQVQDGRATC	17332
3									
HEAVY VARIABLE									
	Sequence	H_FBI	SEQ ID NO.	H_CDR1	SEQ ID NO.	H_CDR2	SEQ ID NO.	H_FBI	SEQ ID NO.
PS-28130	VL77aJL3b	WQKRFQAPRGLIG	17310	K-----IAIN	17316	RIKENT-NHATVYAGAVND	17322	FTTSSGDSNATVYLGNNILKTSQAVTCAR	17334
PS-28687	VL77aJL3b	WQKRFQAPRGLIG	17311	K-----IAIN	17317	RIKENT-NHATVYAGAVND	17323	FTTSSGDSNATVYLGNNILKTSQAVTCAR	17335
3									

Table S7
S7
CDRs defined by Kabat
Alignment numbering defined by Angen Reference (A16)

LIGHT VARIABLE									
	L_F1	SEQ ID NO.	L_CDR1	SEQ ID NO.	L_F2	SEQ ID NO.	L_CDR2	SEQ ID NO.	SEQ ID NO.
PS:28130	E.....	17348	G.....N.....	17355	V.K.....G..	17361	G.....KELAP	17373	17384
12E_x_eFc_variant_									
PS:28687	E.....	17350	G.....N.....	17356	V.K.....G..	17362	G.....KELAP	17374	17386
12E_x_eFc_									
3									
HEAVY VARIABLE									
	H_F1	SEQ ID NO.	H_CDR1	SEQ ID NO.	H_F2	SEQ ID NO.	H_CDR2	SEQ ID NO.	SEQ ID NO.
PS:28130	E.....	17352	K.....L.....	17358	P.....A	17364	Y..M..Y..G..G	17376	17387
12E_x_eFc_variant_									
PS:28687	E.....	17353	K.....L.....	17359	P.....A	17365	Y..M..Y..G..G	17377	17388
12E_x_eFc_									
3									

Table 88
BiTE-scFc Full Sequences

iPS#	Ab	Type	BiTE_scFc
		NA	<i>No nuc. seq. available</i>
iPS:2306863	MA_03-G10_AS_CC_x_I2C0_x_scFc_	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKCLEWVSAISGSGGGTYYAASVKGRFTISRDNKNTLYLQMSSLR AEDTA VYYCATGKGVHLGFDYWGQGITLVTVSSGGGGSGGGSGGGSSSYVLTQPPSVVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVMVYDDNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFCGKTLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTFNKYAMINWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTA VYYCVVRHGNFGNSYISYWAYWGQGITLVTVSSGGGGSGGGGGSGGQT VVTQEPSTVTVSPGTVTLTCGSSTGAVTSGNYPNWVQOKPGQAPRGLIGGKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNATKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 17390) <i>No nuc. seq. available</i>
iPS:2810773	MA_03-G10_AS_CC_x_I2E_x_scFc_	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKCLEWVSAISGSGGGTYYAASVKGRFTISRDNKNTLYLQMSSLR AEDTA VYYCATGKGVHLGFDYWGQGITLVTVSSGGGGSGGGSGGGSSSYVLTQPPSVVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVMVYDDNDRPSGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDYSGQRQVFCGKTLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTFNKYAMINWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNHLKTEDTA VYYCARAGNFGSSYISYWAYWGQGITLVTVSSGGGGSGGGGGSGGQT VVTQEPSTVTVSPGTVTITCGSSTGAVTSGNYPNWVQOKPGQAPRGLIGGKFLAPGTPARFSGSLGKKAALTL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTHTCPPCPAPELLGGPSVFLFPKPKD TLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNATKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 17391) <i>No nuc. seq. available</i>

604

iPS:2810779	MA_10-B5_CC_x_12E_x_scFc_—	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGLSLRSLCAASGFTFSNAWMSWVRQAPGKCLEWVGRIR SRSYGGTTDYAAPVKGRFTISRDDSKNTLFLQMSLKTEDTAVYYCTTPSYSGSYNYFVMDVWGQGTITVSSG GGSGGGGGGGDIQMTQSPSSLSASVGDRTVITRTSQSISSYLNWYQKPGRAPKLLIFAAASLQGGVPSRFSG SGSGTDFLTITSLQPEDFATYYCQQTYSMPFTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGLSLRSLCAASGFTF NKYAINWVRQAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNHLKTEDTAVYYCARAGN FGSSYISYWAYWGQGLTVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTITCGSSTGAVTSNGYNWVQ KKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGD KTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTEPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSPGKGGG SGGG EVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSPGK
		NA	(SEQ ID NO: 17394) <i>No info. seq. available</i>
iPS:2810781	MA_10-B5_CC_x_12E_x_scFc_variant	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGLSLRSLCAASGFTFSNAWMSWVRQAPGKCLEWVGRIR SRSYGGTTDYAAPVKGRFTISRDDSKNTLFLQMSLKTEDTAVYYCTTPSYSGSYNYFVMDVWGQGTITVSSG GGSGGGGGGGGGDIQMTQSPSSLSASVGDRTVITRTSQSISSYLNWYQKPGRAPKLLIFAAASLQGGVPSRFSG SGSGTDFLTITSLQPEDFATYYCQQTYSMPFTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGLSLRSLCAASGFTF NKYAINWVRQAPGKLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTVYLQMNHLKTEDTAVYYCARAGN FGSSYISYWAYWGQGLTVTVSSGGGGGGGGGGGSGTQVTVTQEPSTVSPGGTVTITCGSSTGAVTSNGYNWVQ KKPGQAPRGLIGGTFKFLAPGTPARFSGSLSGKAAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGD KTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMISRTEPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSPGKGGG SGGG EVKFNWYVDGVEVHNAAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSPGK
		NA	(SEQ ID NO: 17395) <i>No info. seq. available</i>

iPS:2306864	MA_98-C7_CC_x_12C0_x_scFc_(Y8P)	AA	MDMRVPAQLLGLLLWLRGARCEVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMS WVRQAPGKCLEWVSSISG SGGGTYAAASVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSGG SGGGSSSYVLTQPPSVVAPGQTARITCGGNIGSKSVHWYQKPGQAPVMVYDDNDRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQVWDY'SPLRHVFGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTFNK YAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGQTVVTOEPSLTVSPGGTVTLTCGSSTGAVTSNGYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLGKKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGGD KTHTCPPCPAPELLGGPSVFLFPKPKDITLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNATKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGKGGG SGGGSGGGSGGGSGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMISRTPETCVVVDVSHEDP EVKFNWYVDGVEVHNATKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVSMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 17396) <i>No info. seq. available</i>
iPS:2810785	MA_98-C7_CC_x_12E_x_scFc_	AA	MDMRVPAQLLGLLLWLRGARCEVQLLES GGGLVQPGGSLRLSCAASGFTFSSHAMS WVRQAPGKCLEWVSSISG SGGGTYAAASVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGLTVTVSSGGGGSGG SGGGSSSYVLTQPPSVVAPGQTARITCGGNIGSKSVHWYQKPGQAPVMVYDDNDRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQVWDY'SPLRHVFGCGTKLTVLSSGGGSEVQLVESGGGLVQPGGSLKLSCAAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCARAGNF SSYISYWAYWGQGLTVTVSSGGGGSGGGGSGGQTVVTOEPSLTVSPGGTVTLTCGSSTGAVTSNGYPNWVQK PGQAPRGLIGGTKFLAPGTPARFSGSLSGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGLTKLTVLGGGGDKTH TCPPCPAPELLGGPSVFLFPKPKDITLMISRTPETCVVVDVSHEDPEVKFNWYVDGVEVHNATKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPGKGGGSG GGGGSGGGSGGGSGGGGSDKTHTCPPCPAPELLGGPSVFLFPKPKDITLMISRTPETCVVVDVSHEDPEV KFNWYVDGVEVHNATKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYCKVSNKALPAPIETISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
		NA	(SEQ ID NO: 17397) <i>No info. seq. available</i>

iPS:2810787	MA_98-C7_CC_x_12E_x_scFc_variant	AA	MDMRVPAQLLGLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSHAMSWVRQAPGKCLEWVSSISG SGGGTYAAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGQGTILVTVSSGGGGGGG SGGGGSSYVLTPPSSVAPGQTARITCGGNNIGSKSVHWYQKPGQAPVMVYDDNDRPSGIPERFSGNSGNT ATLTISRVEAGDEADYYCQVWDY'SPLRHVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIPRSKYNRYATYYADA VKDRFTISRDDSKNTVYLQMNNLK'TEDTAVYYCARAGNFG SSYISW'AYWGQGTILVTVSSGGGGGGGGGGGQTVVTQEPSTVSPGGTVTITCGSSTGAVTSGNYPNWWQKK PGQAPRGLIGGTFKFLAPGTPARFSGSLSGGKAALTLGSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLGGGGDKTH TCPPCPAPPELLGGPSVFLFPPKPKDTLITITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPCEEQYGSTYR CVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSLSLSPKGGGGSG GGSGGGGGGGGGGGGGGGGGGGDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLITITREPEVTCVVVDVSHEDPEV KFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC SVMHEALHNHYTQKSLSLSPGK
			(SEQ ID NO: 17398)

Table 89

BiTE-scFc Fv#1 VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:230686 3	MA_03- G10_AS_CC_x_I2C0_x_scFc_(N3H)_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
		AA	GGNIGSKSVH (SEQ ID NO: 17399)	DDNDRPS (SEQ ID NO: 17435)	QVWDYSGQRQV (SEQ ID NO: 17471)
IPS:281077 3	MA_03- G10_AS_CC_x_I2E_x_scFc_	NA	No nuc. seq available		
		AA	GGNIGSKSVH (SEQ ID NO: 17400)	DDNDRPS (SEQ ID NO: 17436)	QVWDYSGQRQV (SEQ ID NO: 17472)
IPS:281077 5	MA_03- G10_AS_CC_x_I2E_x_scFc_variant_	NA	No nuc. seq available		
		AA	GGNIGSKSVH (SEQ ID NO: 17401)	DDNDRPS (SEQ ID NO: 17437)	QVWDYSGQRQV (SEQ ID NO: 17473)
IPS:230686 7	MA_10- B5_CC_x_I2C0_x_scFc_(H6H)_	NA	No nuc. seq available		
		AA	RTSQSISSYLN (SEQ ID NO: 17402)	AASSLOG (SEQ ID NO: 17438)	QQTYSMPPT (SEQ ID NO: 17474)
IPS:281077 9	MA_10-B5- CC_x_I2E_x_scFc_	NA	No nuc. seq available		
		AA	RTSQSISSYLN (SEQ ID NO: 17403)	AASSLOG (SEQ ID NO: 17439)	QQTYSMPPT (SEQ ID NO: 17475)
IPS:281078 1	MA_10- B5_CC_x_I2E_x_scFc_variant_	NA	No nuc. seq available		
		AA	RTSQSISSYLN (SEQ ID NO: 17404)	AASSLOG (SEQ ID NO: 17440)	QQTYSMPPT (SEQ ID NO: 17476)
IPS:230686 4	MA_98- C7_CC_x_I2C0_x_scFc_(Y8P)_	NA	No nuc. seq available		
		AA	GGNIGSKSVH (SEQ ID NO: 17405)	DDNDRPS (SEQ ID NO: 17441)	QVWDYSPLRHV (SEQ ID NO: 17477)
IPS:281078 5	MA_98-C7- CC_x_I2E_x_scFc_	NA	No nuc. seq available		
		AA	GGNIGSKSVH (SEQ ID NO: 17406)	DDNDRPS (SEQ ID NO: 17442)	QVWDYSPLRHV (SEQ ID NO: 17478)
IPS:281078 7	MA_98- C7_CC_x_I2E_x_scFc_variant_	NA	No nuc. seq available		
		AA	GGNIGSKSVH (SEQ ID NO: 17407)	DDNDRPS (SEQ ID NO: 17443)	QVWDYSPLRHV (SEQ ID NO: 17479)
BiTE-scFc Fv#1 VH CDRs					
IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:230686 3	MA_03- G10_AS_CC_x_I2C0_x_scFc_(N3H)_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
		AA	SYAMS (SEQ ID NO: 17408)	AISGGGGTTYAASVKG (SEQ ID NO: 17444)	GKGVHLGFDY (SEQ ID NO: 17480)
IPS:281077 3	MA_03- G10_AS_CC_x_I2E_x_scFc_	NA	No nuc. seq available		
		AA	SYAMS	AISGGGGTTYAASVKG	GKGVHLGFDY

			(SEQ ID NO: 17409)	(SEQ ID NO: 17445)	(SEQ ID NO: 17481)
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_variant_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:230686	MA_10- B5_CC_x_I2C0_x_scFc_(H6H)_	AA	SYAMS	AISGGGGTTYAASVKG	GKGVHLGFDY
IPS:281077	MA_10- B5_CC_x_I2C0_x_scFc_(H6H)_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281077	MA_10-B5-CC_x_I2E_x_scFc_	AA	NAWMS	RIRRSYGGTTDYAAPVKG	PSYSGSYNYFVSMDV
IPS:281077	MA_10-B5-CC_x_I2E_x_scFc_	NA	(SEQ ID NO: 17411)	(SEQ ID NO: 17447)	(SEQ ID NO: 17483)
IPS:281077	MA_10-B5-CC_x_I2E_x_scFc_	AA	NAWMS	RIRRSYGGTTDYAAPVKG	PSYSGSYNYFVSMDV
IPS:281078	MA_10- B5_CC_x_I2E_x_scFc_variant_	NA	(SEQ ID NO: 17412)	(SEQ ID NO: 17448)	(SEQ ID NO: 17484)
IPS:230686	MA_98- C7_CC_x_I2C0_x_scFc_(Y8P)_	AA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281078	MA_98- C7_CC_x_I2C0_x_scFc_(Y8P)_	NA	NAWMS	RIRRSYGGTTDYAAPVKG	PSYSGSYNYFVSMDV
IPS:281078	MA_98- C7_CC_x_I2C0_x_scFc_(Y8P)_	AA	(SEQ ID NO: 17413)	(SEQ ID NO: 17449)	(SEQ ID NO: 17485)
IPS:281078	MA_98- C7_CC_x_I2C0_x_scFc_(Y8P)_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_	AA	SHAMS	SISGGGGTTYAASVKG	GKGVHLGFDY
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_	NA	(SEQ ID NO: 17414)	(SEQ ID NO: 17450)	(SEQ ID NO: 17486)
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_	AA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_	NA	SHAMS	SISGGGGTTYAASVKG	GKGVHLGFDY
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_	AA	(SEQ ID NO: 17415)	(SEQ ID NO: 17451)	(SEQ ID NO: 17487)
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_variant_	AA	SHAMS	SISGGGGTTYAASVKG	GKGVHLGFDY
IPS:281078	MA_98- C7_CC_x_I2E_x_scFc_variant_	AA	(SEQ ID NO: 17416)	(SEQ ID NO: 17452)	(SEQ ID NO: 17488)

Table 90

BiTE-scFc Fy#2 VL CDRs

IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:230686	MA_03- G10_AS_CC_x_I2C0_x_scFc_(N3H)_	NA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_	AA	GSSTGAVTSGNYPN	GTKFLAP	VLWYSNRWV
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_	NA	(SEQ ID NO: 17417)	(SEQ ID NO: 17453)	(SEQ ID NO: 17489)
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_	AA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_	AA	GSSTGAVTSGNYPN	GTKFLAP	VLWYSNRWV
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_	NA	(SEQ ID NO: 17418)	(SEQ ID NO: 17454)	(SEQ ID NO: 17490)
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_	AA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_variant_	AA	GSSTGAVTSGNYPN	GTKFLAP	VLWYSNRWV
IPS:281077	MA_03- G10_AS_CC_x_I2E_x_scFc_variant_	NA	(SEQ ID NO: 17419)	(SEQ ID NO: 17455)	(SEQ ID NO: 17491)
IPS:230686	MA_10- B5_CC_x_I2C0_x_scFc_(H6H)_	AA	No nuc. seq available	No nuc. seq available	No nuc. seq available
IPS:230686	MA_10- B5_CC_x_I2C0_x_scFc_(H6H)_	AA	GSSTGAVTSGNYPN	GTKFLAP	VLWYSNRWV

			(SEQ ID NO: 17420 <i>No nuc. seq available</i>)	(SEQ ID NO: 17456 <i>No nuc. seq available</i>)	(SEQ ID NO: 17492 <i>No nuc. seq available</i>)
IPS:281077 9	MA_10-B5_CC_x_I2E_x_scFc__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17421) <i>No nuc. seq available</i>	GTKFLAP (SEQ ID NO: 17457) <i>No nuc. seq available</i>	VLWYSNRWV (SEQ ID NO: 17493) <i>No nuc. seq available</i>
IPS:281078 1	MA_10-B5_CC_x_I2E_x_scFc_variant__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17422) <i>No nuc. seq available</i>	GTKFLAP (SEQ ID NO: 17458) <i>No nuc. seq available</i>	VLWYSNRWV (SEQ ID NO: 17494) <i>No nuc. seq available</i>
IPS:230686 4	MA_98-C7_CC_x_I2C0_x_scFc_(Y8P)_	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17423) <i>No nuc. seq available</i>	GTKFLAP (SEQ ID NO: 17459) <i>No nuc. seq available</i>	VLWYSNRWV (SEQ ID NO: 17495) <i>No nuc. seq available</i>
IPS:281078 5	MA_98-C7_CC_x_I2E_x_scFc__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17424) <i>No nuc. seq available</i>	GTKFLAP (SEQ ID NO: 17460) <i>No nuc. seq available</i>	VLWYSNRWV (SEQ ID NO: 17496) <i>No nuc. seq available</i>
IPS:281078 7	MA_98-C7_CC_x_I2E_x_scFc_variant__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 17425)	GTKFLAP (SEQ ID NO: 17461)	VLWYSNRWV (SEQ ID NO: 17497)
BiTE-scFc F#2 VH CDRs					
IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:230686 3	MA_03-G10_AS_CC_x_I2C0_x_scFc_(N3H)_	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	KYAMN (SEQ ID NO: 17426) <i>No nuc. seq available</i>	RIRSKYNNTATYYADSVKD (SEQ ID NO: 17462) <i>No nuc. seq available</i>	HGNFGNSYISYWAY (SEQ ID NO: 17498) <i>No nuc. seq available</i>
IPS:281077 3	MA_03-G10_AS_CC_x_I2E_x_scFc__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	KYAIN (SEQ ID NO: 17427) <i>No nuc. seq available</i>	RIRSKYNNTATYYADAVKD (SEQ ID NO: 17463) <i>No nuc. seq available</i>	AGNFGSSYISYWAY (SEQ ID NO: 17499) <i>No nuc. seq available</i>
IPS:281077 5	MA_03-G10_AS_CC_x_I2E_x_scFc_variant__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	KYAIN (SEQ ID NO: 17428) <i>No nuc. seq available</i>	RIRSKYNNTATYYADAVKD (SEQ ID NO: 17464) <i>No nuc. seq available</i>	AGNFGSSYISYWAY (SEQ ID NO: 17500) <i>No nuc. seq available</i>
IPS:230686 7	MA_10-B5_CC_x_I2C0_x_scFc_(H6H)_	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	KYAMN (SEQ ID NO: 17429) <i>No nuc. seq available</i>	RIRSKYNNTATYYADSVKD (SEQ ID NO: 17465) <i>No nuc. seq available</i>	HGNFGNSYISYWAY (SEQ ID NO: 17501) <i>No nuc. seq available</i>
IPS:281077 9	MA_10-B5_CC_x_I2E_x_scFc__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	KYAIN (SEQ ID NO: 17430) <i>No nuc. seq available</i>	RIRSKYNNTATYYADAVKD (SEQ ID NO: 17466) <i>No nuc. seq available</i>	AGNFGSSYISYWAY (SEQ ID NO: 17502) <i>No nuc. seq available</i>
IPS:281078 1	MA_10-B5_CC_x_I2E_x_scFc_variant__	NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>
		AA	KYAIN (SEQ ID NO: 17431) <i>No nuc. seq available</i>	RIRSKYNNTATYYADAVKD (SEQ ID NO: 17467) <i>No nuc. seq available</i>	AGNFGSSYISYWAY (SEQ ID NO: 17503) <i>No nuc. seq available</i>
		NA	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>	<i>No nuc. seq available</i>

iPS:230686 4	MA_98- C7_CC_x_12C0_x_scFc_(Y8P)_	AA	KYAMN (SEQ ID NO: 17432) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADSVKD (SEQ ID NO: 17468) <i>No nuc. seq. available</i>	HGNFGNSYISYWAY (SEQ ID NO: 17504) <i>No nuc. seq. available</i>
		NA			
iPS:281078 5	MA_98-C7_CC_x_12E_x_scFc_	AA	KYAIN (SEQ ID NO: 17433) <i>No nuc. seq. available</i>	RIRSKYNNYATYYADAVKD (SEQ ID NO: 17469) <i>No nuc. seq. available</i>	AGNFGSSYISYWAY (SEQ ID NO: 17505) <i>No nuc. seq. available</i>
		NA			
iPS:281078 7	MA_98- C7_CC_x_12E_x_scFc_variant_	AA	KYAIN (SEQ ID NO: 17434)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 17470)	AGNFGSSYISYWAY (SEQ ID NO: 17506)

BiTE-scFc Variable Region Sequences

[illegible]

Abstract

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IPS:281078	MA_10- RE_CC_X_12E_X_wRC_variant_P#2	VH3J-15D01-210RP2JH4	RVLQJFES-GBELVQFQBSILALSCAGS-PTF6	17579	E-----YALH	17622	WVQJAPQCLUBWA	17665	RIREBN-IMHANTYAGAVD	17708	RFTIIEGKSNITVLQJNNILATETAVTCAR	17751	AMFSSB-----YISWAV	17794	WQJQTLVTVGS	17837
IPS:281078	MA_96- CT_CC_X_12E_X_wRC_P#2	VH3J-15D01-210RP2JH4	RVLQJFES-GBELVQFQBSILALSCAGS-PTF6	17580	E-----YALH	17623	WVQJAPQCLUBWA	17666	RIREBN-IMHANTYAGAVD	17709	RFTIIEGKSNITVLQJNNILATETAVTCAR	17752	AMFSSB-----YISWAV	17795	WQJQTLVTVGS	17838
IPS:281078	MA_96- CT_CC_X_12E_X_wRC_variant_P#2	VH3J-15D01-210RP2JH4	RVLQJFES-GBELVQFQBSILALSCAGS-PTF6	17581	E-----YALH	17624	WVQJAPQCLUBWA	17667	RIREBN-IMHANTYAGAVD	17710	RFTIIEGKSNITVLQJNNILATETAVTCAR	17753	AMFSSB-----YISWAV	17796	WQJQTLVTVGS	17839
		Granular														
IPS:230685	MA_10- RE_CC_X_12C9_X_wRC_1R6H_P#1	VH3J-15D01-100RP2JH6	RVLQJFES-GBELVQFQBSILALSCAGS-PTF6	17582	H CDB1 H-----AMNS	17625	WVQJAPQCLUBWQ	17668	RIREBS-VOBTTQIAAPVQ3	17711	RFTIIEGKSNITVLQJNNILATETAVTCCT	17754	H CDB1 PRESENTX-----AMFSSWAV	17797	H PB4 WQJQTLVTVGS	17840
IPS:281077	MA_10- RE_P#1	VH3J-15D01-100RP2JH6	RVLQJFES-GBELVQFQBSILALSCAGS-PTF6	17584	H-----AMNS	17627	WVQJAPQCLUBWQ	17670	RIREBS-VOBTTQIAAPVQ3	17713	RFTIIEGKSNITVLQJNNILATETAVTCCT	17756	PRESENTX-----AMFSSWAV	17799	WQJQTLVTVGS	17842
IPS:281078	MA_10- RE_CC_X_12E_X_wRC_variant_P#1	VH3J-15D01-100RP2JH6	RVLQJFES-GBELVQFQBSILALSCAGS-PTF6	17585	H-----AMNS	17628	WVQJAPQCLUBWQ	17671	RIREBS-VOBTTQIAAPVQ3	17714	RFTIIEGKSNITVLQJNNILATETAVTCCT	17757	PRESENTX-----AMFSSWAV	17800	WQJQTLVTVGS	17843

Table 2
HFE, aE, Variable Region Consensus Protein Alignment
CDRs defined by Kabat
All amino acid numbering defined by Angen Reference (Ato)

CDR	SEQ ID NO.	K	PR	SEQ ID NO.	K	PR	SEQ ID NO.	K	PR	SEQ ID NO.	K	PR	SEQ ID NO.	K	PR	SEQ ID NO.	K	PR	SEQ ID NO.
CDR1	17844	T	17887	17930	17943	17953	17973	17984	17994	18004	18014	18024	18034	18044	18054	18064	18074	18084	18094
CDR2	17845	T	17888	17931	17944	17954	17974	17846	17889	17932	17945	17955	17975	17847	17890	17933	17946	17956	17966
CDR3	17846	T	17889	17932	17945	17955	17975	17847	17890	17933	17946	17956	17976	17848	17891	17934	17947	17957	17967
CDR4	17847	T	17890	17933	17946	17956	17976	17848	17891	17934	17947	17957	17977	17849	17892	17935	17948	17958	17968
CDR5	17848	T	17891	17934	17947	17957	17977	17849	17892	17935	17948	17958	17978	17850	17893	17936	17949	17959	17969
CDR6	17849	T	17892	17935	17948	17958	17978	17850	17893	17936	17949	17959	17979	17851	17894	17937	17950	17960	17970
CDR7	17850	T	17893	17936	17949	17959	17979	17851	17894	17937	17950	17960	17980	17852	17895	17938	17951	17961	17971
CDR8	17851	T	17894	17937	17950	17960	17980	17852	17895	17938	17951	17961	17981	17853	17896	17939	17952	17962	17972
CDR9	17852	T	17895	17938	17951	17961	17981	17853	17896	17939	17952	17962	17982	17854	17897	17940	17953	17963	17973
CDR10	17853	T	17896	17939	17952	17962	17982	17854	17897	17940	17953	17963	17983	17855	17898	17941	17954	17964	17974
CDR11	17854	T	17897	17940	17953	17963	17983	17855	17898	17941	17954	17964	17984	17856	17899	17942	17955	17965	17975
CDR12	17855	T	17898	17941	17954	17964	17984	17856	17899	17942	17955	17965	17985	17857	17900	17943	17956	17966	17976
CDR13	17856	T	17899	17942	17955	17965	17985	17857	17900	17943	17956	17966	17986	17858	17901	17944	17957	17967	17977
CDR14	17857	T	17900	17943	17956	17966	17986	17858	17901	17944	17957	17967	17987	17859	17902	17945	17958	17968	17978
CDR15	17858	T	17901	17944	17957	17967	17987	17859	17902	17945	17958	17968	17988	17860	17903	17946	17959	17969	17979
CDR16	17859	T	17902	17945	17958	17968	17988	17860	17903	17946	17959	17969	17989	17861	17904	17947	17960	17970	17980
CDR17	17860	T	17903	17946	17959	17969	17989	17861	17904	17947	17960	17970	17990	17862	17905	17948	17961	17971	17981
CDR18	17861	T	17904	17947	17960	17970	17990	17862	17905	17948	17961	17971	17991	17863	17906	17949	17962	17972	17982
CDR19	17862	T	17905	17948	17961	17971	17991	17863	17906	17949	17962	17972	17992	17864	17907	17950	17963	17973	17983
CDR20	17863	T	17906	17949	17962	17972	17992	17864	17907	17950	17963	17973	17993	17865	17908	17951	17964	17974	17984
CDR21	17864	T	17907	17950	17963	17973	17993	17865	17908	17951	17964	17974	17994	17866	17909	17952	17965	17975	17985
CDR22	17865	T	17908	17951	17964	17974	17994	17866	17909	17952	17965	17975	17995	17867	17910	17953	17966	17976	17986
CDR23	17866	T	17909	17952	17965	17975	17995	17867	17910	17953	17966	17976	17996	17868	17911	17954	17967	17977	17987
CDR24	17867	T	17910	17953	17966	17976	17996	17868	17911	17954	17967	17977	17997	17869	17912	17955	17968	17978	17988
CDR25	17868	T	17911	17954	17967	17977	17997	17869	17912	17955	17968	17978	17998	17870	17913	17956	17969	17979	17989
CDR26	17869	T	17912	17955	17968	17978	17998	17870	17913	17956	17969	17979	17999	17871	17914	17957	17970	17980	17990
CDR27	17870	T	17913	17956	17969	17979	17999	17871	17914	17957	17970	17980	18000	17872	17915	17958	17971	17981	17991
CDR28	17871	T	17914	17957	17970	17980	18000	17872	17915	17958	17971	17981	18001	17873	17916	17959	17972	17982	17992
CDR29	17872	T	17915	17958	17971	17981	18001	17873	17916	17959	17972	17982	18002	17874	17917	17960	17973	17983	17993
CDR30	17873	T	17916	17959	17972	17982	18002	17874	17917	17960	17973	17983	18003	17875	17918	17961	17974	17984	17994
CDR31	17874	T	17917	17960	17973	17983	18003	17875	17918	17961	17974	17984	18004	17876	17919	17962	17975	17985	17995
CDR32	17875	T	17918	17961	17974	17984	18004	17876	17919	17962	17975	17985	18005	17877	17920	17963	17976	17986	17996
CDR33	17876	T	17919	17962	17975	17985	18005	17877	17920	17963	17976	17986	18006	17878	17921	17964	17977	17987	17997
CDR34	17877	T	17920	17963	17976	17986	18006	17878	17921	17964	17977	17987	18007	17879	17922	17965	17978	17988	17998
CDR35	17878	T	17921	17964	17977	17987	18007	17879	17922	17965	17978	17988	18008	17880	17923	17966	17979	17989	17999
CDR36	17879	T	17922	17965	17978	17988	18008	17880	17923	17966	17979	17989	18009	17881	17924	17967	17980	17990	18000
CDR37	17880	T	17923	17966	17979	17989	18009	17881	17924	17967	17980	17990	18010	17882	17925	17968	17981	17991	18001
CDR38	17881	T	17924	17967	17980	17990	18010	17882	17925	17968	17981	17991	18011	17883	17926	17969	17982	17992	18002
CDR39	17882	T	17925	17968	17981	17991	18011	17883	17926	17969	17982	17992	18012	17884	17927	17970	17983	17993	18003
CDR40	17883	T	17926	17969	17982	17992	18012	17884	17927	17970	17983	17993	18013	17885	17928	17971	17984	17994	18004
CDR41	17884	T	17927	17970	17983	17993	18013	17885	17928	17971	17984	17994	18014	17886	17929	17972	17985	17995	18005
CDR42	17885	T	17928	17971	17984	17994	18014	17886	17929	17972	17985	17995	18015	17887	17930	17973	17986	17996	18006
CDR43	17886	T	17929	17972	17985	17995	18015	17887	17930	17973	17986	17996	18016	17888	17931	17974	17987	17997	18007
CDR44	17887	T	17930	17973	17986	17996	18016	17888	17931	17974	17987	17997	18017	17889	17932	17975	17988	17998	18008
CDR45	17888	T	17931	17974	17987	17997	18017	17889	17932	17975	17988	17998	18018	17890	17933	17976	17989	17999	18009
CDR46	17889	T	17932	17975	17988	17998	18018	17890	17933	17976	17989	17999	18019	17891	17934	17977	17990	18000	18010
CDR47	17890	T	17933	17976	17989	17999	18019	17891	17934	17977	17990	18000	18020	17892	17935	17978	17991	18001	18011
CDR48	17891	T	17934	17977	17990	18000	18020	17892	17935	17978	17991	18001	18021	17893	17936	17979	17992	18002	18012
CDR49	17892	T	17935	17978	17991	18001	18021	17893	17936	17979	17992	18002	18022	17894	17937	17980	17993	18003	18013
CDR50	17893	T	17936	17979	17992	18002	18022	17894	17937	17980	17993	18003	18023	17895	17938	17981	17994	18004	18014
CDR51	17894	T	17937	17980	17993	18003	18023	17895	17938	17981	17994	18004	18024	17896	17939	17982	17995	18005	18015
CDR52	17895	T	17938	17981	17994	18004	18024	17896	17939	17982	17995	18005	18025	17897	17940	17983	17996	18006	18016
CDR53	17896	T	17939	17982	17995	18005	18025	17897	17940	17983	17996	18006	18026	17898	17941	17984	17997	18007	18017
CDR54	17897	T	17940	17983	17996	18006	18026	17898	17941	17984	17997	18007	18027	17899	17942	17985	17998	18008	18018
CDR55	17898	T	17941	17984	17997	18007	18027	17899	17942	17985	17998	18008	18028	17900	17943	17986	17999	18009	18019
CDR56	17899	T	17942	17985	17998	18008	18028	17900	17943	17986	17999	18009	18029	17901	17944	17987	18000	18010	18020
CDR57	17900	T	17943	17986	17999	18009	18029	17901	17944	17987	18000	18010	18030	17902	17945	17988	18001	18011	18021
CDR58	17901	T	17944	17987	18000	18010	18030	17902	17945	17988	18001	18011	18031	17903	17946	17989	18002	18012	18022
CDR59	17902	T	17945	17988	18001	18011	18031	17903	17946	17989	18002	18012	18032	17904	17947	17990	18003	18013	18023
CDR60	17903	T	17946	17989	18002	18012	18032	17904	17947	17990	18003	18013	18033	17905	17948	17991	18004	18014	18024
CDR61	17904	T	17947	17990	18003	18013</													

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PS-281078	MA-10- RE_CC_X12E_X_wFC_variant_Pw2	VTH3-15021-210RP2JH4	B	17880	K.....X1M	17923	P.....A	17966	Y..M...Y..Da..D	18009	V.....M.....A..	18052	.GNF.SB.....YI..W.	18095		18138
PS-281078	MA-96- RE_CC_X12E_X_wFC_Pw2	VTH3-15021-210RP2JH4	B	17881	K.....Y1M	17924	P.....A	17967	Y..M...Y..Da..D	18010	V.....M.....A..	18053	.GNF.SB.....YI..W.	18096		18139
PS-281078	MA-96- CT_CC_X12E_X_wFC_variant_Pw2	VTH3-15021-210RP2JH4	B	17882	K.....X1M	17925	P.....A	17968	Y..M...Y..Da..D	18011	V.....M.....A..	18054	.GNF.SB.....YI..W.	18097		18140
		Granite	H FBI	17883	H FBI	17926	H FBI	17969	H FBI	18012	H FBI	18055	H FBI	18098	H FBI	18141
PS-230685	MA-10- RE_CC_X12C9_X_wFC_BkH_Pw1	VTH3-15031-100RP2JH6	Q.....	17884		17927	C.....	17970	..R.PB.X.....	18013	F.....	18056	PS.SB257.....M.FSV...	18099		18142
PS-281078	MA-10-B5- RE_CC_X12E_X_wFC_Pw1	VTH3-15031-100RP2JH6	Q.....	17885		17928	C.....	17971	..R.PB.X.....	18014	F.....	18057	PS.SB257.....M.FSV...	18100		18143
PS-281078	MA-10- RE_CC_X12E_X_wFC_variant_Pw1	VTH3-15031-100RP2JH6	Q.....	17886		17929	C.....	17972	..R.PB.X.....	18015	F.....	18058	PS.SB257.....M.FSV...	18101		18144

Table 94
BiTE Full Sequences

iPS#	Ab	Type	BiTE
		NA	<i>No info. seq available</i>
iPS:2810771	MA_03-G10_AS_CC_x_I2E6	AA	MDMRVPAQLLGLLLLWLRGARCEVQLLESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKCLEWVSAISGGGGTTYAASVKGRFTISRDN KNTLYLQMSSLRAEDTAVYYCATGKGVHLGFDYWGQGLVTVSSGGG GSGGGGGGGSSYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQ KPGQAPVMVVDNDNRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYC QVWDYSGQRQVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADA VKDR FTISRDDSKNTVYLQMNNLKTEDTAVYYCARAGNFGSSYISYWYWGQ GTLVTVSSGGGGGGGGGGGSGQTVVTQEPSLTVSPGGTVTITCGSSTG AVTSGNYPNWVQKKPGQAPRGLIGTKFLAPGTPARFSGSLSGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLHHHHHHH
			(SEQ ID NO: 18145)
		NA	<i>No info. seq available</i>

iPS:2810777	MA_10-B5_CC_x_I2E6_	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVGRIRSRSYGGTTDYAAPVKGRFTISR DSKNTLFLQMNSLKTEDTAVYYCTTPSYSGSYNYFSVMDVWVGQGT TVSSGGGGGGGGGGGGDIQMTQSPSSLSASVGDRTITCRISQSISS LNWYQKPKGRAPKLLIFASSLQGGVPSRFGSGSGTDFTLTISSLQPEDF ATYYCQQTYSMPFTFGCGTKVEIKSGGGSEVQLVESGGGLVQPGGSLK LSCAASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADAVK DRFTISRDDSKNTVYLQMNLLKTEDTAVYYCARAGNFGSSYISYWAYW GQGTLVTVSSGGGGGGGGGGGSGTQTVVTQEPSTVSPGGTVTITCGSS TGAVTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAA LTLSGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLHHHHHH	(SEQ ID NO: 18146 <i>No info. seq. available</i>)
		NA		
iPS:2810783	MA_98-C7_CC_x_I2E6	AA	MDMRVPAQLLGLLLWLRGARCEVQLVESGGGLVQPGGSLRLSCAASG FTFSNAWMSWVRQAPGKCLEWVSSISGGGGTYAAASVKGRFTISRDN KNTLYLQMNSLRAEDTAVYYCATGKGVHLGFDYWGGQTLTVSSGGG GSGGGGGGGGGSSVLTQPPSVSVAPGQTARITCGGNIGSKSVHWYQQ KPGQAPVMVYDDNDRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYC QVWDYSPLRHVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLS AASGFTFNKYAINWVRQAPGKLEWVARIRSKYNNYATYYADAVKDRF TISRDDSKNTVYLQMNLLKTEDTAVYYCARAGNFGSSYISYWAYWGGQ TLVTVSSGGGGGGGGGGGSGTQTVVTQEPSTVSPGGTVTITCGSSTGA VTSGNYPNWVQKKPGQAPRGLIGGKFLAPGTPARFSGSLSGGKAAATL SGVQPEDEAEYYCVLWYSNRWVFGSGTKLTVLHHHHHH	(SEQ ID NO: 18147)

Table 95

IPS#	Ab	Type	CDR1	CDR2	CDR3
BiTE Fv#1 VL CDRs					
IPS:281077 1	MA_03-G10_AS_CC_x_12E6	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GGNIGSKSVH (SEQ ID NO: 18148)	DDNDRPS (SEQ ID NO: 18160)	QVWDYSGQRQV (SEQ ID NO: 18172)
IPS:281077 7	MA_10-B5_CC_x_12E6_	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	RTSQSISSVYL (SEQ ID NO: 18149)	AASSLQ (SEQ ID NO: 18161)	QQTYSMPFT (SEQ ID NO: 18173)
IPS:281078 3	MA_98-C7_CC_x_12E6	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GGNIGSKSVH (SEQ ID NO: 18150)	DDNDRPS (SEQ ID NO: 18162)	QVWDYSPLRHV (SEQ ID NO: 18174)

BiTE Fv#1 VH CDRs					
IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:281077 1	MA_03-G10_AS_CC_x_12E6	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	SYAMS (SEQ ID NO: 18151)	AISGGGGTYYAASVKG (SEQ ID NO: 18163)	GKGVHLGFDY (SEQ ID NO: 18175)
IPS:281077 7	MA_10-B5_CC_x_12E6_	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	NAWMS (SEQ ID NO: 18152)	RIRRSYGGTTDYAAPVKG (SEQ ID NO: 18164)	PSYSGSYNYFVSMDV (SEQ ID NO: 18176)
IPS:281078 3	MA_98-C7_CC_x_12E6	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	SHAMS (SEQ ID NO: 18153)	SISGGGGTYYAASVKG (SEQ ID NO: 18165)	GKGVHLGFDY (SEQ ID NO: 18177)

Table 96

BiTE Fv#2 VL CDRs					
IPS#	Ab	Type	CDR1	CDR2	CDR3
IPS:281077 1	MA_03-G10_AS_CC_x_12E6	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 18154)	GTKFLAP (SEQ ID NO: 18166)	VLWYSNRWV (SEQ ID NO: 18178)
IPS:281077 7	MA_10-B5_CC_x_12E6_	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 18155)	GTKFLAP (SEQ ID NO: 18167)	VLWYSNRWV (SEQ ID NO: 18179)
IPS:281078 3	MA_98-C7_CC_x_12E6	NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available
		AA	GSSTGAVTSGNYPN (SEQ ID NO: 18156)	GTKFLAP (SEQ ID NO: 18168)	VLWYSNRWV (SEQ ID NO: 18180)
BiTE Fv#2 VH CDRs					
IPS#	Ab	Type	CDR1	CDR2	CDR3
		NA	No nuc. seq. available	No nuc. seq. available	No nuc. seq. available

IPS:281077 1	MA_03-G10_AS_CC_x_12E6	AA	KYAIN (SEQ ID NO: 18157 <i>No nuc. seq. available</i>)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 18169 <i>No nuc. seq. available</i>)	AGNFGSSYISYWAY (SEQ ID NO: 18181 <i>No nuc. seq. available</i>)
		NA			
		AA	KYAIN (SEQ ID NO: 18158 <i>No nuc. seq. available</i>)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 18170 <i>No nuc. seq. available</i>)	AGNFGSSYISYWAY (SEQ ID NO: 18182 <i>No nuc. seq. available</i>)
IPS:281077 7	MA_10-B5_CC_x_12E6_	AA			
		NA			
IPS:281078 3	MA_98-C7_CC_x_12E6	AA	KYAIN (SEQ ID NO: 18159)	RIRSKYNNYATYYADAVKD (SEQ ID NO: 18171)	AGNFGSSYISYWAY (SEQ ID NO: 18183)

Table 97
BTE Variable Region Sequences

IP#	Alt	Type	LC Region	HC Region	HC Variable Region	LC Variable Region	HC Region	LC Region	HC Variable Region
HPS-2H1077 1	MA_03-410_AS_CC_x_12E6	NA	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532
		AA	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18184)	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18187)	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18190)	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18193)	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18196)	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18199)	SVLTTPPNSVAPQQTARITCGNNIGSKSVHWYQKSPQAPQAPVAVY DNDPESGIPERFSGNSONTATLTISRVEAGDEADYYCQWWDYSGQRH VFQGGTKLTVL (SEQ ID NO: 18202)
	MA_10-4E_CC_x_12E6_	NA	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532
		AA	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18185)	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18188)	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18191)	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18194)	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18197)	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18200)	DIONTOSISLSASVGDRAVITTCRTSOSISSYLAWYQKSPQAPKLLIFAF SSLQGGVPSRFSGSGCTDFTLTISLQPHDEATYCCQYTSMPITFCGCT KVEIK (SEQ ID NO: 18203)
HPS-2H1078 3	MA_98-C7_CC_x_12E6	AA	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532	5'-TGT-129-255-532

[illegible]622

[illegible]623

CLAIMS

What is claimed is:

1. An isolated antibody construct comprising a binding domain that binds to a pMAGE-HLA on the surface of a target cell, wherein the binding domain binds to the same epitope as an antibody or antibody construct that comprises:

- a) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or
- b) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or
- c) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or
- d) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or
- f) a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or
- g) a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or
- h) a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or
- i) a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

2. An isolated antibody construct comprising a first domain that binds to a pMAGE-HLA on the surface of a target cell, and a second domain that binds to human CD3 on the surface of a T cell, wherein the first domain binds to the same epitope as an antibody or antibody construct that comprises:

- a) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or
- b) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or
- c) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or
- d) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123; or
- f) a VH region as depicted in SEQ ID NO: 629, and a VL region as depicted in SEQ ID NO: 628; or
- g) a VH region as depicted in SEQ ID NO: 577, and a VL region as depicted in SEQ ID NO: 576; or
- h) a VH region as depicted in SEQ ID NO: 684, and a VL region as depicted in SEQ ID NO: 685; or
- i) a VH region as depicted in SEQ ID NO: 557, and a VL region as depicted in SEQ ID NO: 556; or
- j) a VH region as depicted in SEQ ID NO: 561, and a VL region as depicted in SEQ ID NO: 560.

3. An isolated antibody construct that binds to an epitope comprising a pMAGE-HLA, wherein the antibody construct binds to at least one of the following MAGEB2 peptide (SEQ ID NO: 1) residues: Asp4, Gly5, Glu6, Glu7, His8, Ser9, or Val10.

4. An isolated antibody construct that binds to an epitope comprising both a MAGEB2 peptide (SEQ ID NO: 1) and an HLA-A2/MHC, wherein the antibody construct binds to at least one of the following residues HLA-A2 residues: Arg65, Lys66, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Glu154, Gln155, Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Lys68, Ser71, Arg75, Gly79, Thr80, Arg82, Gly83, or Glu89.

5. An isolated antibody construct that binds to an epitope comprising both a MAGEB2 peptide (SEQ ID NO: 1) and an HLA-A2/MHC, wherein the antibody construct binds to at least one of the following MAGEB2 peptide residues: Asp4, Gly5, Glu6, Glu7, His8, Ser9, or Val10, and wherein the antibody construct further binds to at least one of the following residues HLA-A2 residues: Arg65, Lys66, Ala69, Gln72, Thr73, Val76, Lys146, Ala149, Ala150, His151, Glu154, Gln155, Gly16, Arg17, Gly18, Glu19, Pro20, Gln43, Lys68, Ser71, Arg75, Gly79, Thr80, Arg82, Gly83, or Glu89.
6. An isolated antibody construct that binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VH region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein CDR-H3 comprises a lysine at position 2, a valine at position 4, and/or a histidine at position 5.
7. An isolated antibody construct that binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VH region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein CDR-H2 comprises a glycine at position 5 and/or a tyrosine at position 11.
8. An isolated antibody construct that binds to an epitope comprising a MAGEB2 peptide (SEQ ID NO: 1), wherein the antibody construct comprises a VL region comprising a CDR-L1, a CDR-L2, and a CDR-L3, wherein CDR-L3 comprises a tryptophan at position 3 and/or a tyrosine at position 5.
9. An isolated antibody construct that binds to an epitope comprising both a MAGEB2 peptide (SEQ ID NO: 1) and an HLA-A2/MHC, wherein the antibody construct comprises at least one of the following heavy chain amino acid residues: Ser30, Ser31, His32, Tyr32, Ala33, Ser52, Gly53, Ser54, Gly56, Gly57, Tyr59, Lys100, Gly101, Val102, His103, Leu104, or Gly105.
10. The antibody of claim 9, further comprising at least one of the following light chain amino acid residues: Asn25, Asn26, Gly28, Ser29, Lys30, Ser31, His33, Tyr48, Asp49, Asp50, Asn51, Asp52, Arg53, Asn65, Phe66, Ser66, Gly67, Trp90, Tyr92, Arg93, Leu95, Gln95.
11. The antibody construct according to claims 2-10, wherein if present, the second domain binds to human CD3 epsilon and to *Callithrix jacchus* or *Saimiri sciureus* CD3 epsilon.
12. The antibody construct according to claim 1 -11, wherein the antibody construct comprises a first binding domain and a second binding domain, wherein:
- a) the antibody construct is a single chain antibody construct,
 - b) the first domain is in the format of an scFv,
 - c) the second domain is in the format of an scFv,
 - d) the first and the second domain are connected via a linker, and/or

e) the antibody construct comprises a domain providing an extended serum half-life.

13. The antibody construct according to any of the preceding claims, wherein the antibody construct binds to a MAGEA4 peptide (SEQ ID NO: 2) and/or a MAGEA8 peptide (SEQ ID NO: 3).

14. The antibody construct according to any one of the preceding claims, wherein the first domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

- a) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 439, CDR-H2 as depicted in SEQ ID NO: 440, and CDR-H3 as depicted in SEQ ID NO: 441, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 223, CDR-L2 as depicted in SEQ ID NO: 224 and CDR-L3 as depicted in SEQ ID NO: 225; or
- b) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 361, CDR-H2 as depicted in SEQ ID NO: 362, and CDR-H3 as depicted in SEQ ID NO: 363, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 145, CDR-L2 as depicted in SEQ ID NO: 146 and CDR-L3 as depicted in SEQ ID NO: 147; or
- c) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 523, CDR-H2 as depicted in SEQ ID NO: 524, and CDR-H3 as depicted in SEQ ID NO: 525, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 307, CDR-L2 as depicted in SEQ ID NO: 308 and CDR-L3 as depicted in SEQ ID NO: 309; or
- d) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 331, CDR-H2 as depicted in SEQ ID NO: 332, and CDR-H3 as depicted in SEQ ID NO: 333, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 115, CDR-L2 as depicted in SEQ ID NO: 116 and CDR-L3 as depicted in SEQ ID NO: 117; or
- e) a VH region comprising CDR-H1 as depicted in SEQ ID NO: 337, CDR-H2 as depicted in SEQ ID NO: 338, and CDR-H3 as depicted in SEQ ID NO: 339, and a VL region comprising CDR-L1 as depicted in SEQ ID NO: 121, CDR-L2 as depicted in SEQ ID NO: 122 and CDR-L3 as depicted in SEQ ID NO: 123.

15. The antibody construct according to any one of the preceding claims, wherein the first domain comprises a VH region having an amino acid sequence as depicted in SEQ ID NO: 629, 577, 685, 557, or 561.

16. The antibody construct according to any one of the preceding claims, wherein the first domain comprises a VL region having an amino acid sequence as depicted in SEQ ID NO: 628, 576, 684, 556, or 560.

17. The antibody construct according to any one of the preceding claims, wherein the first domain comprises a VL region and a VH region having an amino acid sequence as depicted in SEQ ID NOs: 628 + 629, 576 + 577, 684 + 685, 556 + 557, or 560 + 561.

18. A polynucleotide encoding an antibody construct as defined in any one of the preceding claims.
19. A vector comprising a polynucleotide as defined in claim 18.
20. A host cell transformed or transfected with the polynucleotide as defined in claim 18 or with the vector as defined in claim 19.
21. A process for producing an antibody construct as defined in any one of the preceding claims, said process comprising culturing a host cell as defined in claim 20 under conditions allowing the expression of said antibody construct and recovering the produced antibody construct from the culture.
22. A pharmaceutical composition comprising an antibody construct as defined in any one of the preceding claims, or produced according to the process of claim 21.
23. The antibody construct according to any one of the preceding claims, or produced according to the process of claim 21, for use in the prevention, treatment or amelioration of a disease, preferably a neoplasm.
24. The antibody construct according to any of the preceding claims, wherein the disease or neoplasm is a cancer.
25. The antibody construct according to claim 24, wherein the cancer is a lung cancer, liver cancer, or head and neck cancer.
26. A kit comprising an antibody construct as defined in any one of the preceding claims, an antibody construct produced according to the process of claim 21, a polynucleotide as defined in claim 18, a vector as defined in claim 19, and/or a host cell as defined in claim 20.

FIGURE 1

MAGEB2 and similar peptides

	1	2	3	4	5	6	7	8	9	10	
MAGEB2	G	V	Y	D	G	E	E	H	S	V	(SEQ ID NO: 1)
MAGEA4	G	V	Y	D	G	R	E	H	T	V	(SEQ ID NO: 2)
MAGEA8	G	L	Y	D	G	R	E	H	S	V	(SEQ ID NO: 3)
KEA	G	V	I	D	G	H	I	Y	A	V	(SEQ ID NO: 18461)
MB	G	L	S	D	G	E	W	Q	L	V	(SEQ ID NO: 18462)
ADF	G	V	M	A	G	D	I	Y	S	V	(SEQ ID NO: 18463)
DPYSL4	G	L	Y	D	G	P	M	H	E	V	(SEQ ID NO: 18464)
CNPD2	G	V	Y	G	G	S	V	H	E	A	(SEQ ID NO: 18465)
MYOF	F	V	Y	D	E	P	G	H	A	V	(SEQ ID NO: 18466)
COX14	T	V	Y	G	G	Y	L	C	S	V	(SEQ ID NO: 18467)
STXBP5	Y	T	Y	D	E	A	I	H	S	V	(SEQ ID NO: 18468)
SLK	F	I	V	D	G	V	E	V	S	V	(SEQ ID NO: 18469)

FIGURE 2A

MASS SPEC: MAGEB2 PEPTIDE-HLA-A*02:01 IS EXPRESSED IN CANCER AND NOT IN NORMAL TISSUES

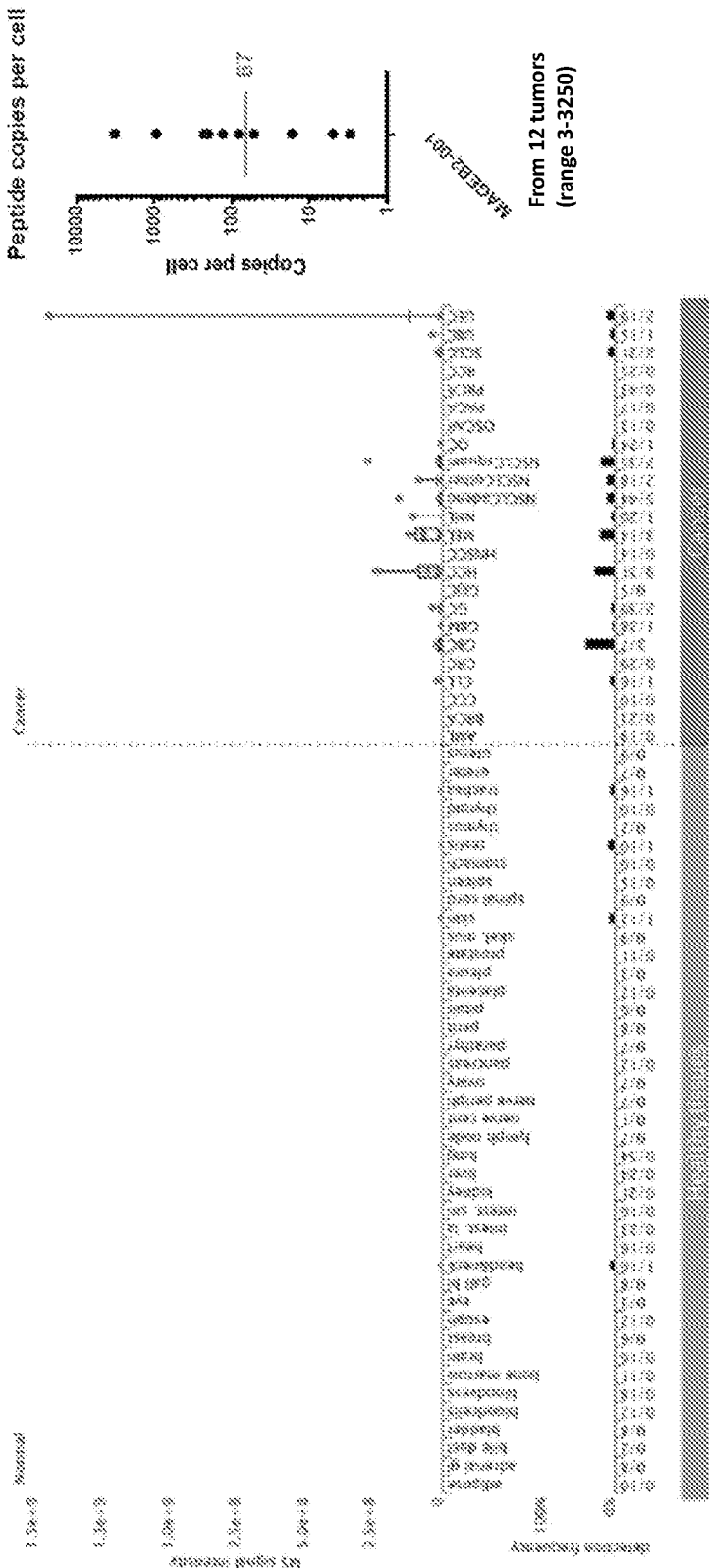


FIGURE 2B

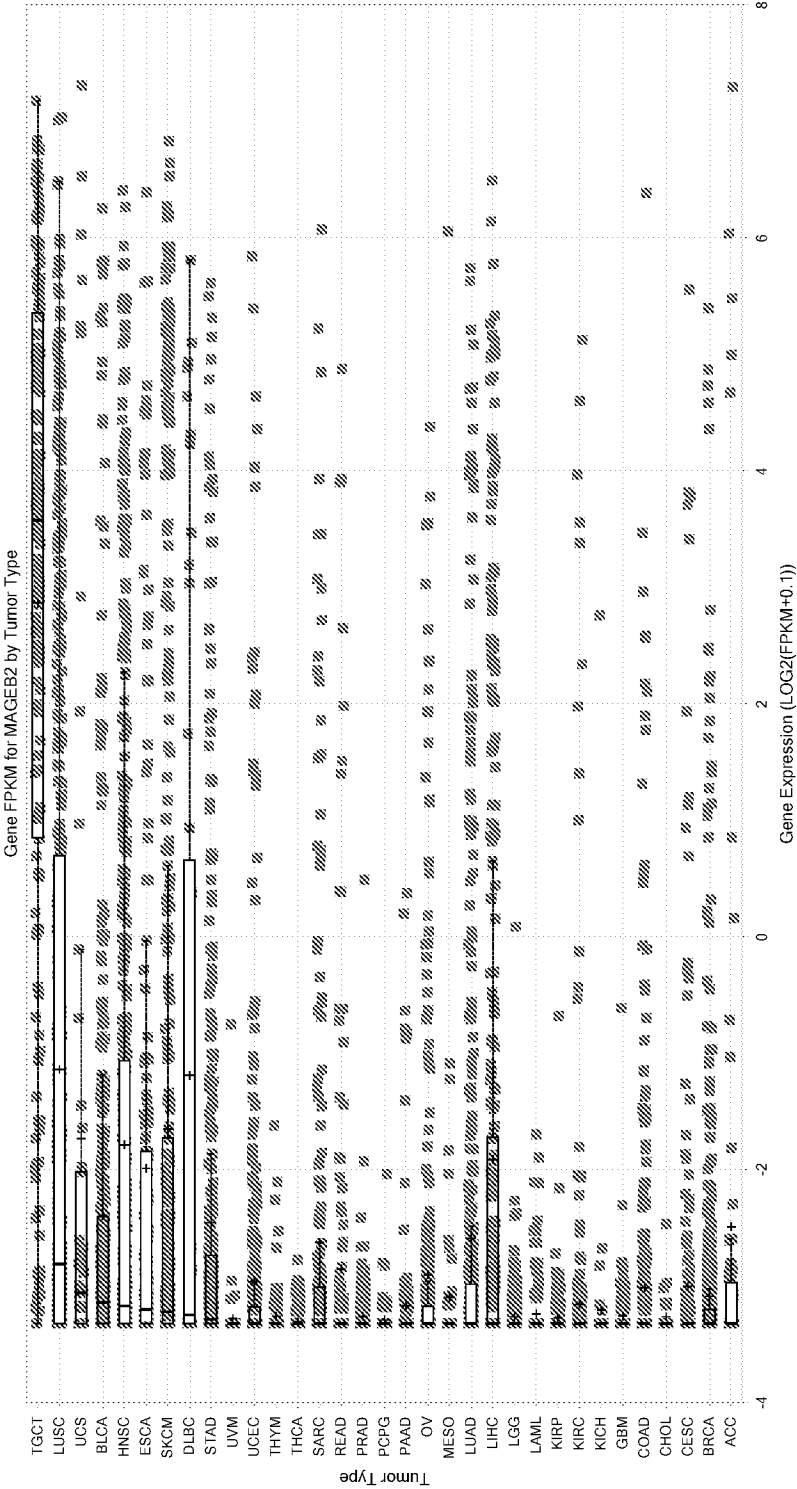


FIGURE 2C

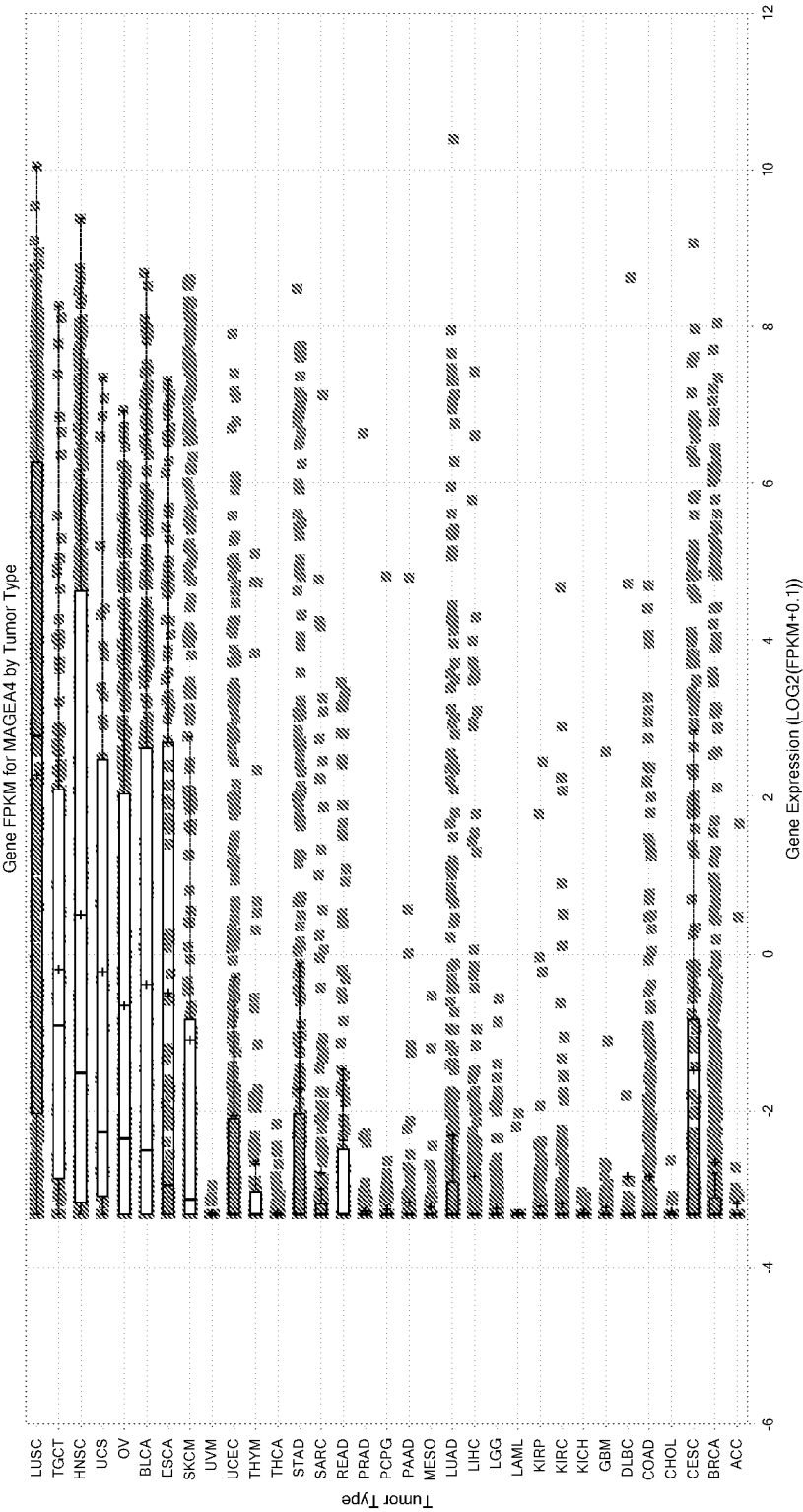


FIGURE 2D

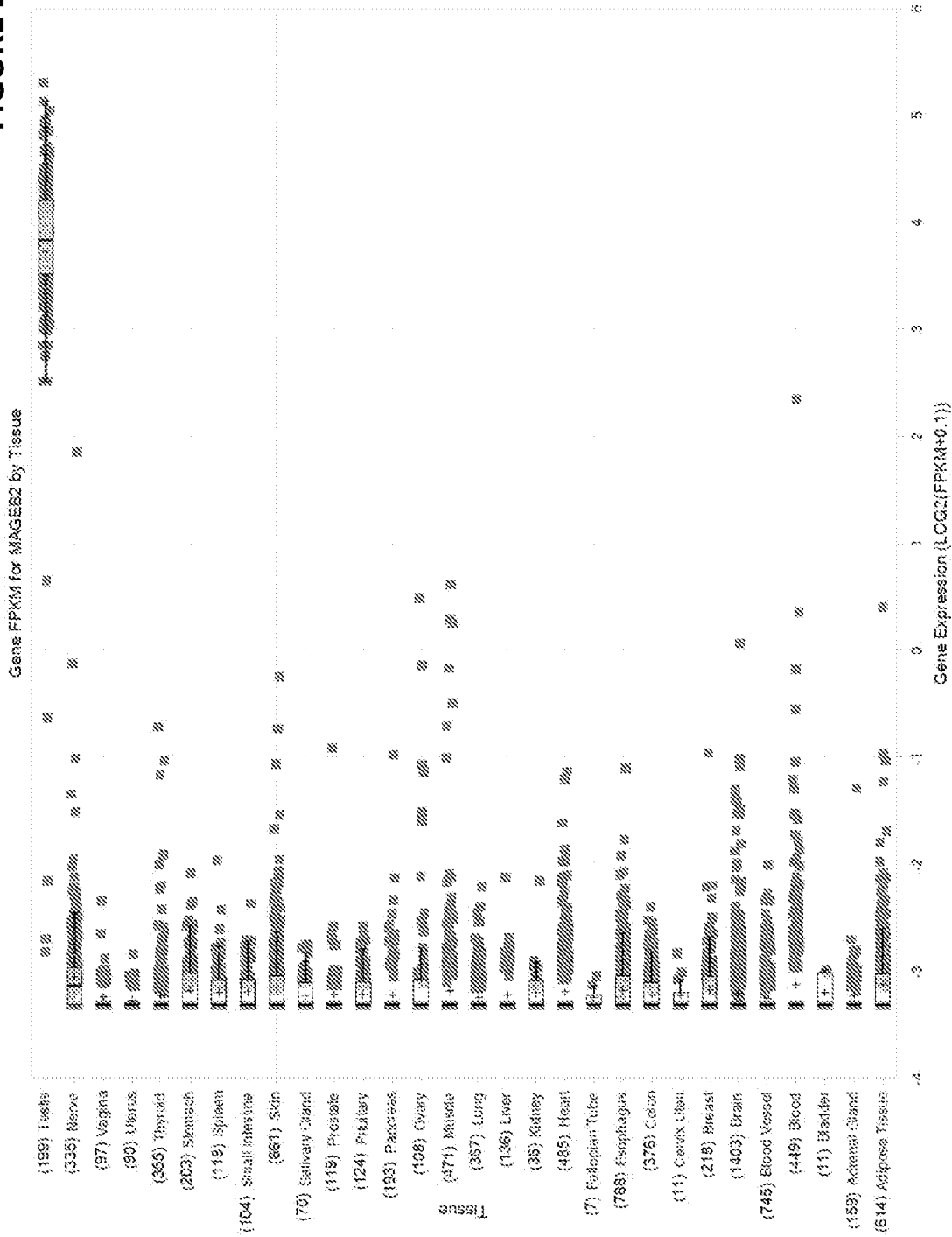


FIGURE 2E

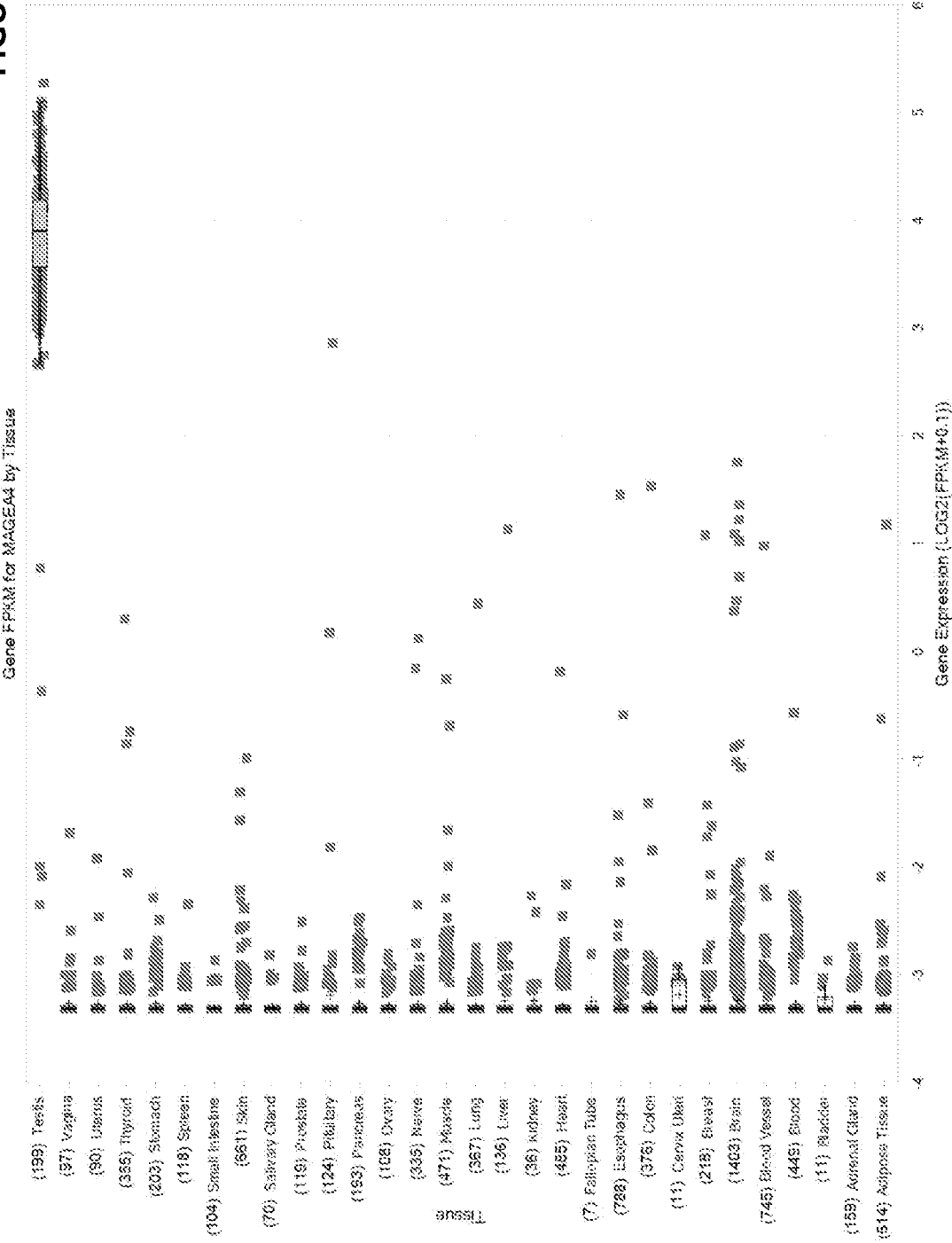


FIGURE 2F

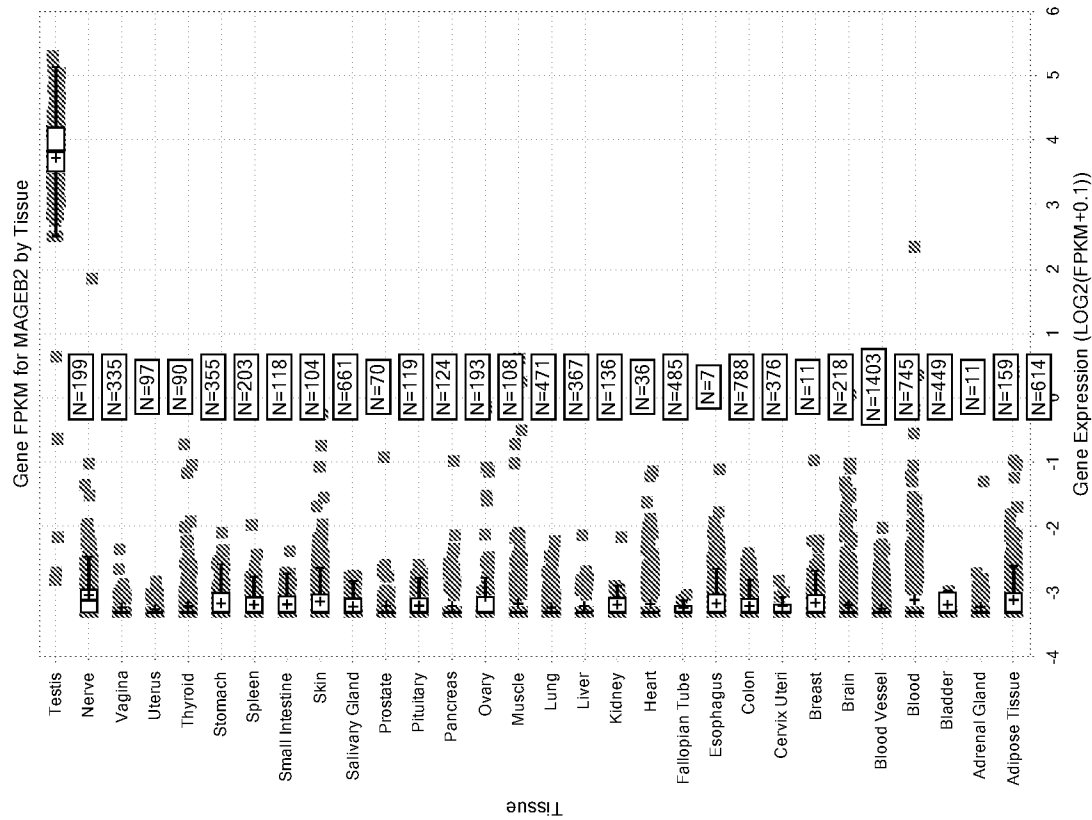


FIGURE 3A

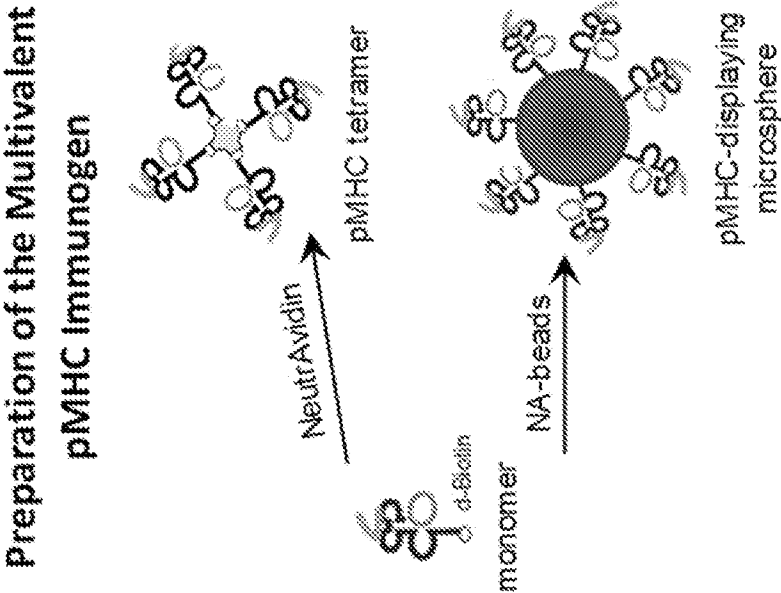


FIGURE 3B

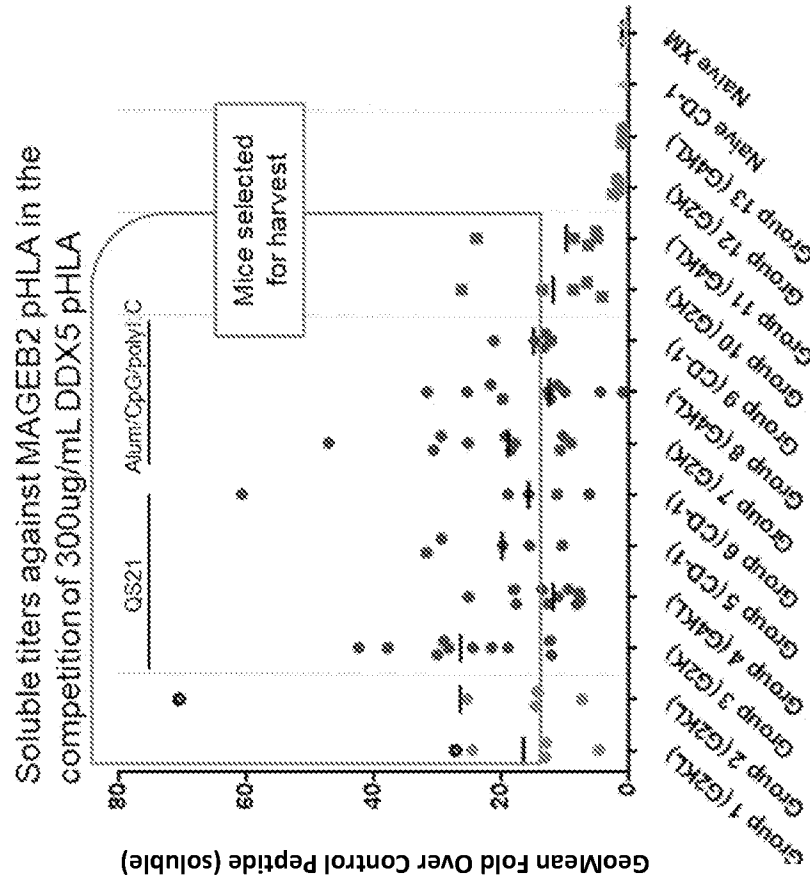
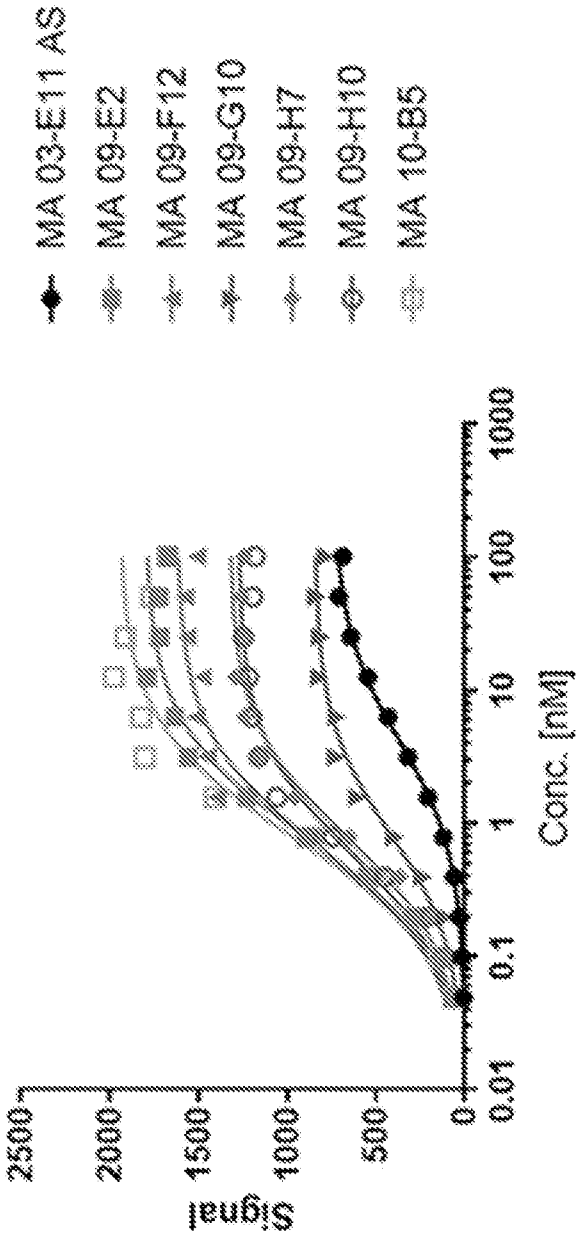


FIGURE 4A

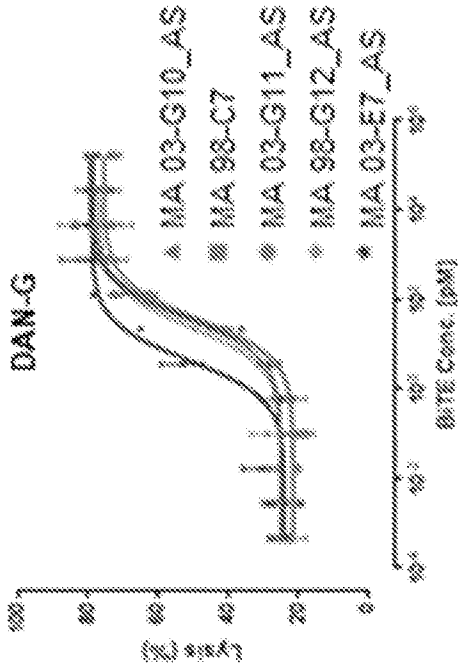
Evaluation of MAGEB2 pMHC HLE bispecific antibody constructs in vitro affinity and efficacy



Cell-based affinity determination by fluorescence cytometry and nonlinear regression (one site - specific binding) analysis on T2 cells loaded with MAGEB2 peptide. Tested MAGEB2 pMHC HLE bispecific antibody constructs are 1 = MA 03-E11_AS; 2 = MA 09-E2; 3 = MA 09-F12; 4 = MA 09-G10; 5 = MA 09-H7; 6 = MA 09-H10 and 7 = MA 10-B5.

FIGURE 4B

Evaluation of MAGEB2 pMHC HLE bispecific antibody constructs in vitro affinity and efficacy



Cytotoxicity assay on the MAGEB2 pMHC bearing cell line DAN-G. Tested MAGEB2 pMHC HLE bispecific antibody constructs are 1 = MA 03-G10_AS; 2 = MA 98-C7; 3 = MA 03-G11_AS; 4 = MA 98-G12_AS and 5= MA 03-E7_AS.

FIGURE 5A

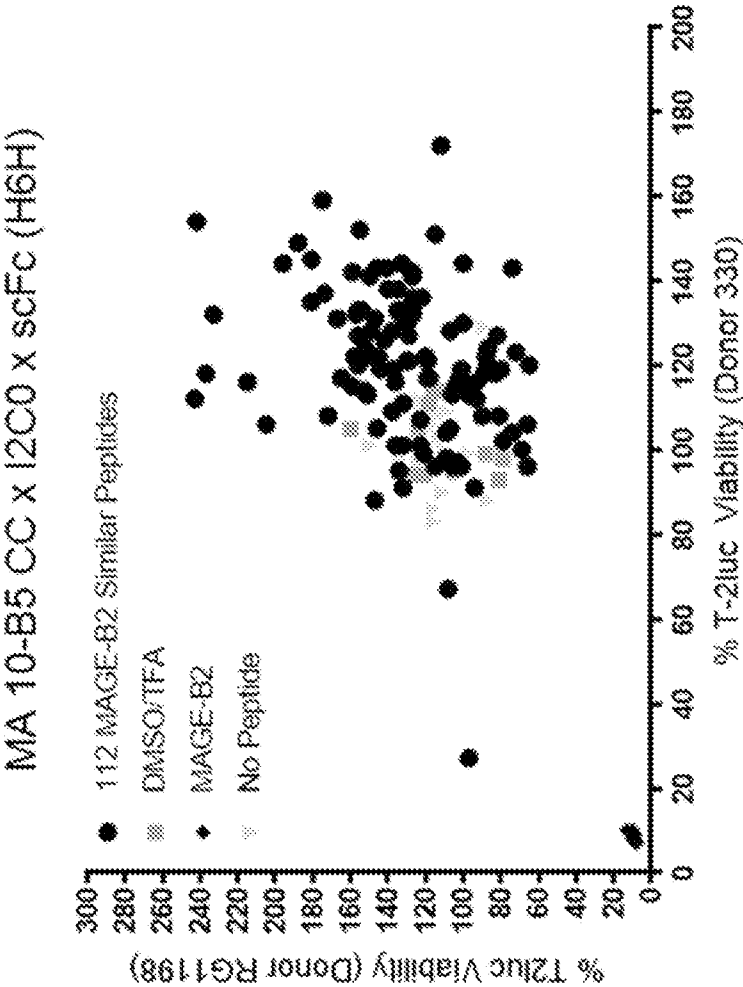


FIGURE 5B

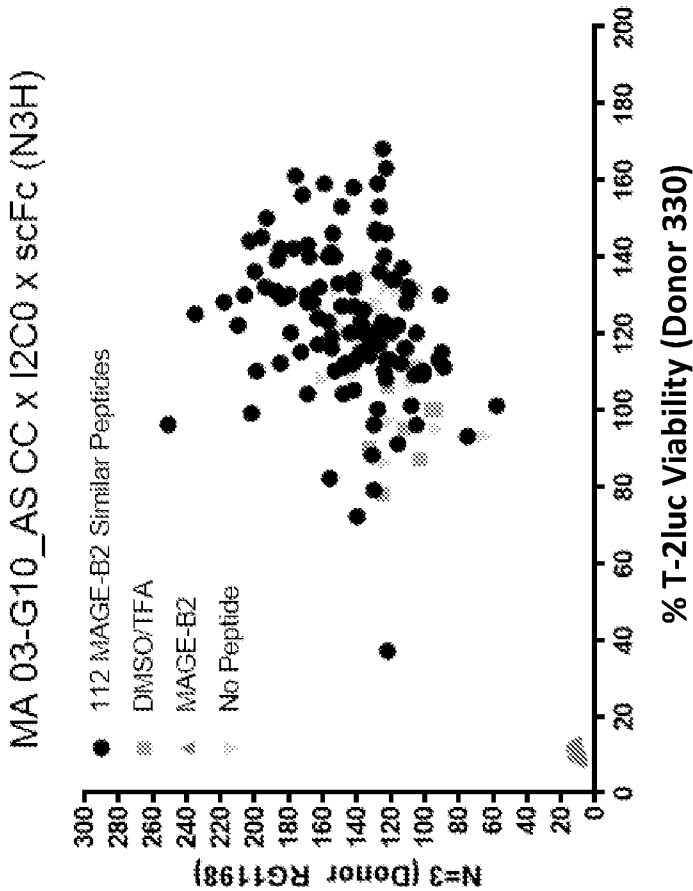


FIGURE 6A

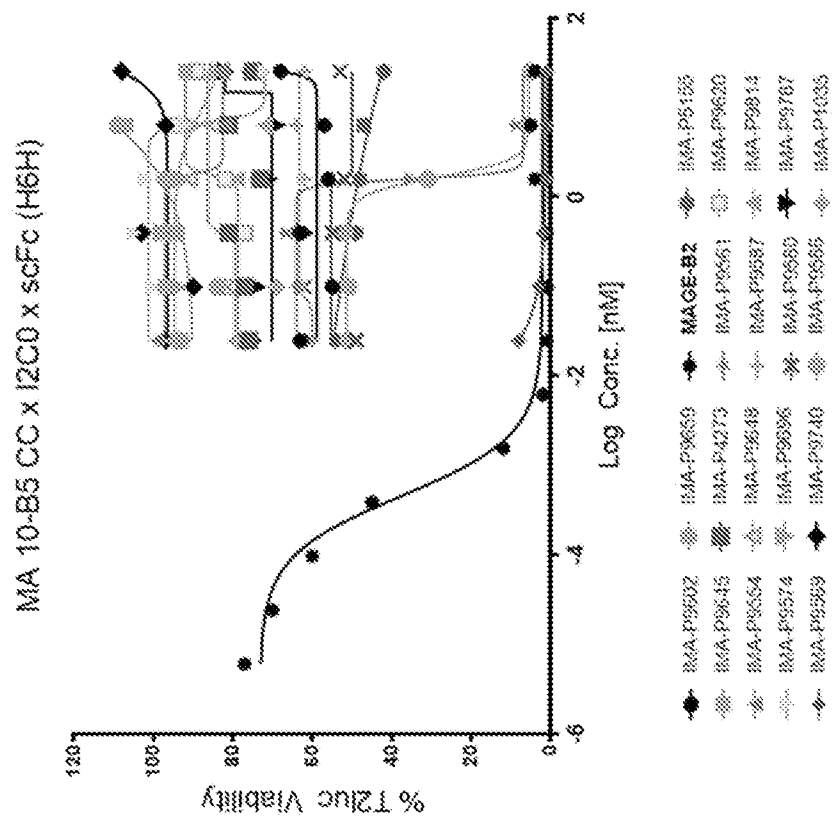


FIGURE 7

SCREENING OF MAGE-B2 9-MER PEPTIDES

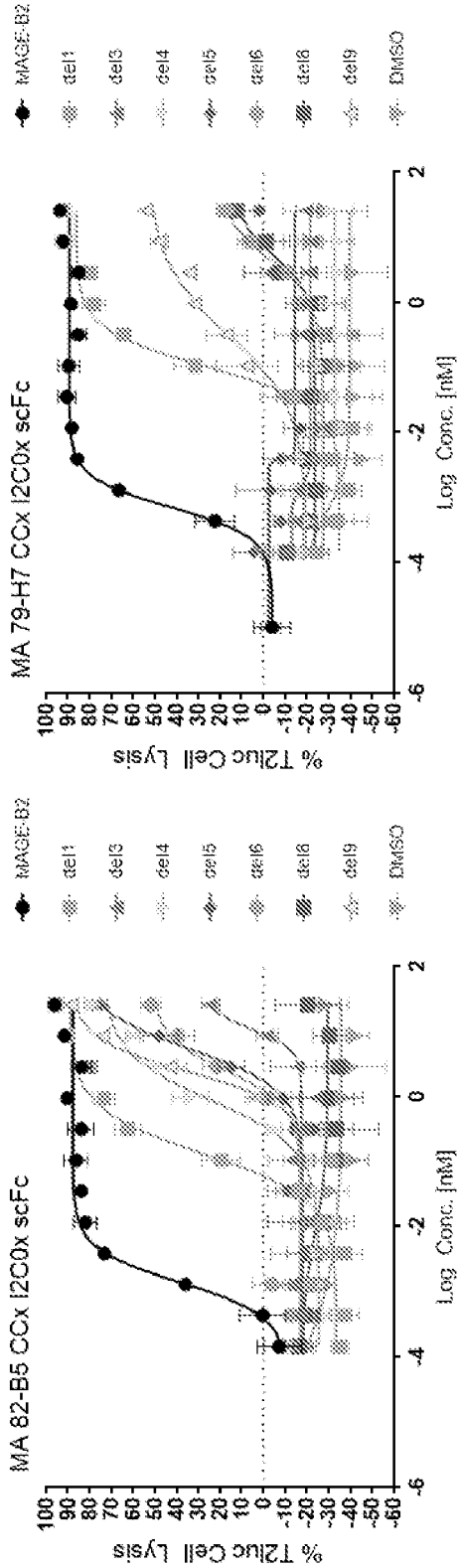


FIGURE 8

TDCC activity of Ten BiTE molecules on cell lines with known MAGEB2 pMHC copies per cell

BiTE	DANG (660 cpc)		NCI-H1792 (473 cpc)		SK-MEL (174 cpc)		SNU-475 (17 cpc)	
	EC50 (pM)	Max Killing (%)	EC50 (pM)	Max Killing (%)	EC50 (pM)	Max Killing (%)	EC50 (pM)	Max Killing (%)
C4K	183.7	96.2	319.4	64.0	112.4	93.8	1470.0	89.9
D1U	62.5	97.2	92.6	79.0	42.5	97.6	1400.0	90.6
H6H	47.9	91.7	55.2	66.4	25.8	90.8	1456.0	14.3
L6A	28.7	95.7	23.3	79.0	9.4	96.9	10943.0	32.8
L7E	10.3	97.6	8.6	77.1	6.6	98.6	2799.0	56.7
N3H	53.4	95.0	21.90	64.6	20.8	96.1	3577.0	21.7
O4R	38.4	96.1	24.8	83.2	14.2	97.1	14815.0	28.3
Q4C	160.9	91.5	148.1	69.5	66.3	87.9	N/A	13.4
V8T	76.1	93.6	N/A	44.3	46.2	94.1	N/A	17.5
Y8P	28.2	93.3	33.5	64.1	15.3	95.9	N/A	28.8

"cpc" = copies per cell

FIGURE 9
TDCC plots of 3 BiTE molecules on cell lines with intermediate-low expression of MAGEB2

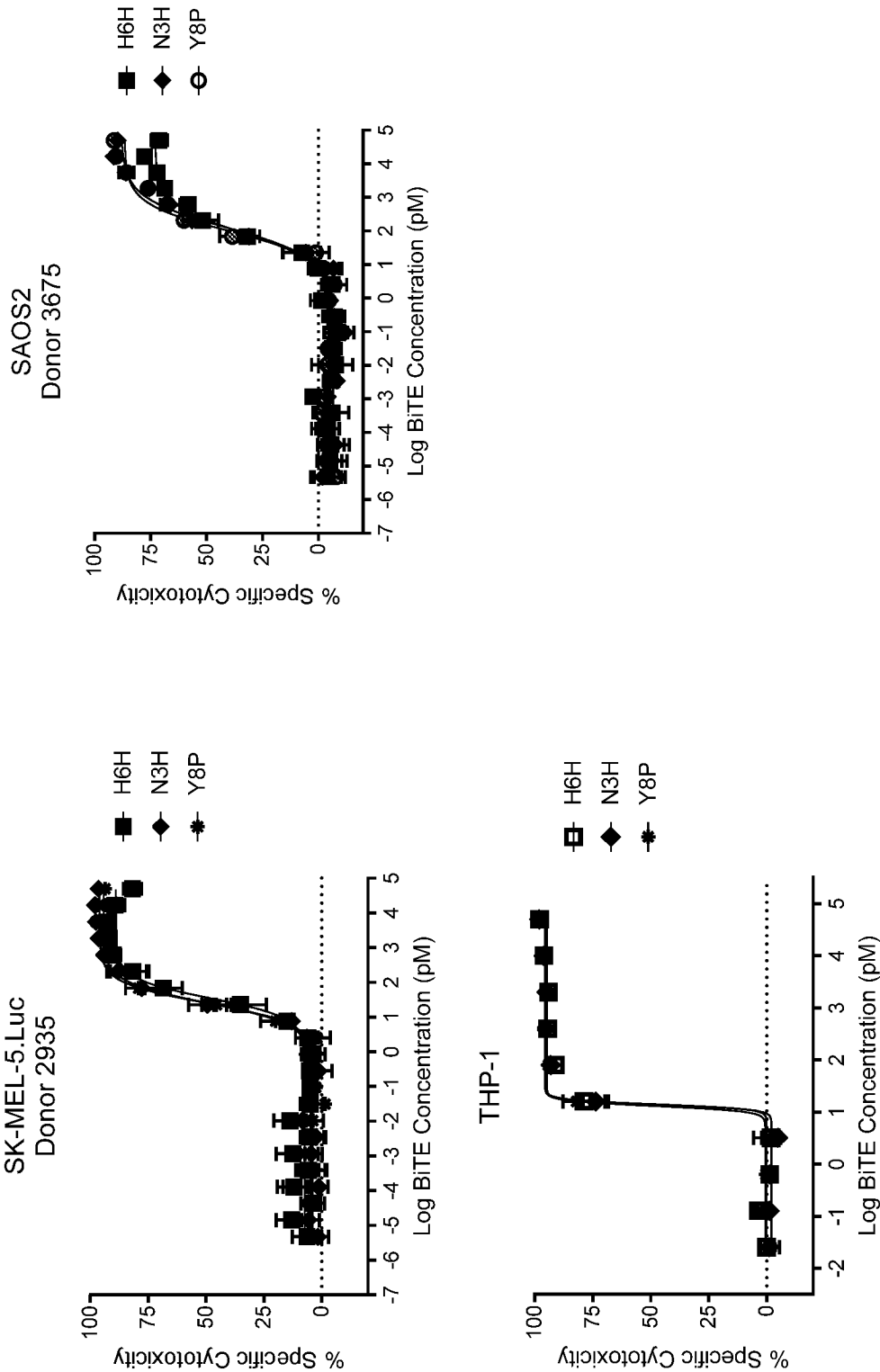


FIGURE 10

Activity of BiTE Molecules on MAGEB2 (+) and MAGEB2 (-) Cells

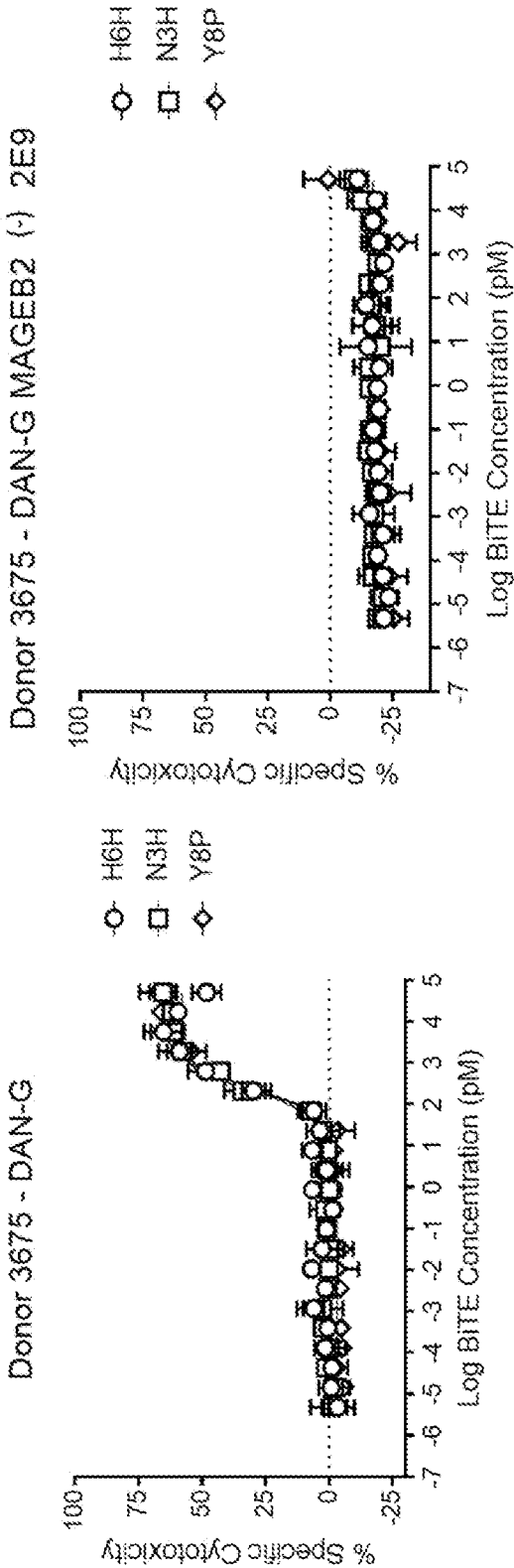


FIGURE 11A

MAGEB2 BiTE Specificity on Normal Cells
(cardiac myocytes, endothelial & epithelial cells)

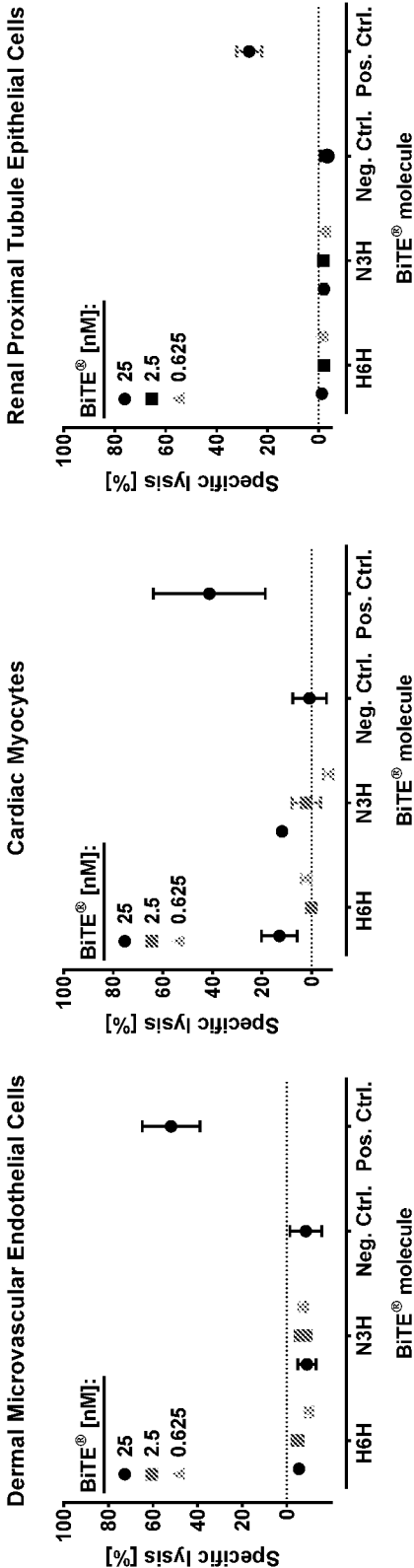


FIGURE 11B

MAGEB2 BiTE Specificity on MAGE-B2(-) Cells

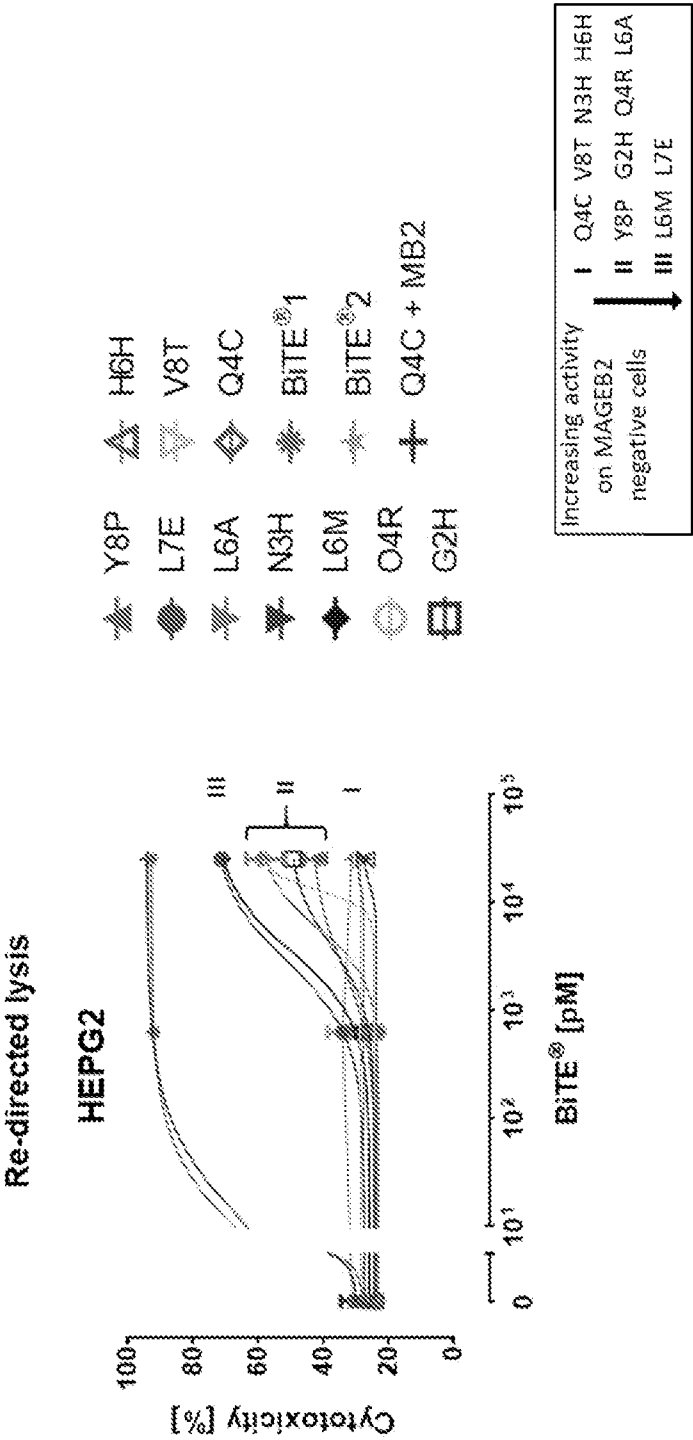


FIGURE 12A

TDCC Activity on MAGEA4(+) MAGEB2(-) HLA-A*02:01 Cell Lines

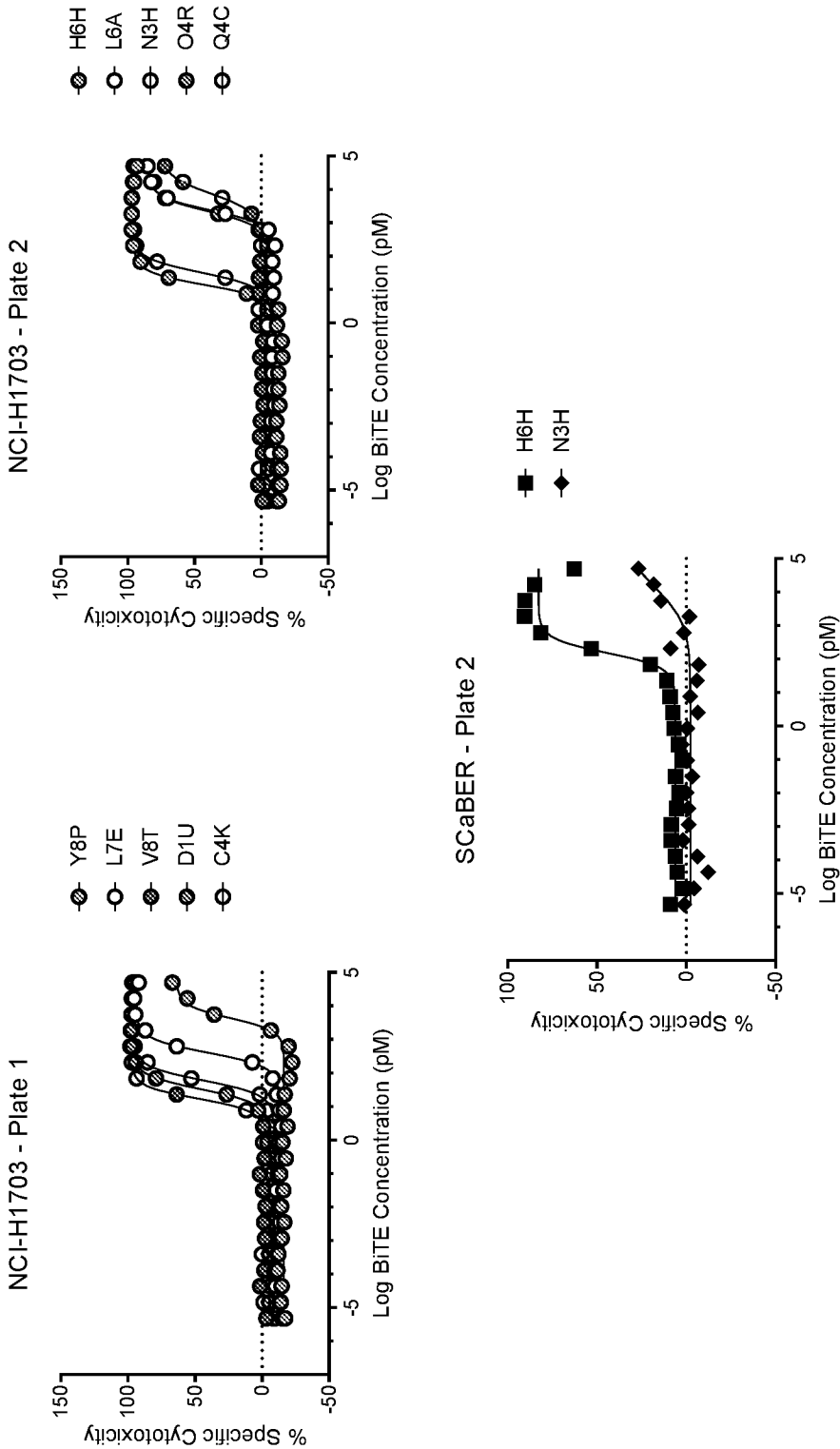


FIGURE 12B

TDCC Activity on MAGEA4(+) MAGEB2(-) HLA-A*02:01 Cell Lines

ID	Family	NCI-H1703		SCaBER	
		EC50 (pM)	Max	EC50 (pM)	Max
Y8P	4	4338	67	516	21
L7E	4	406	92	1293	32
G2H	4	4436	74	ND	28
L6A	4	2352	85	2360	36
L6M	4	424	88	1869	33
N3H	4	7533	72	12549	27
O4R	4	2224	86	ND	36
V8T	7	17	95	238	47
H6H	7	14	93	154	63
Q4C	7	33	96	348	75

Family 7 molecules show activity against MAGE-A4 expressing cell lines;
Family 4 molecules to not cross-react with MAGE-A4 expressing cell lines

FIGURE 13A

MAGE-B2 peptide interactions with MHC

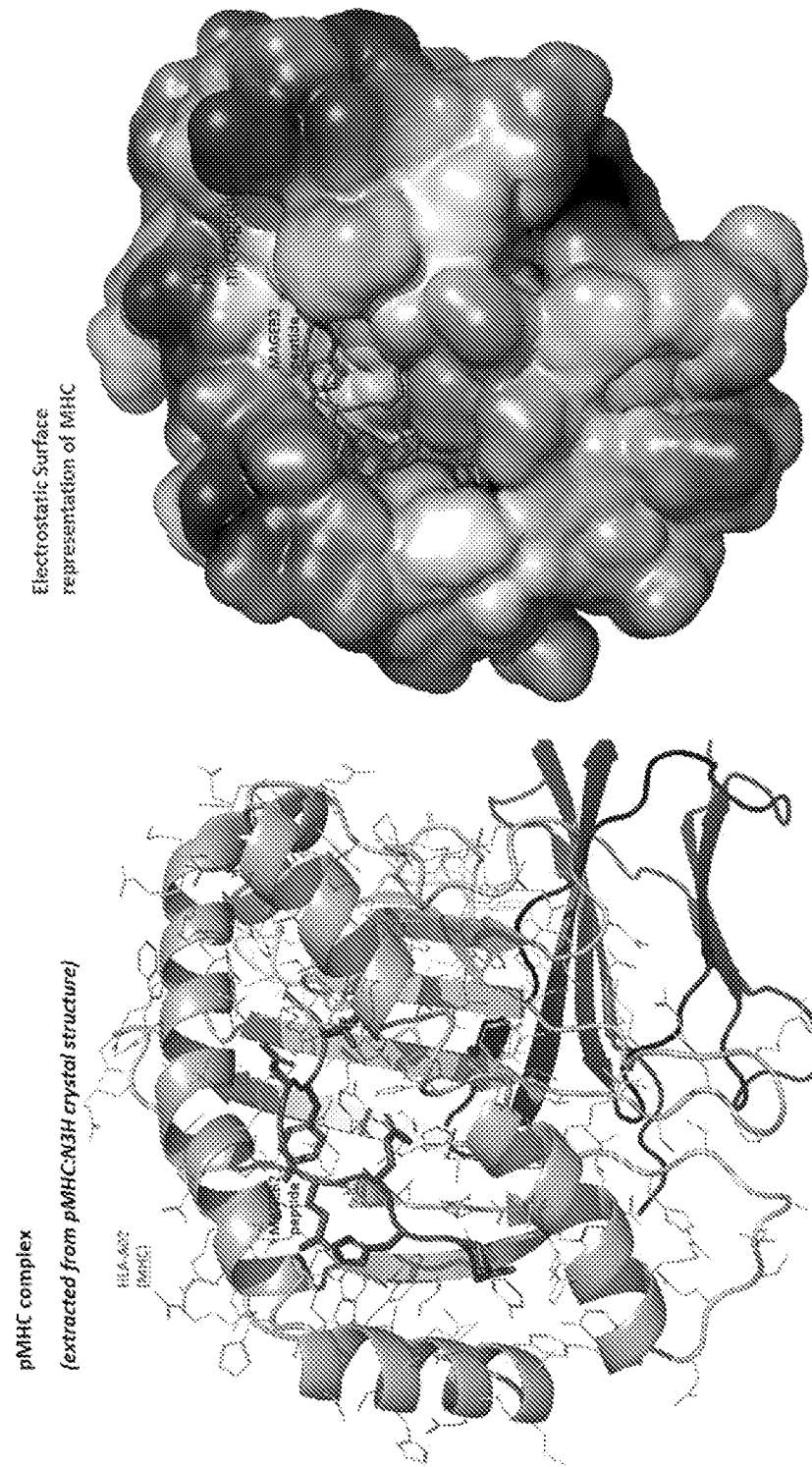


FIGURE 13B

Specificity of MAGEB2 Peptide to Particular HLA-A*02 Serotypes

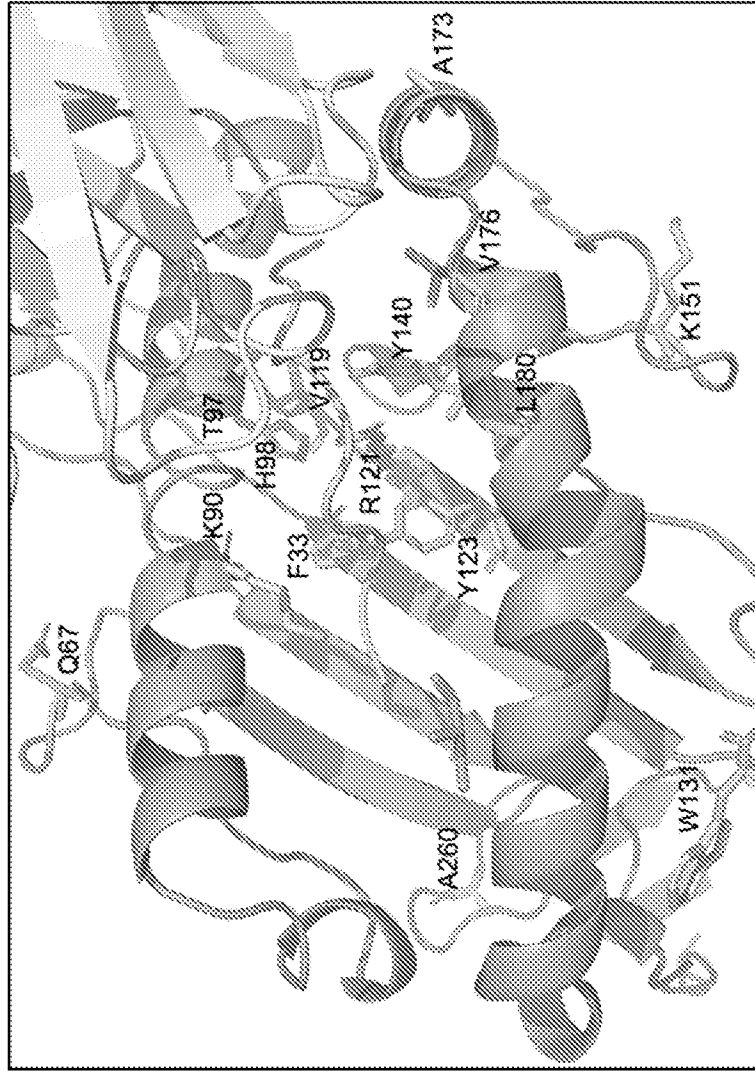


FIGURE 14

Family 4 L7E_{scFv} Bound MAGE-B2 HLA-A: Overall Structure at 1.9 Å

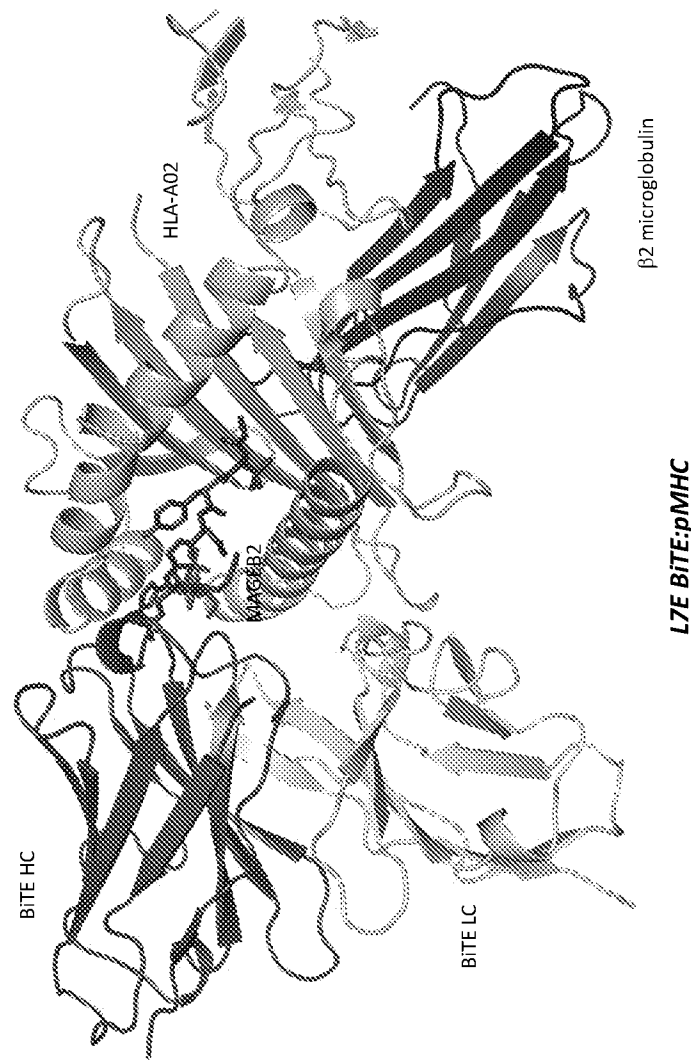


FIGURE 15

Family 4 L7E_{scFv} Bound MAGE-B2 HLA-A: Overall Structure at 1.9 Å

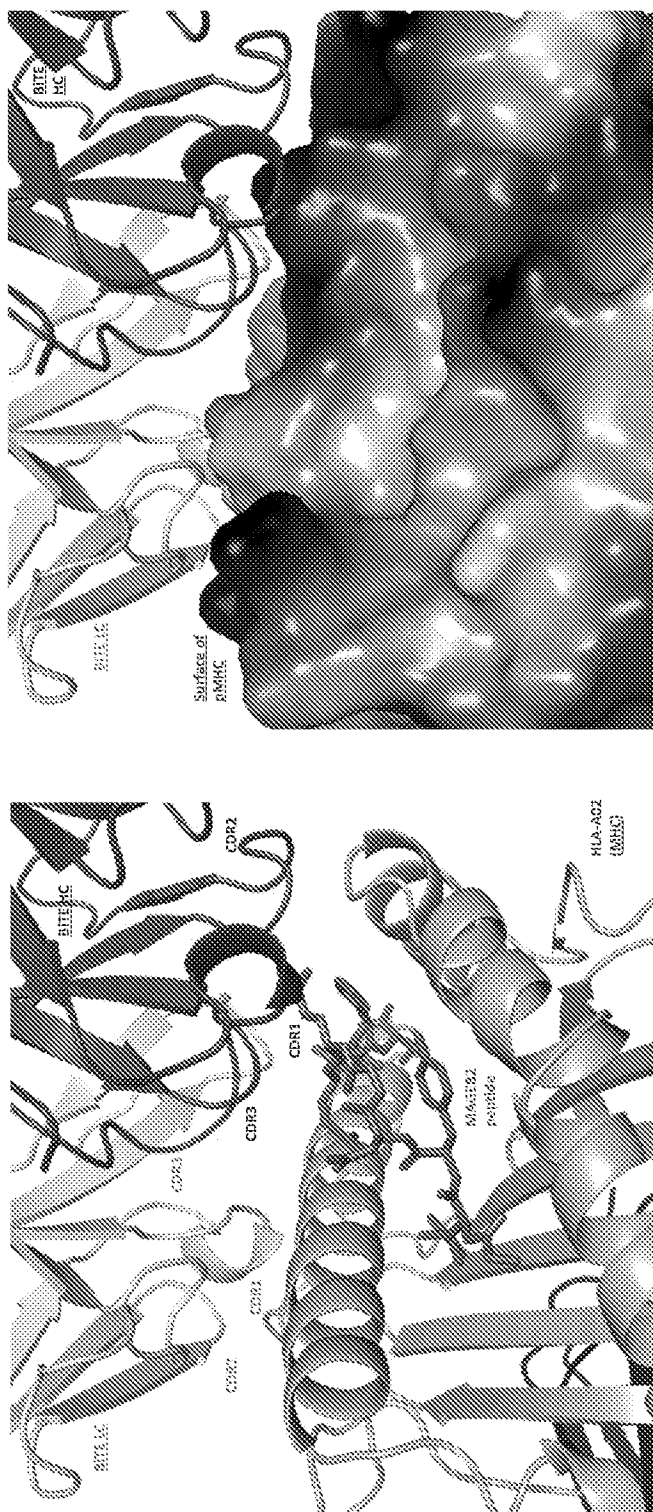


FIGURE 16

Family 4 L7E_{scFv} Bound MAGE-B2 HLA-A: Overall Structure at 1.9 Å

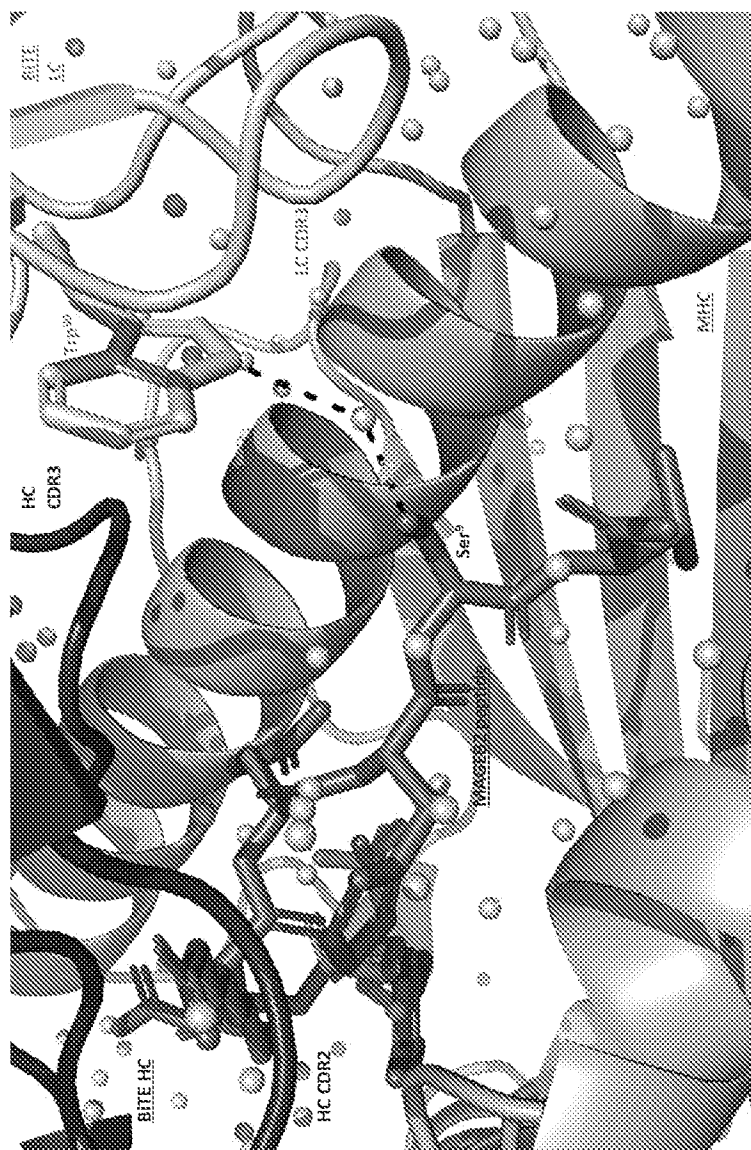
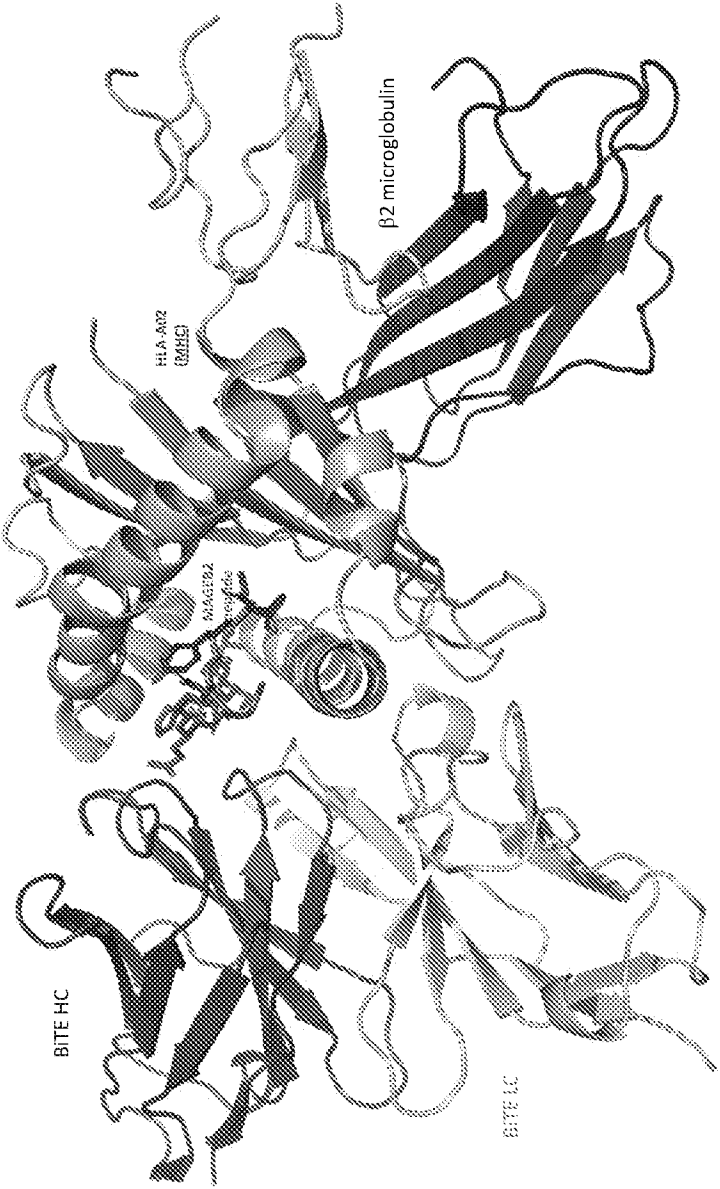


FIGURE 17

H6N scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions



H6N BITE:pMHC

FIGURE 18

H6N scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions

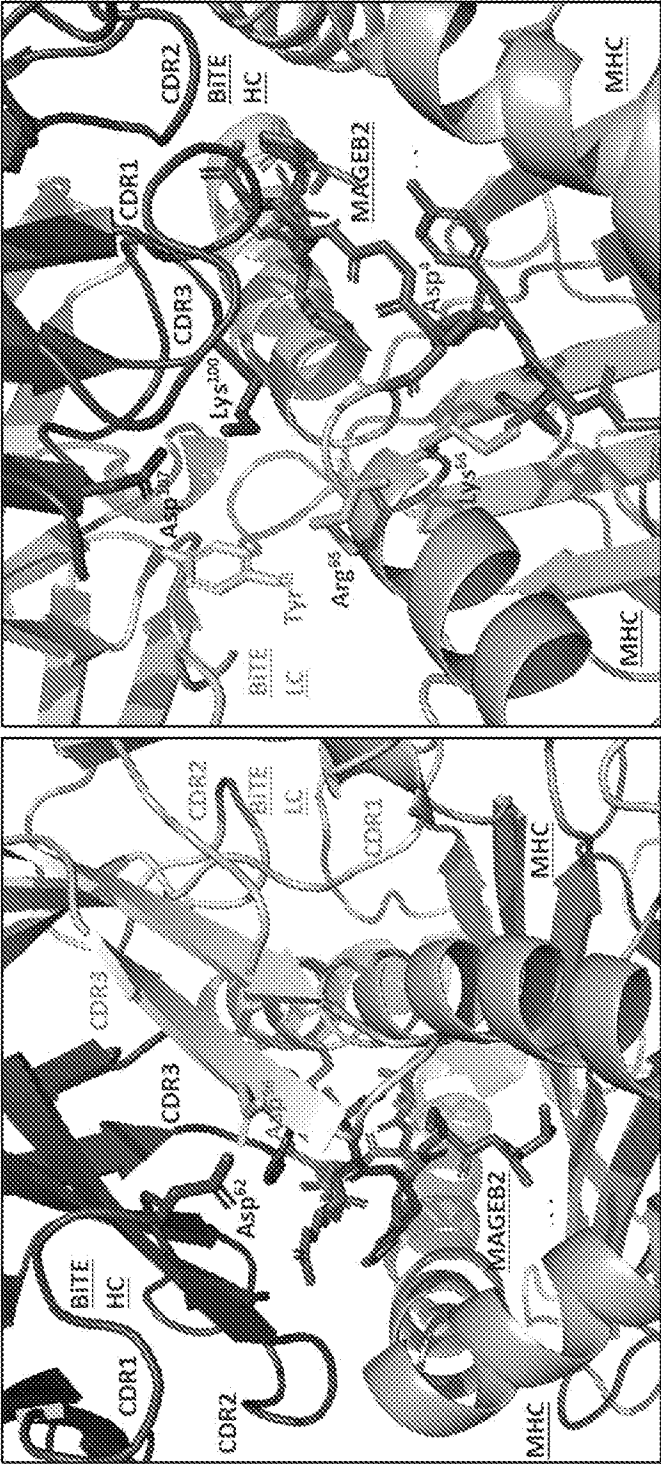


FIGURE 19

H6N scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions

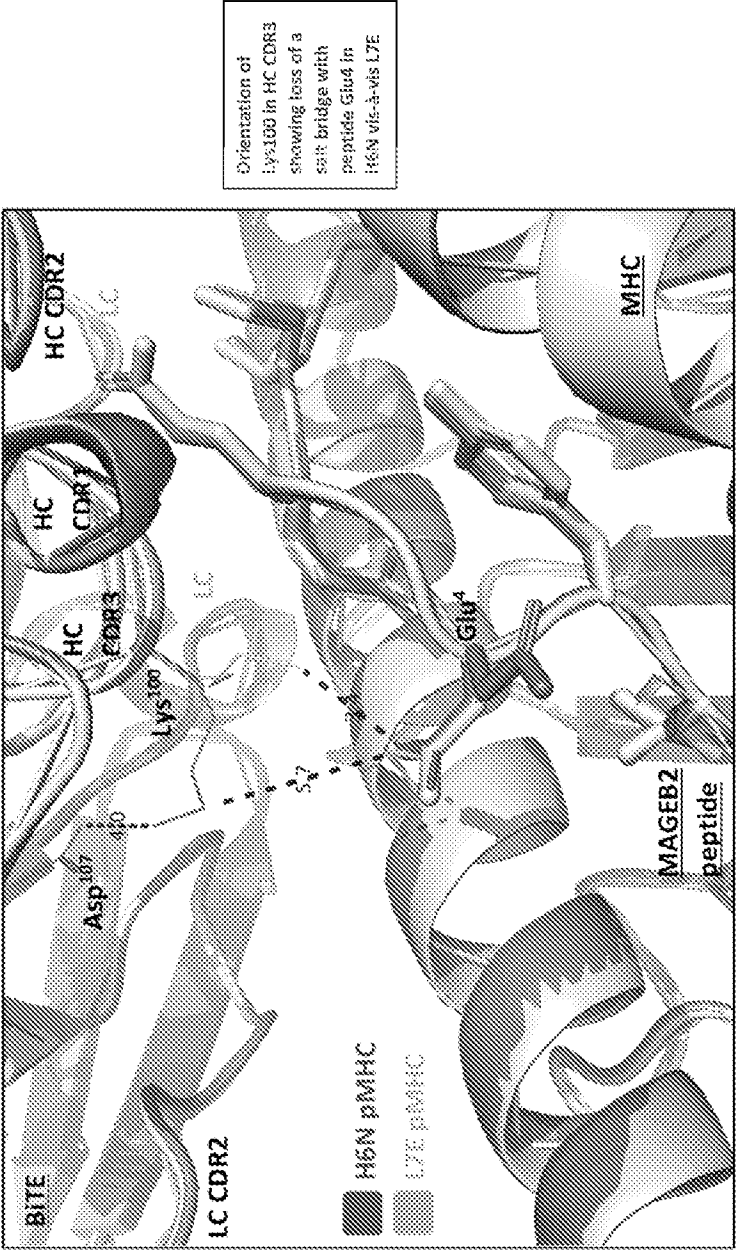
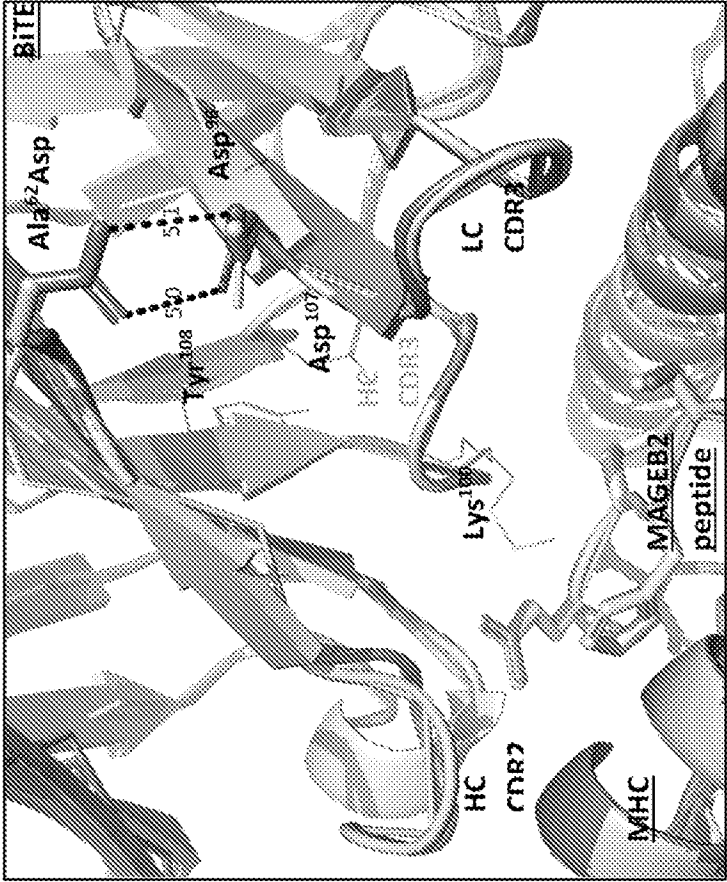


FIGURE 20

H6N scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions



Asp62 in H6N vis-à-vis Ala62: Asp62 seems to stabilize LC CDR3

H6N pMHC
L7E pMHC

FIGURE 21

N3H scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions

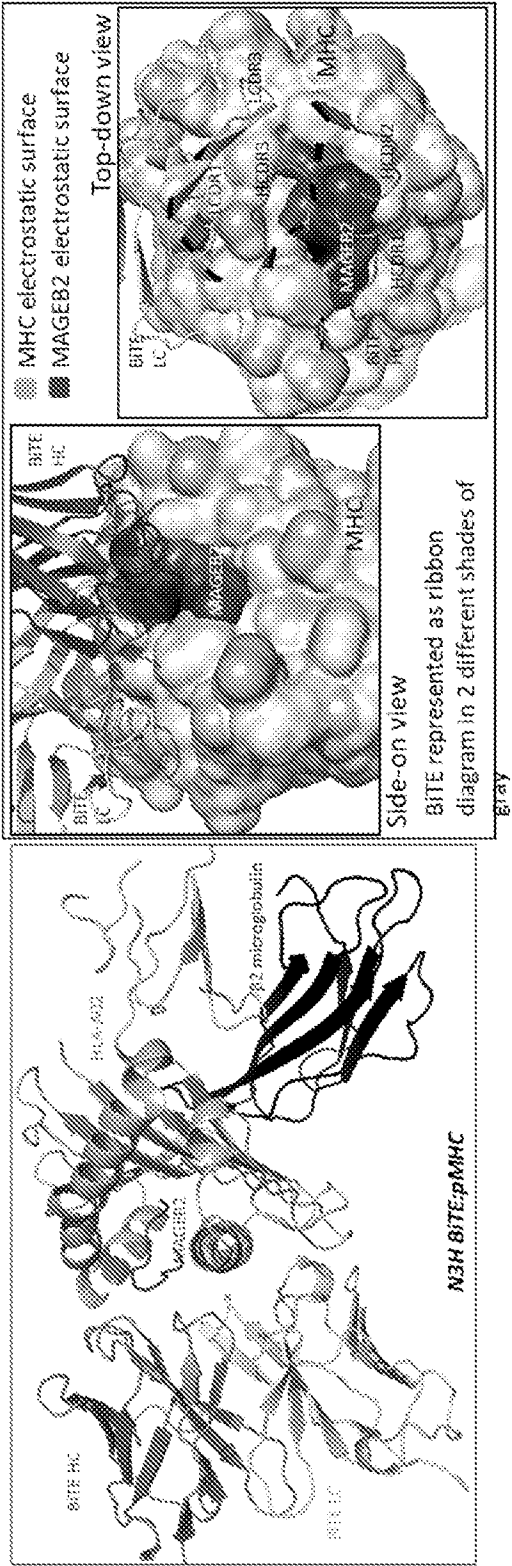


FIGURE 22

N3H scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions

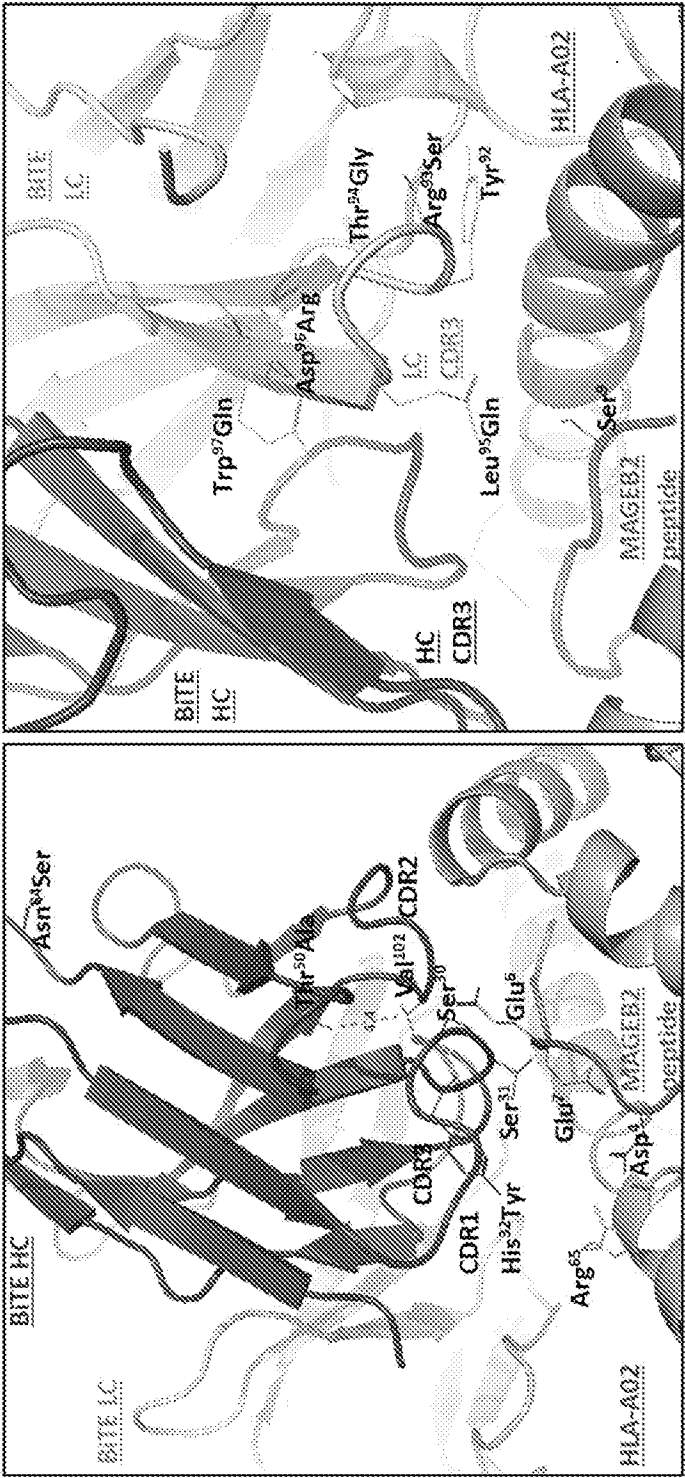


FIGURE 23
N3H scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions

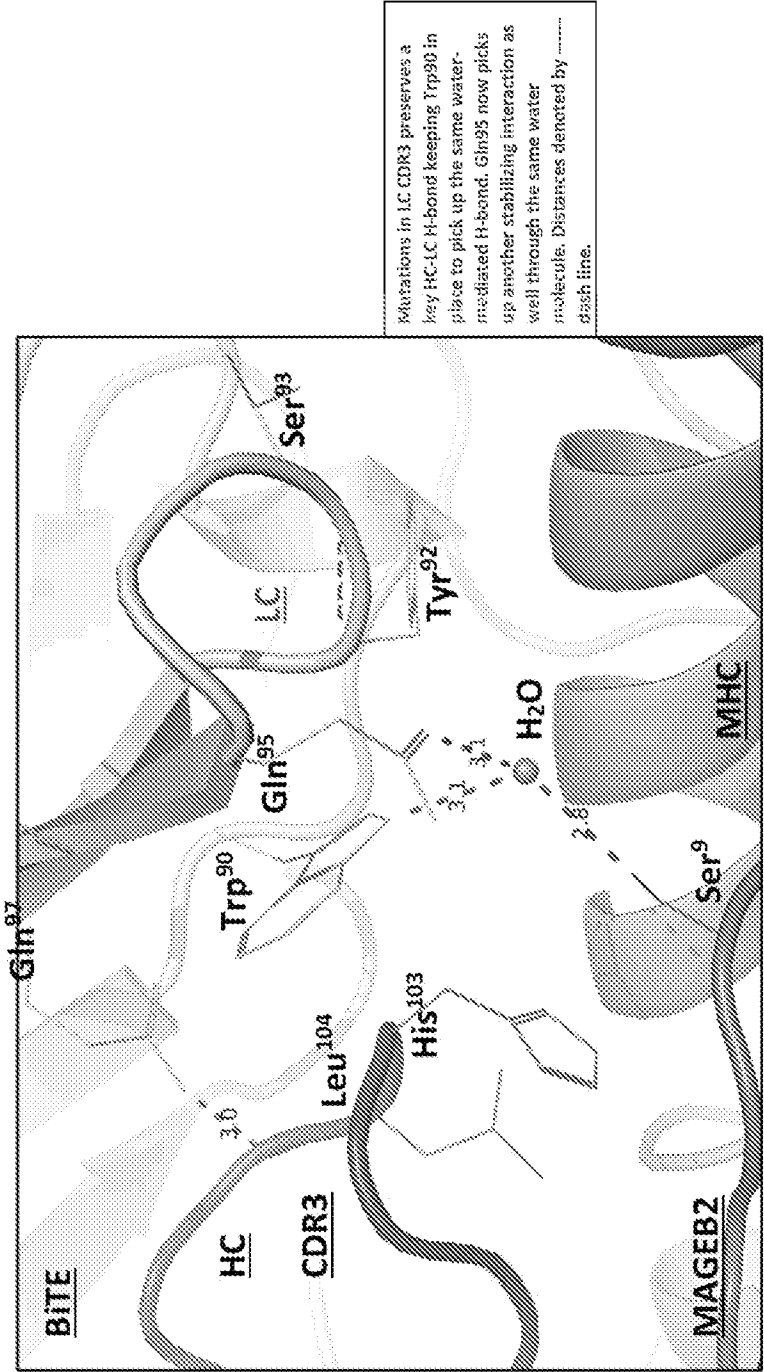


FIGURE 24
N3H scFv Heavy Chain Makes Direct Interactions with MAGEB2 Peptide, Light Chain Makes HLA and MAGEB2 Interactions

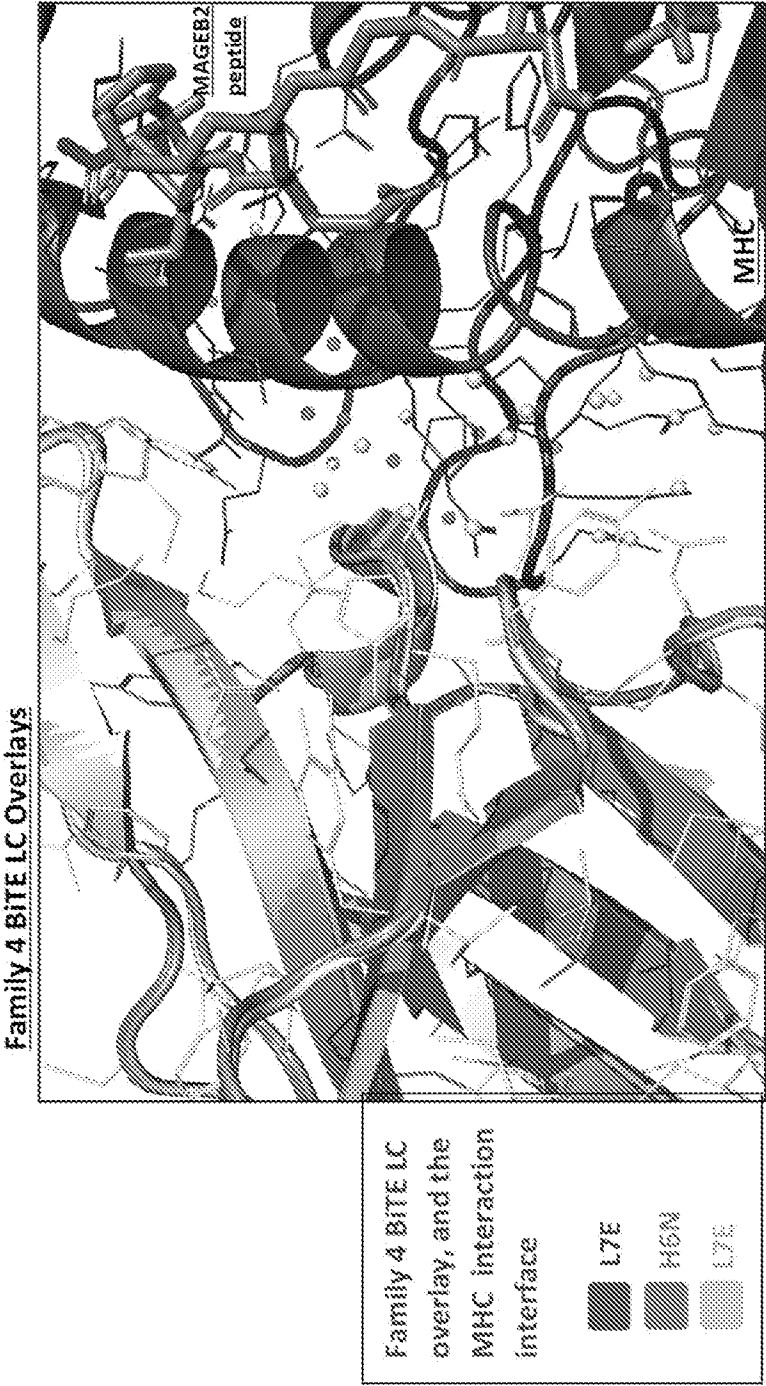


FIGURE 25

Sequence alignment of the Family 4 BiTE® Molecules

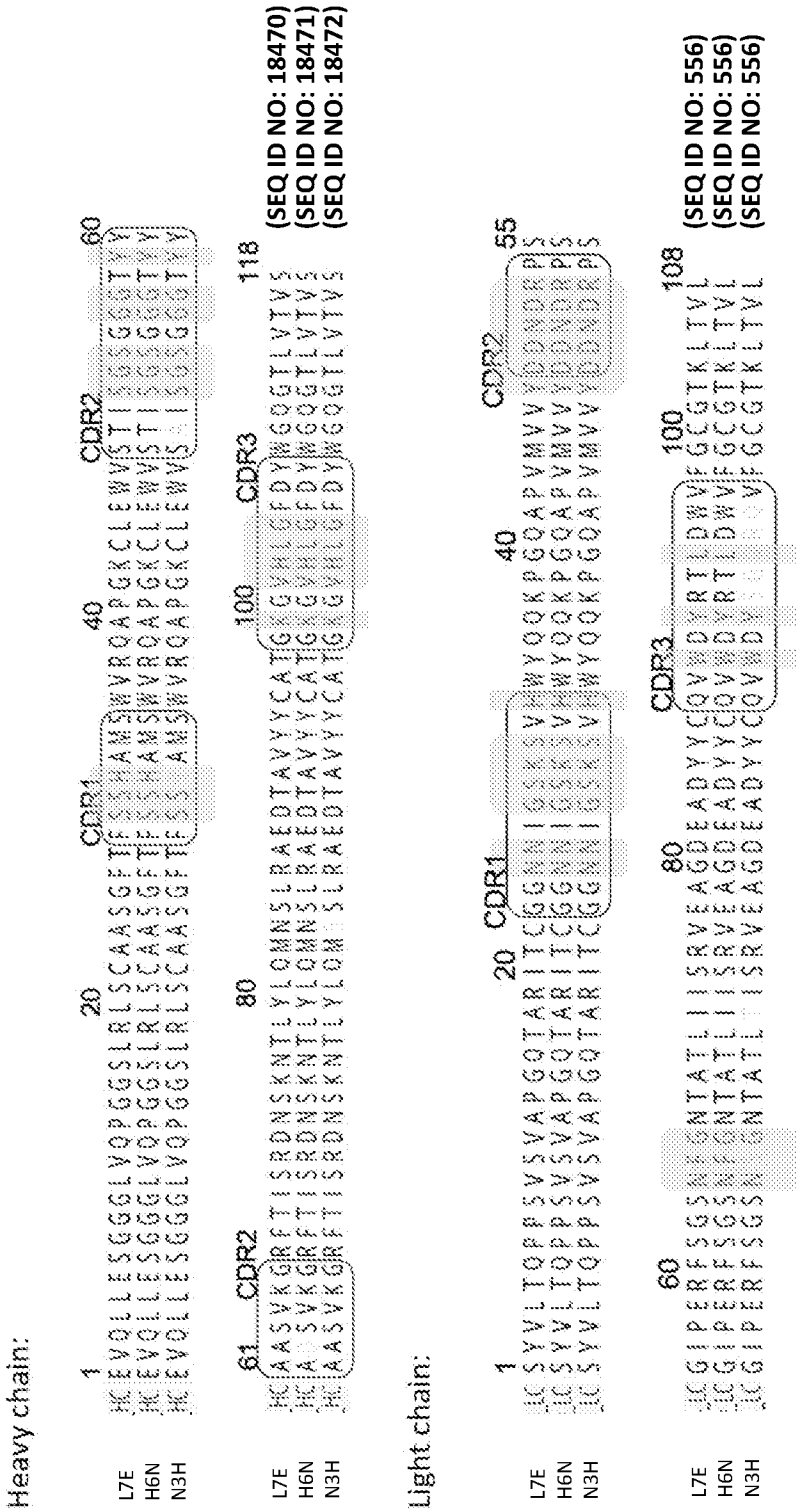


FIGURE 26

Sequence alignment of the Family 7 BiTE® Molecules

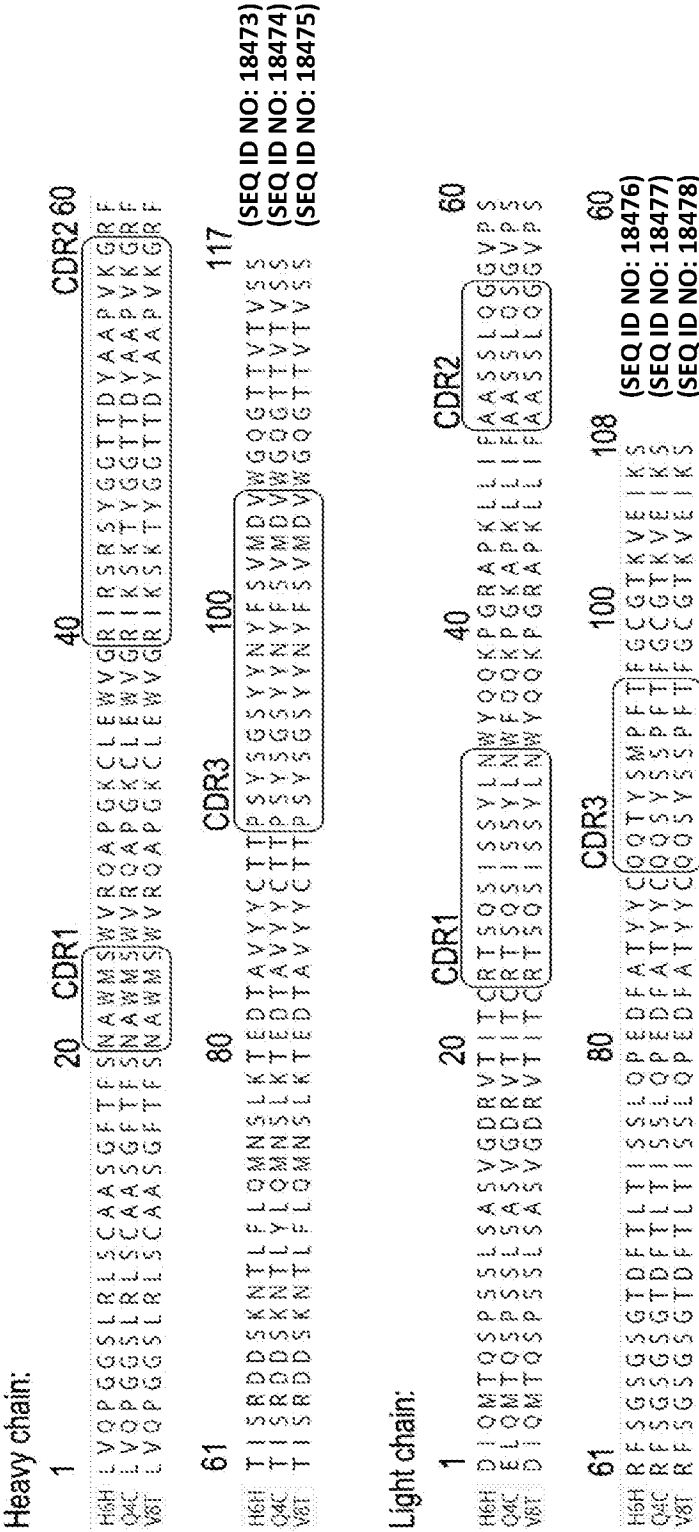


FIGURE 27

Maximum IL-2 production by HLA-A*02:06 and HLA-A*02:07 Expressing BLCLs

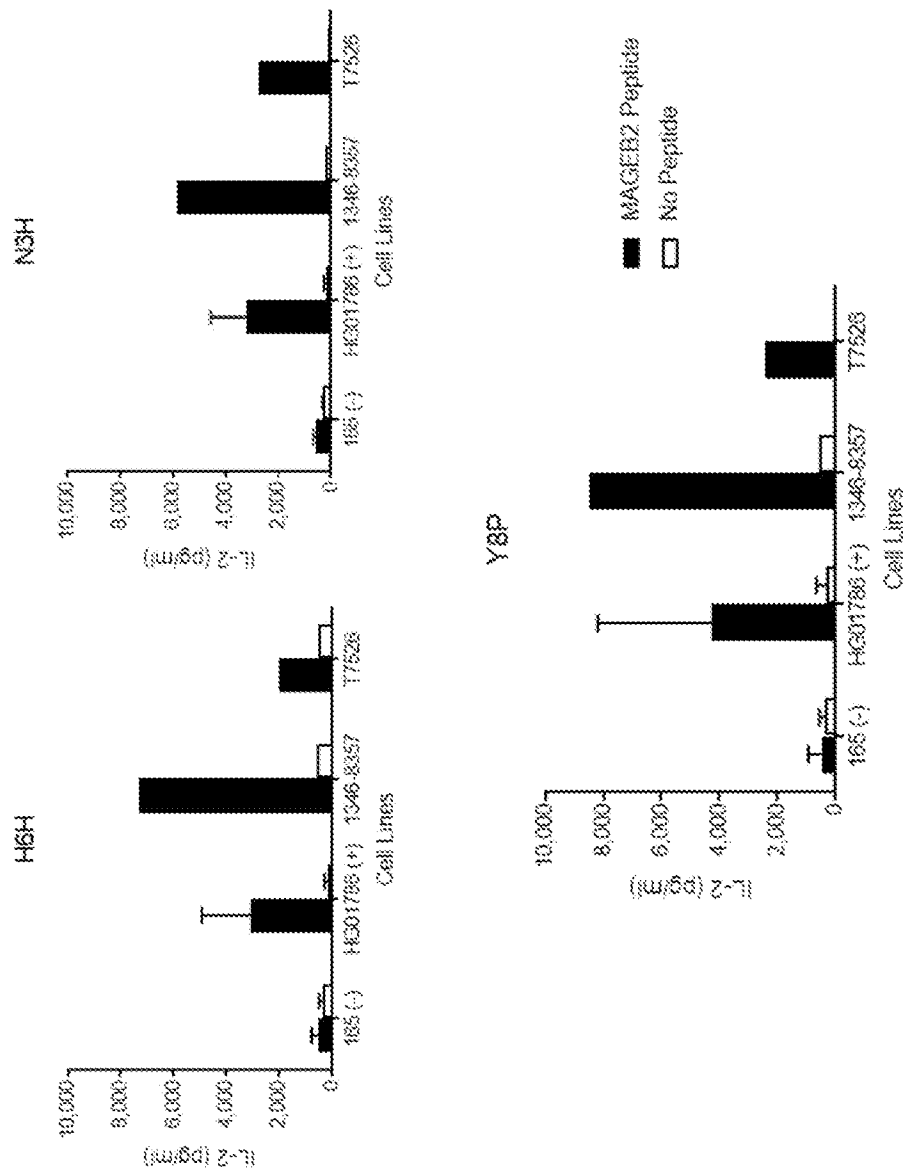


FIGURE 28

Structure of 10B5 (H6H) Binding MAGEB2 HLA-A at 2.02 Å

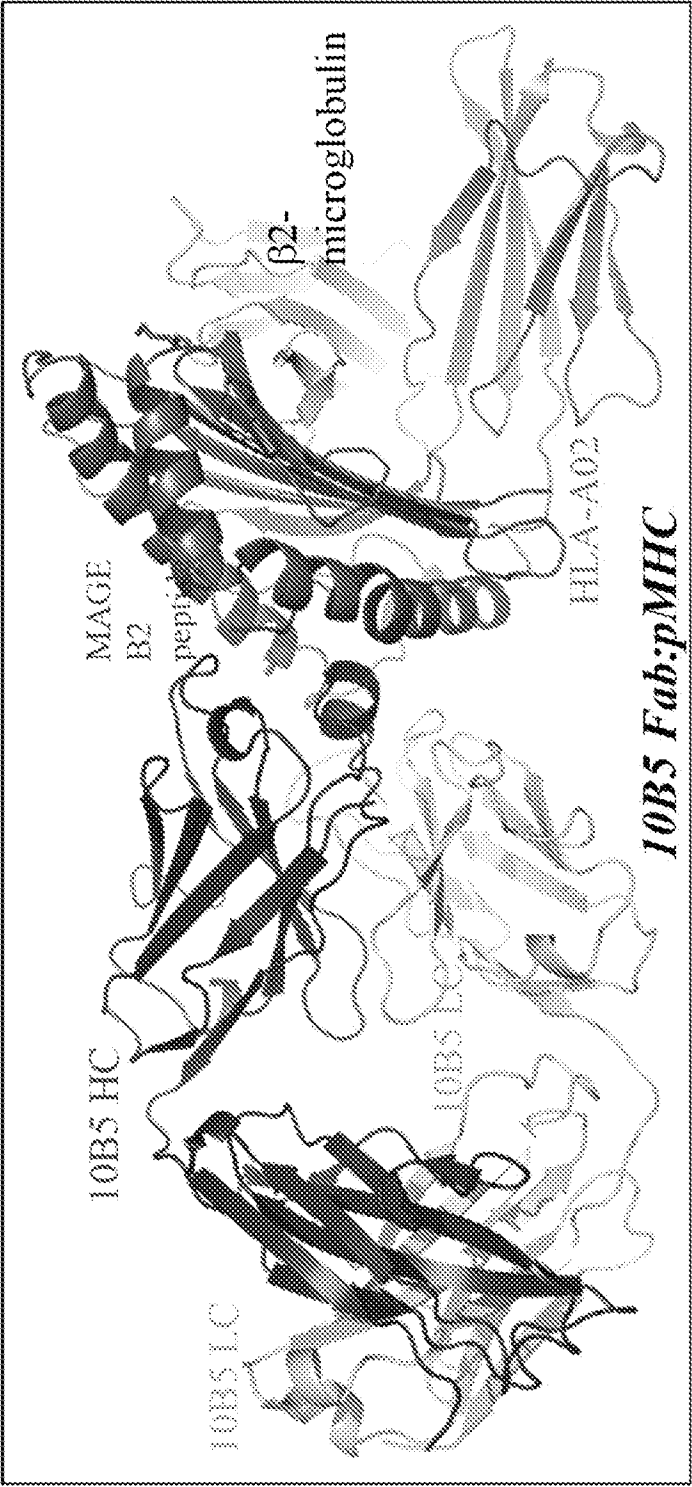
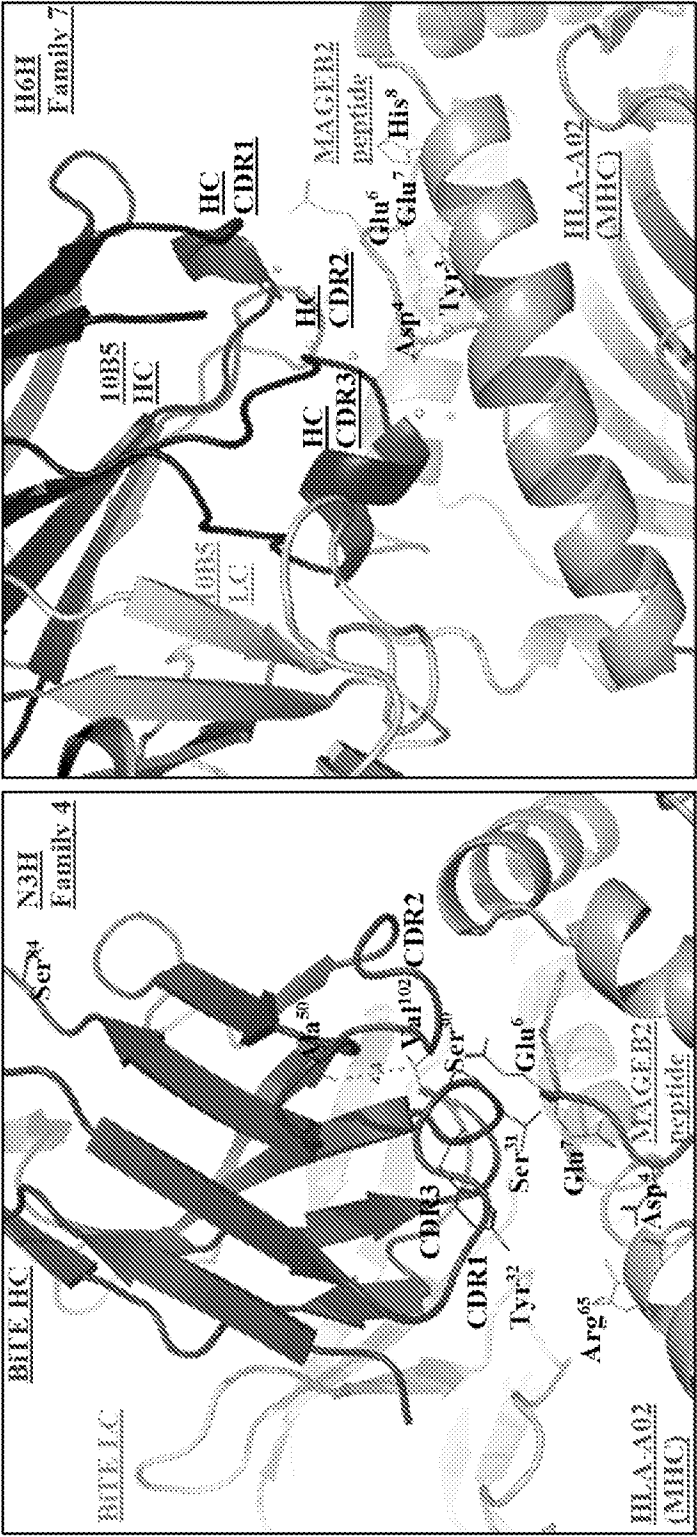


FIGURE 29

Structures of N3H and 10B5 (H6H)



Water Mediated Bonding Network of the
10B5 (H6H) Fab and MAGEB2 pMHC

FIGURE 30

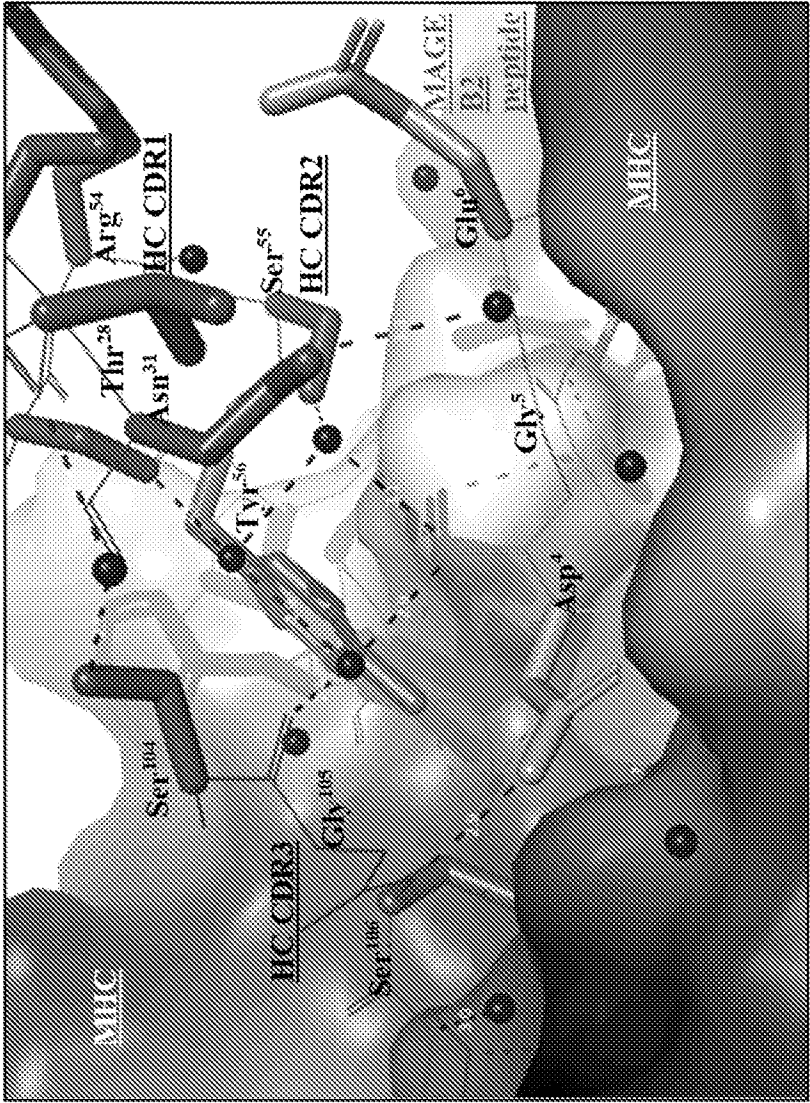


FIGURE 31

10B5 (H6H) Fab and MAGEB2 pMHC Complementary Surfaces

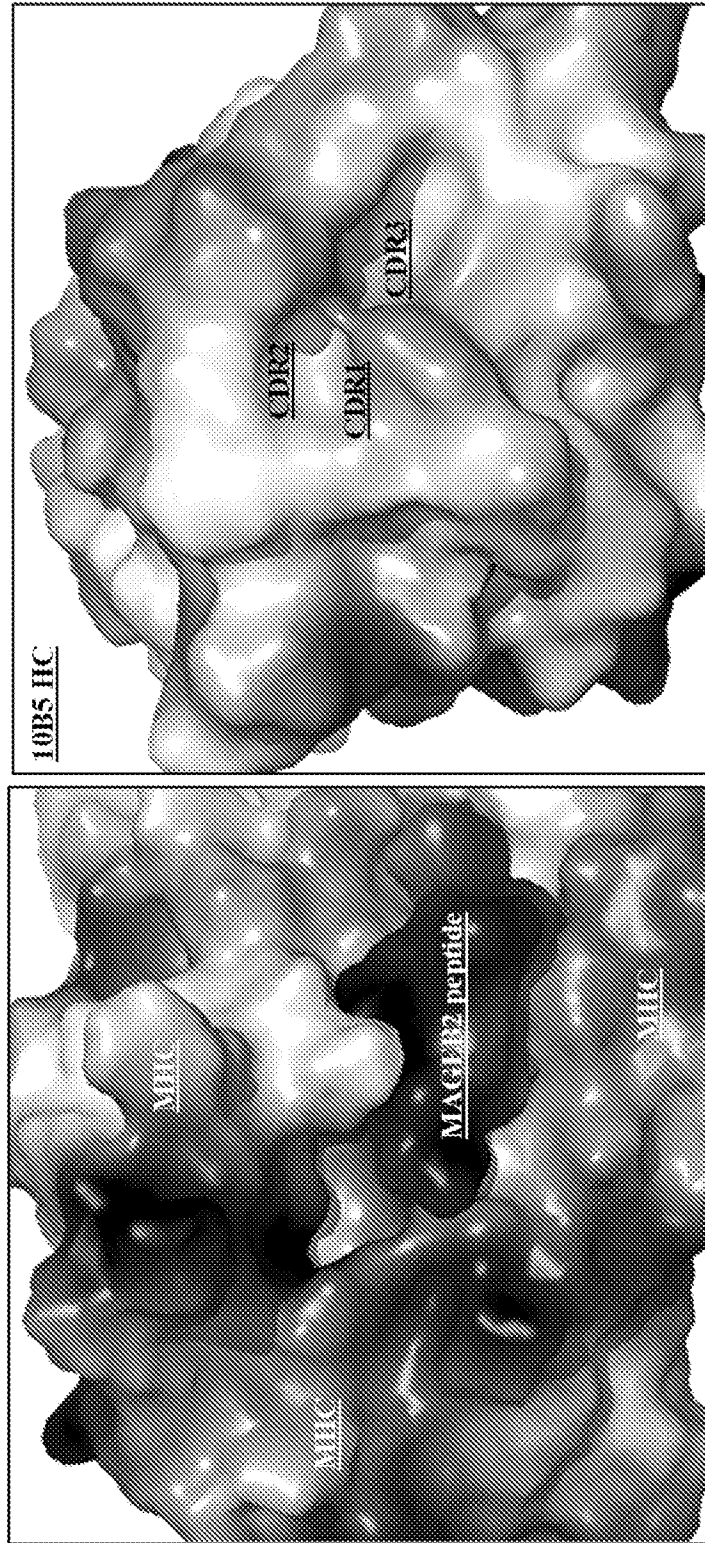
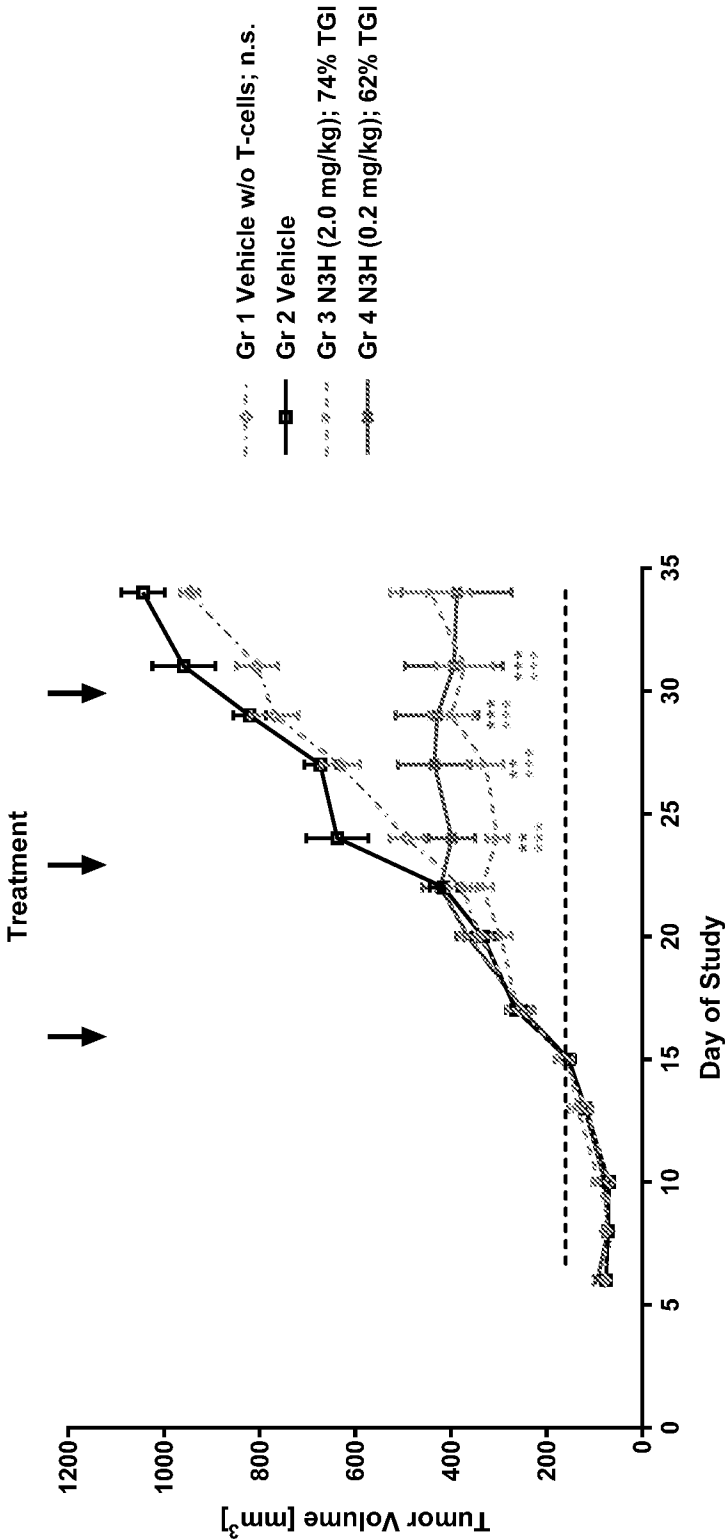


FIGURE 32

MEAN Tumor Volume With SEM following treatment with N3H



Data were analyzed by one-way ANOVA with Dunnett's post-hoc test: *, p<0.05; **, p<0.01; ***, p<0.001; no analysis on day 34 as only 4/10 animals in group 2 were alive
TGI: Tumor growth inhibition days 15-34 (group median)

FIGURE 33

Individual Animal Tumor Volume following treatment with N3H

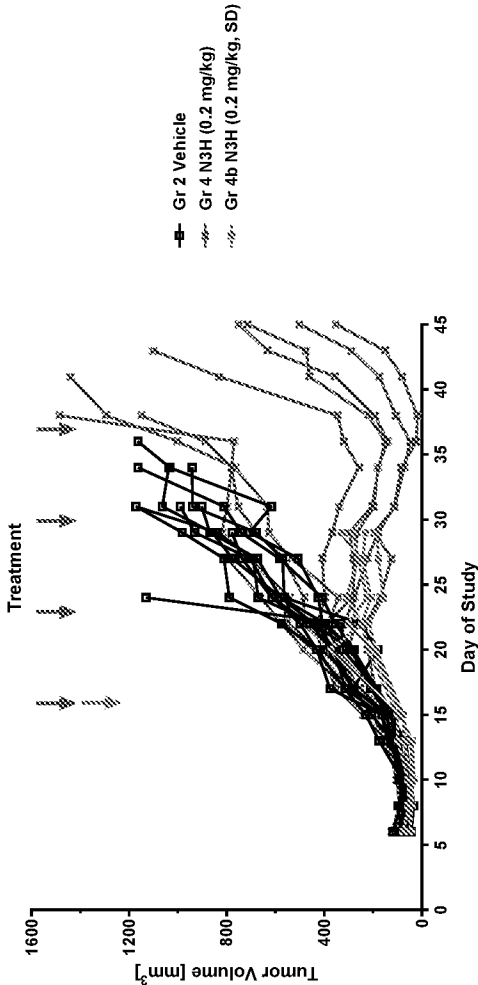
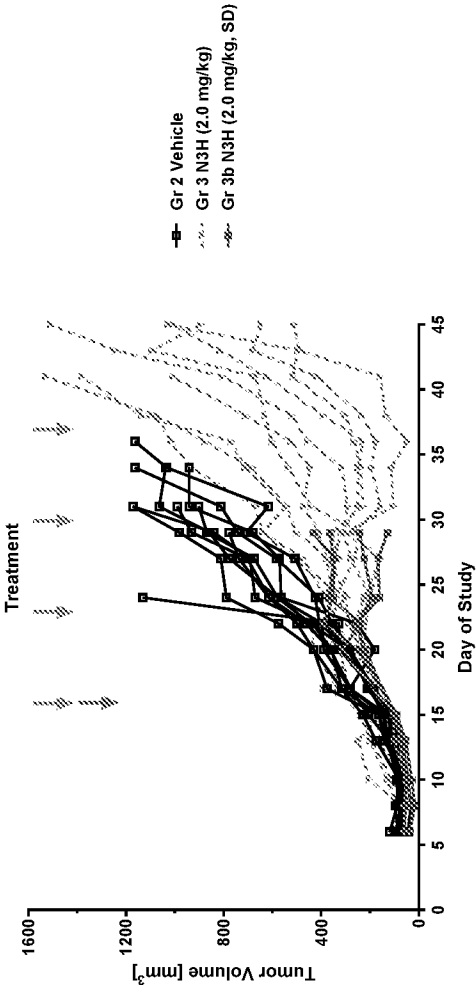
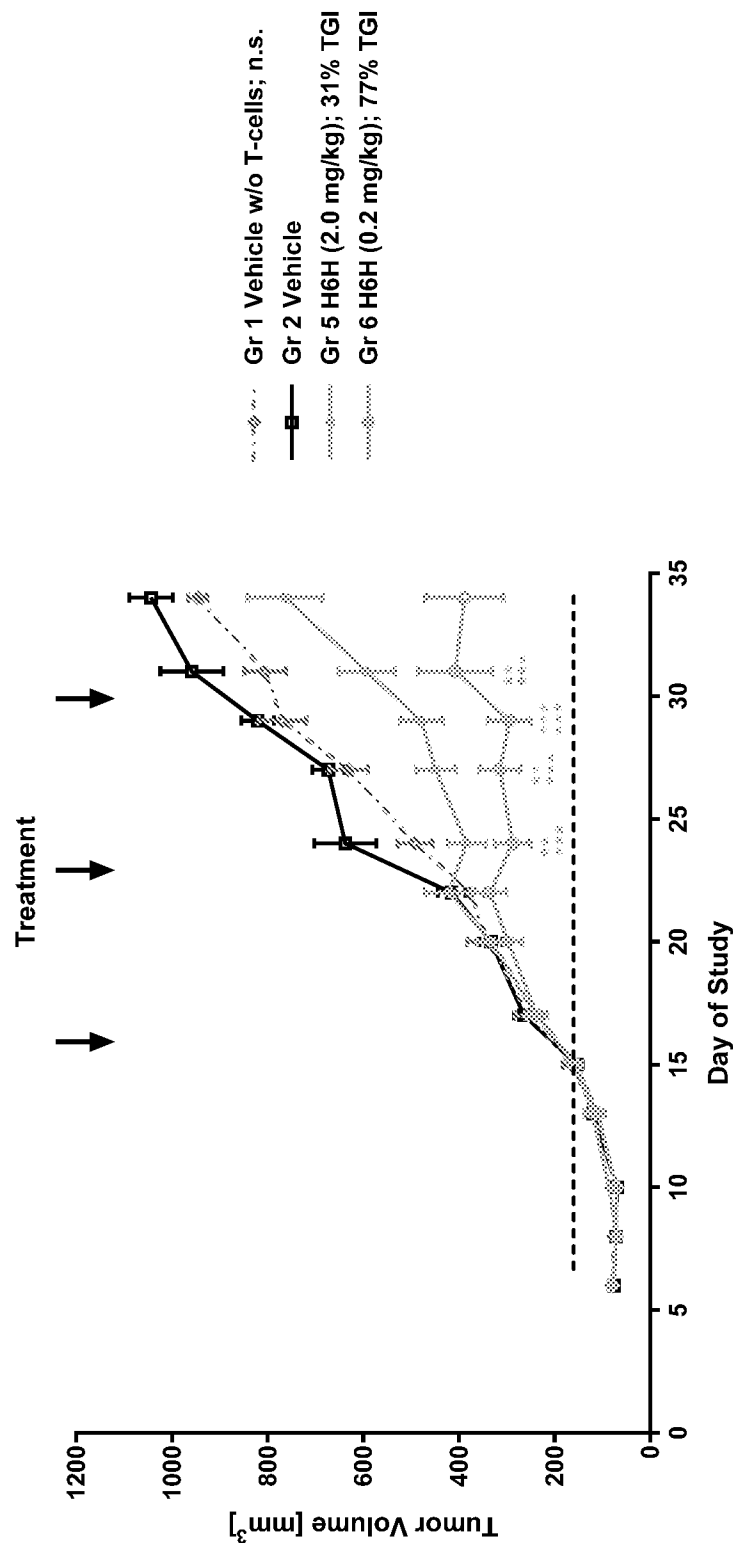


FIGURE 34

MEAN Tumor Volume With SEM following treatment with H6H



Data were analyzed by one-way ANOVA with Dunnett's post-hoc test: *: p<0.05; **: p<0.01; ***: p<0.001; no analysis on day 34 as only 4/10 animals in group 2 were alive
TGI: Tumor growth inhibition days 15-34 (group median)

FIGURE 35
Individual Animal Tumor Volume following treatment with H6H

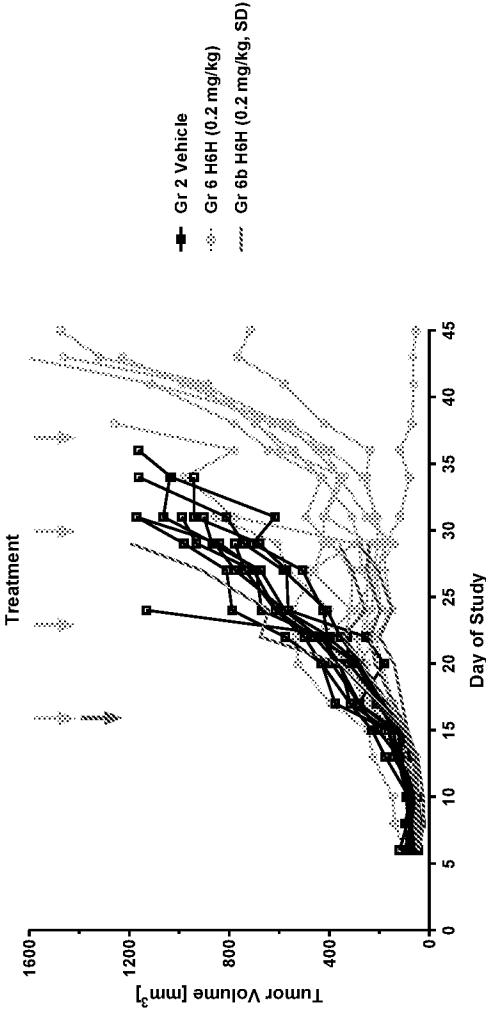
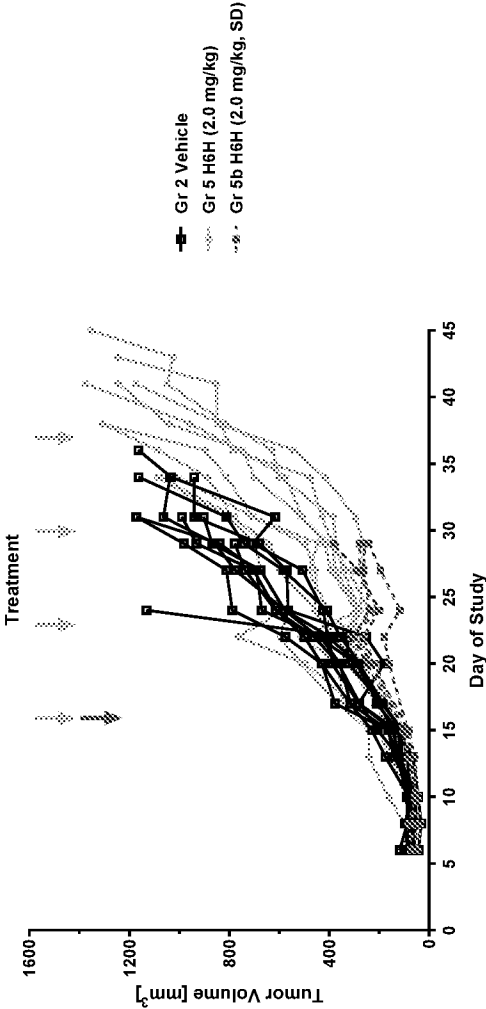


FIGURE 36

Pharmacokinetic Summary

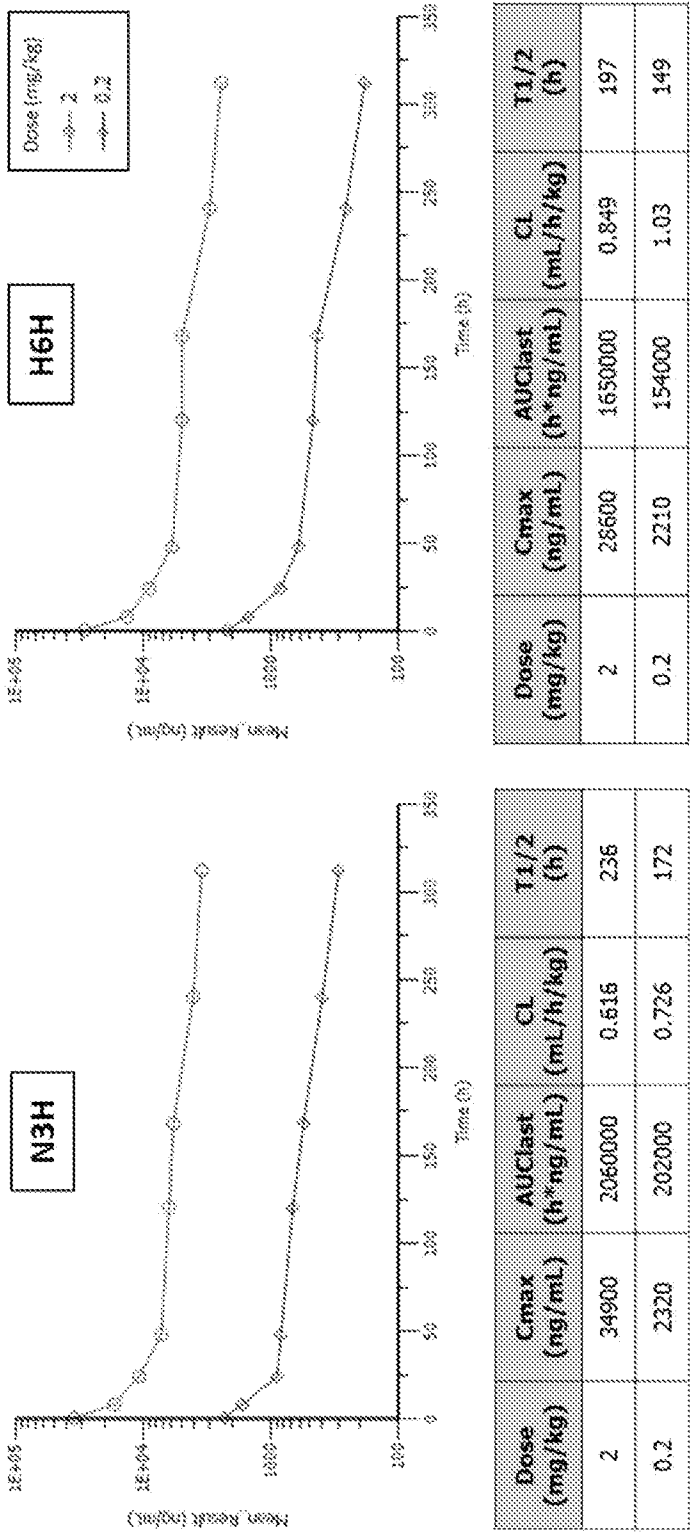
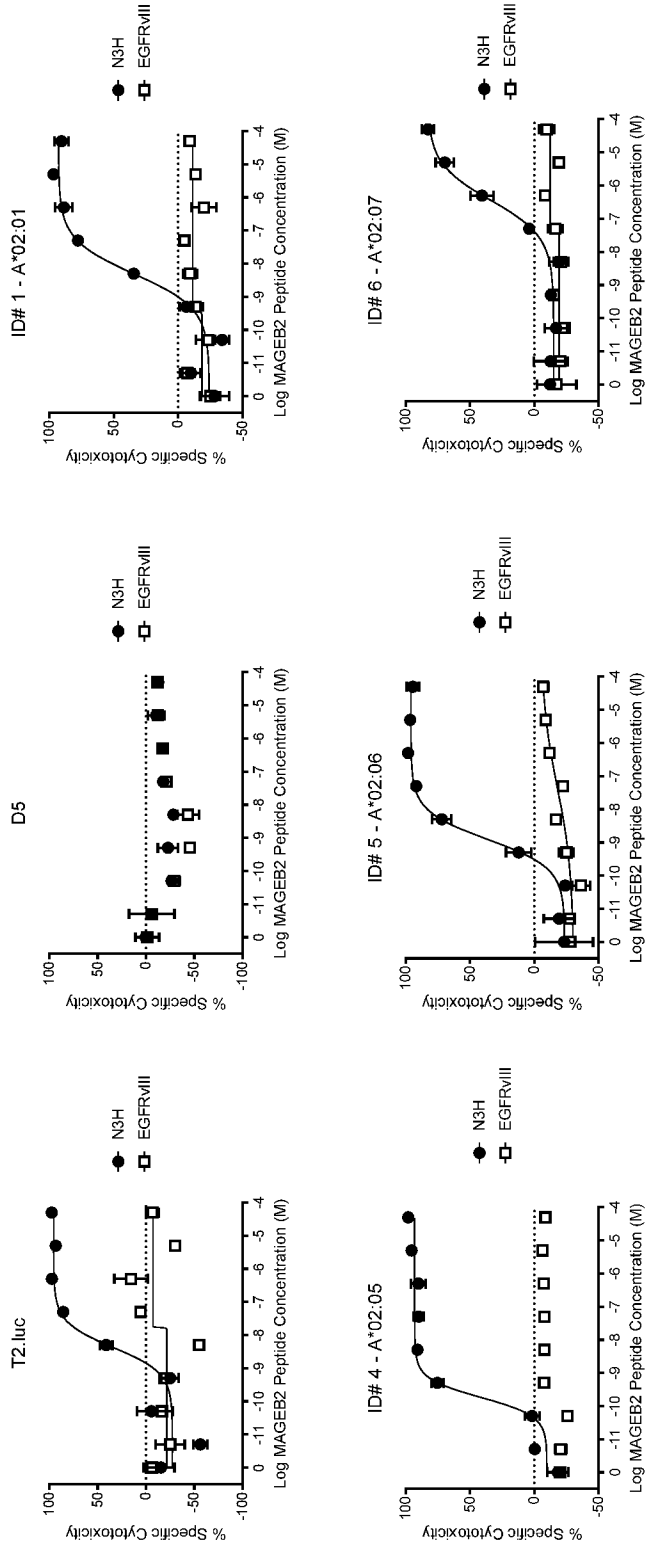


FIGURE 37

Results for N3H Against Various HLA*02 Expressing Cells



Hla-a2 FACS STAINING AFTER PEPTIDE PULSE

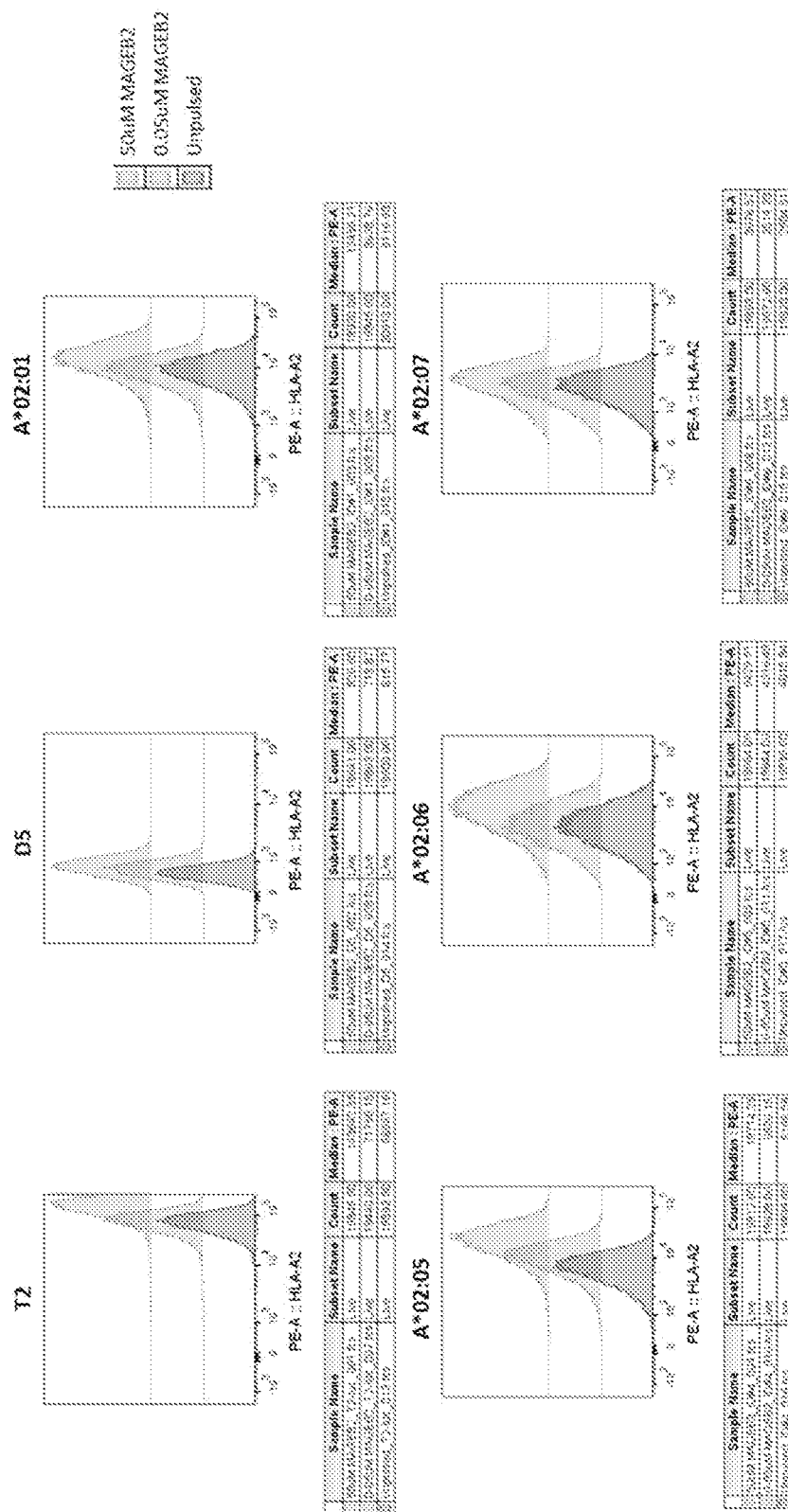


FIGURE 39

Hla-a2 FACS STAINING AFTER PEPTIDE PULSE

**Gating set on D5 cells for each concentration

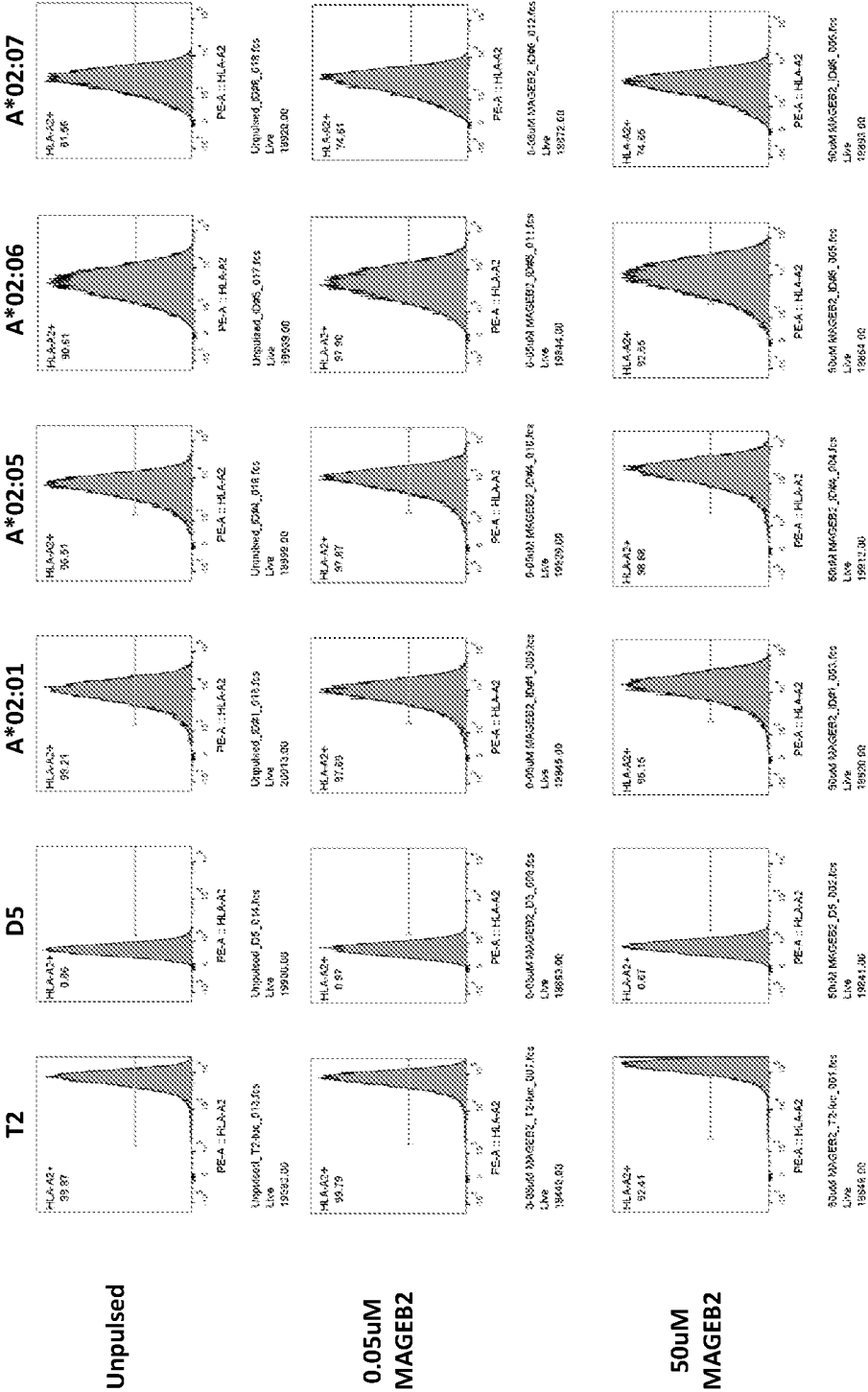


FIGURE 40

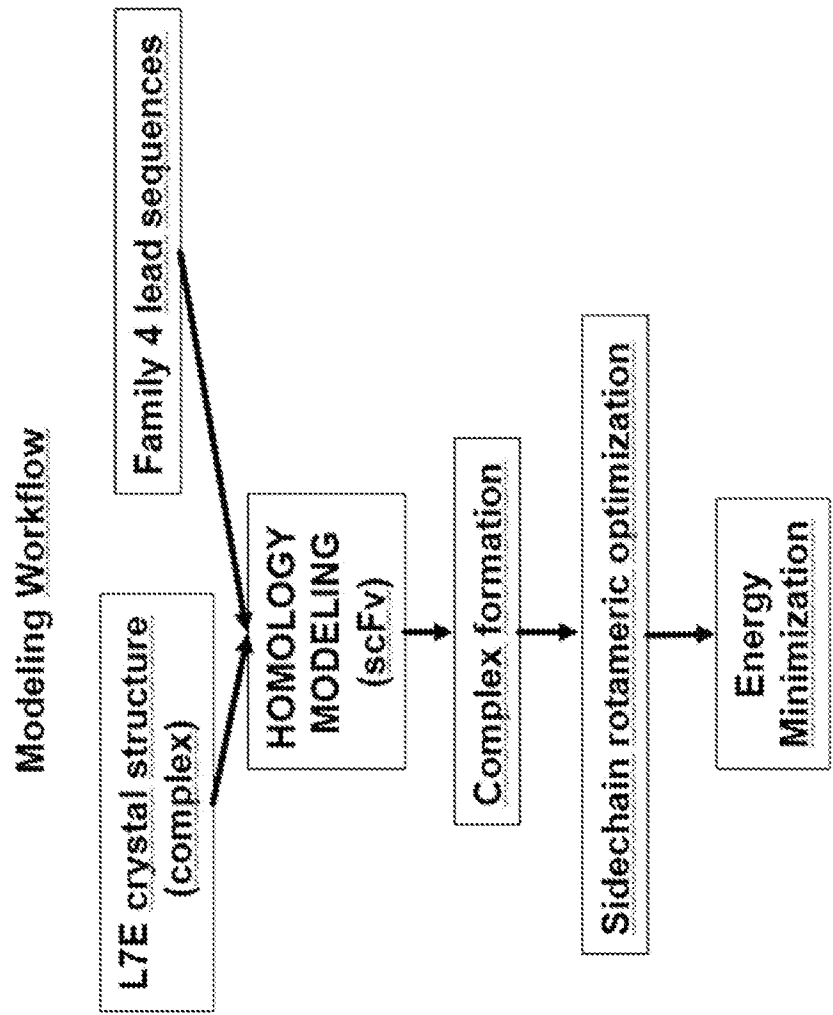


FIGURE 41

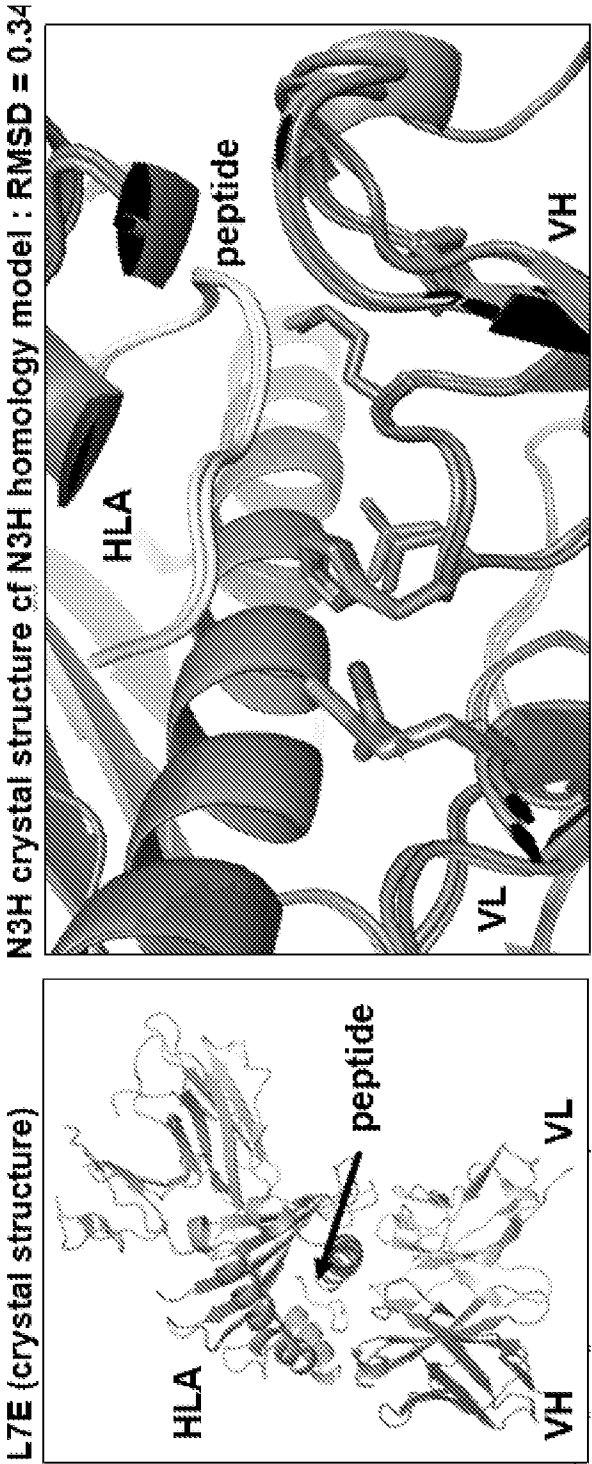


FIGURE 42

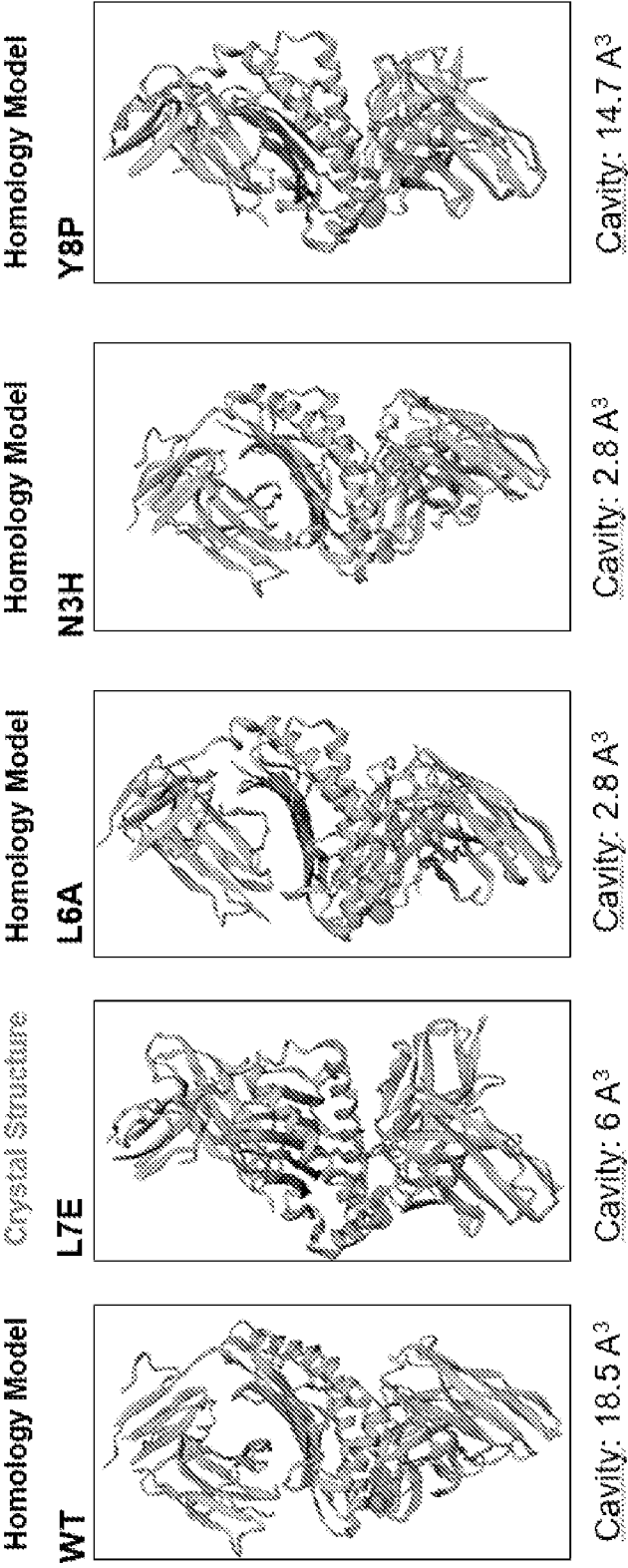


FIGURE 43

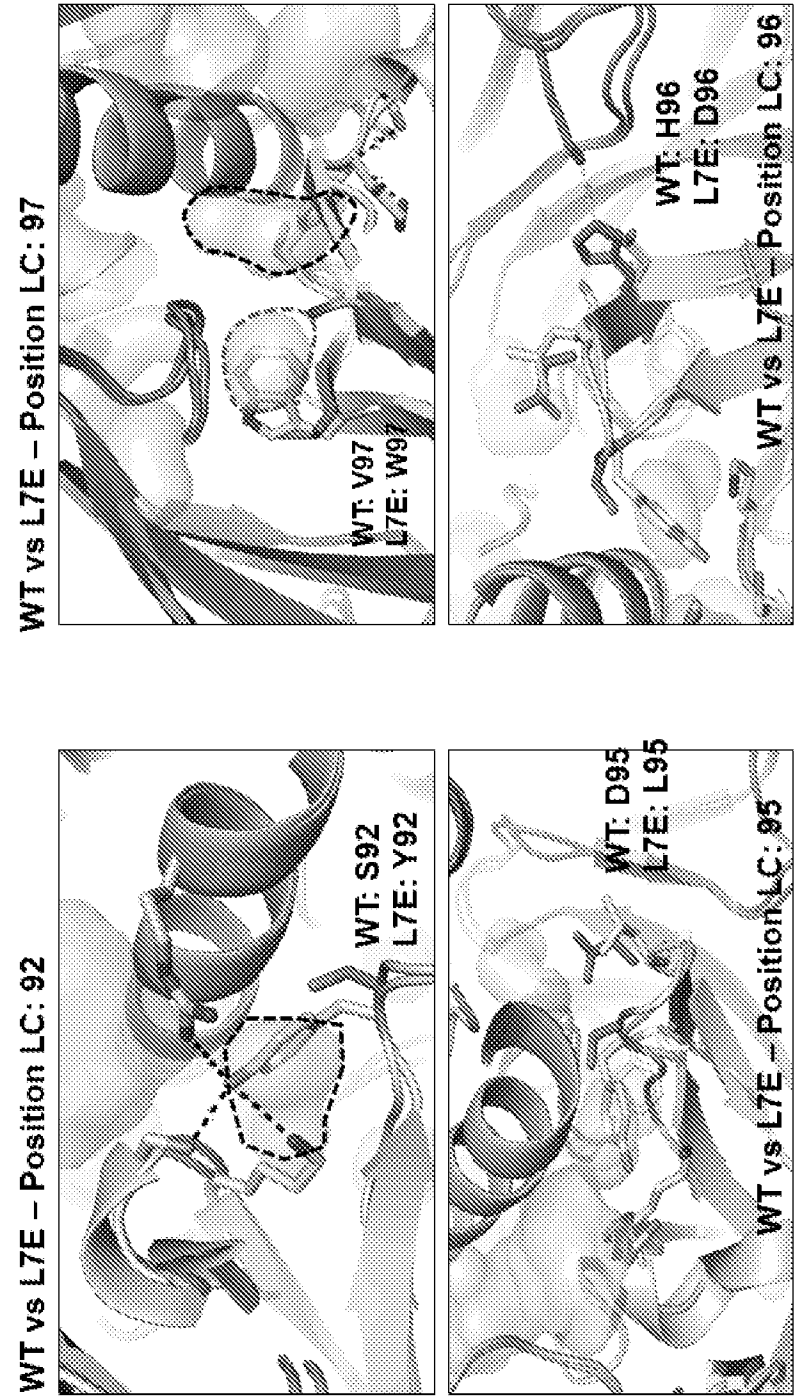


FIGURE 44

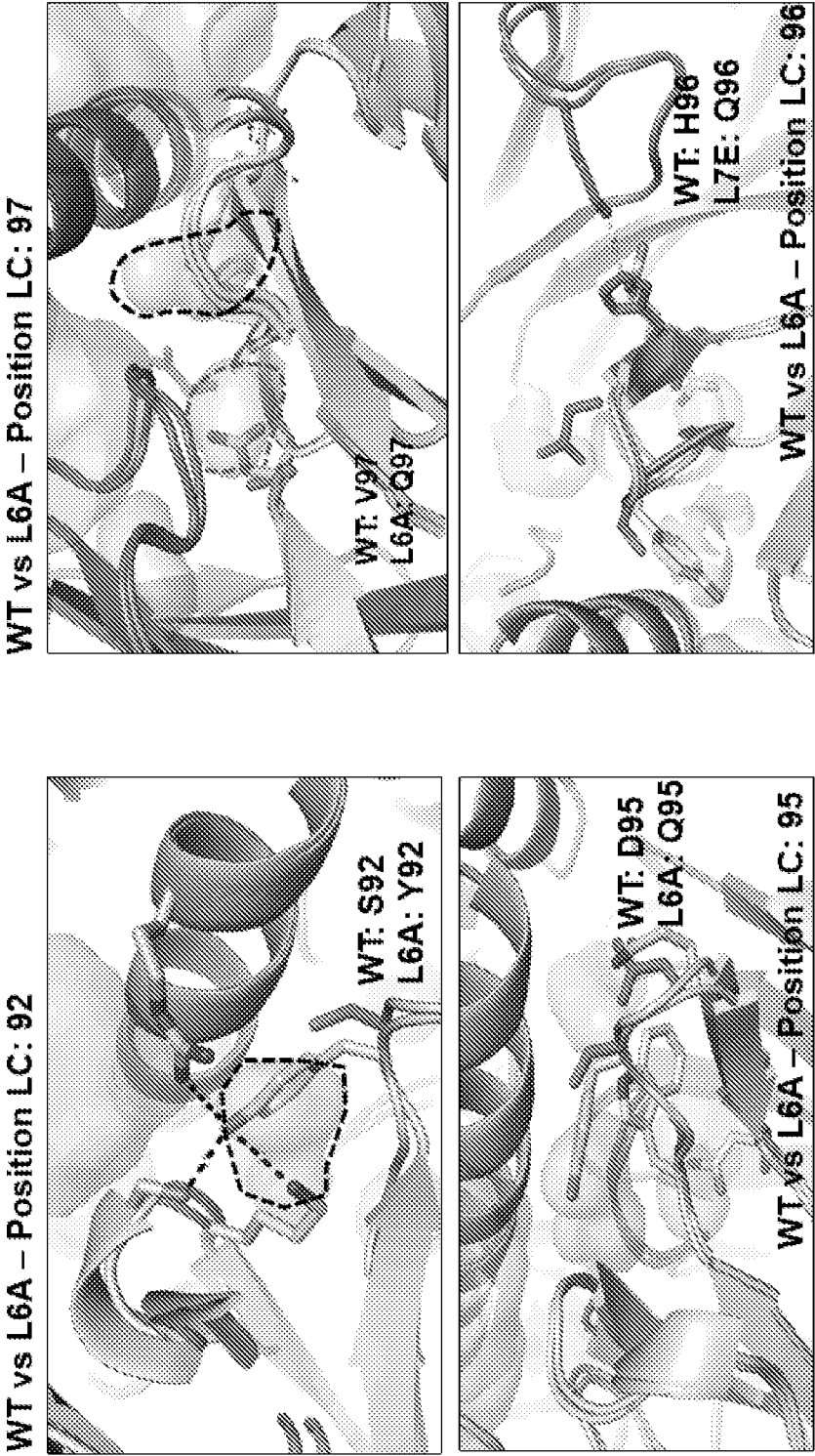


FIGURE 45

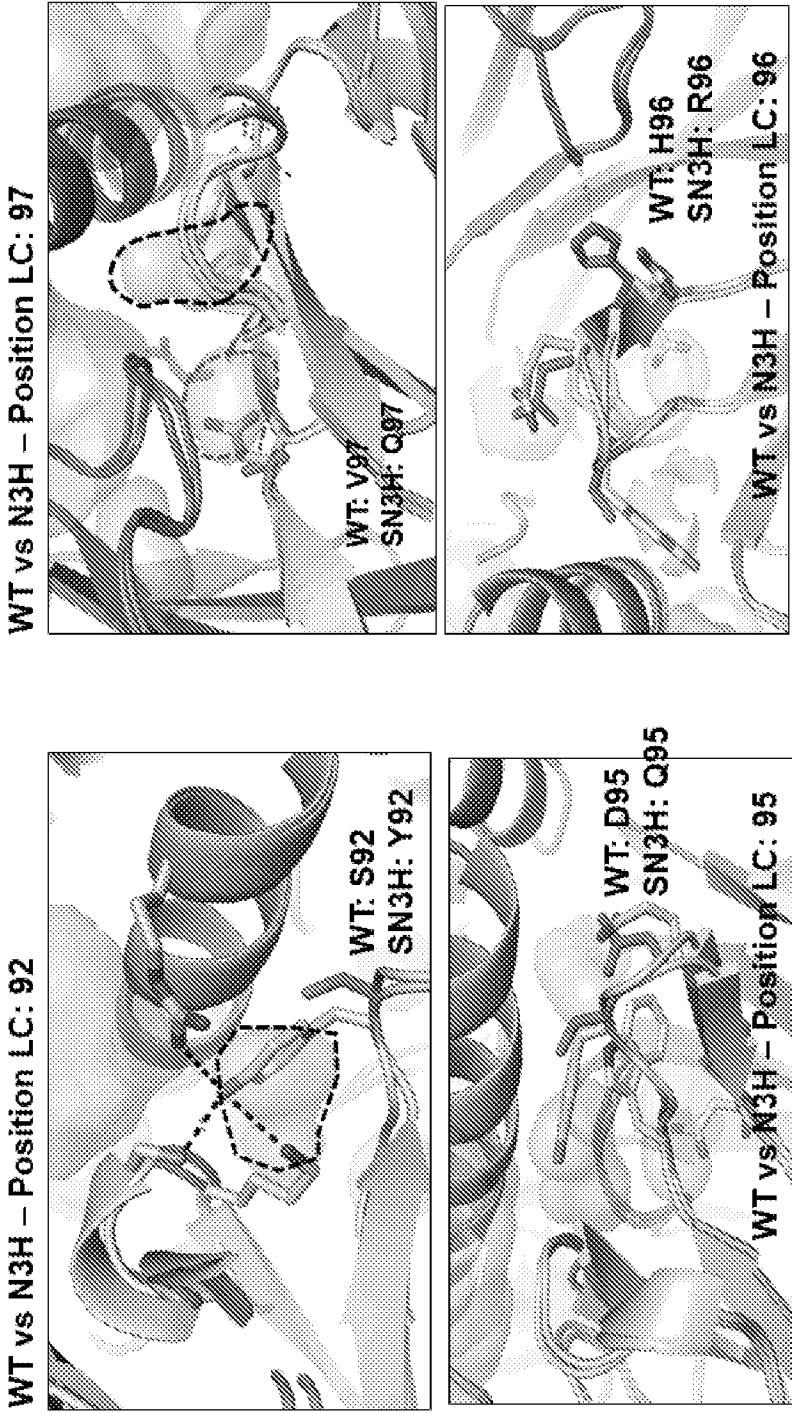
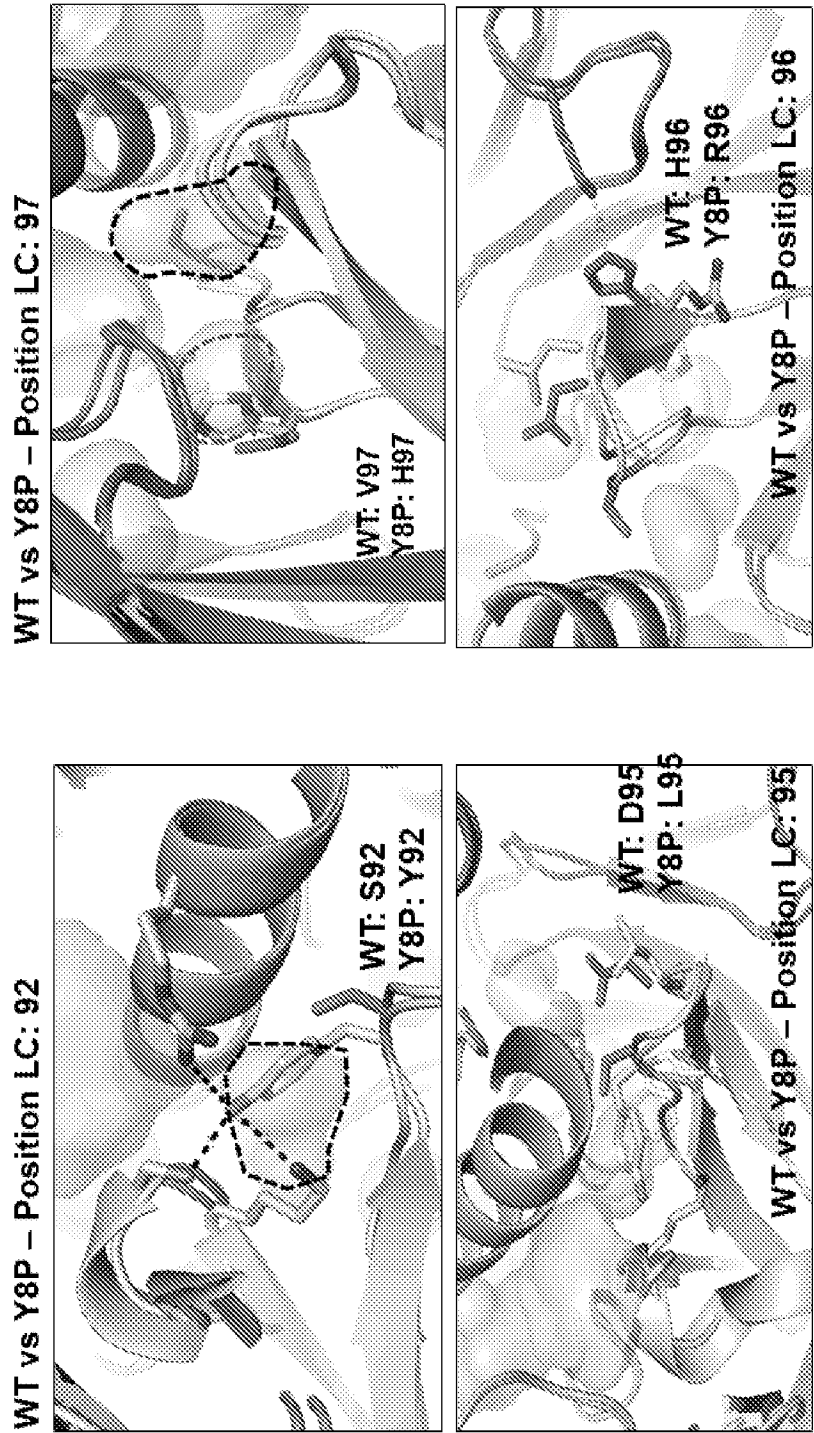


FIGURE 46



Parental

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	Trp
7	Phe	Asp	Arg	Phe	Trp	Trp	Trp	Trp	Trp
8	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
9	Arg	Asp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
10	Pro	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Cys	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Gln	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
13	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Enthalpy	18.0	19.0	19.8	19.2	19.2	19.2	19.2	19.2	19.2
Count									

dStability < 0									
Rank	53a9r32	54sp95	54His96	54His96	54His96	54His96	54His96	54His96	54His96
1	Asp	Leu	Asp	His	Val	Val	Val	Val	Val
2	Ser	Phe	Val	Met	Val	Val	Val	Val	Val
3	Gln	Trp	Leu	Leu	Val	Val	Val	Val	Val
4	Val	Arg	Trp	Met	Leu	Leu	Leu	Leu	Leu
5	Asp	Gln	His	Leu	Trp	Val	Val	Val	Val
6	Leu	Lys	Trp	Arg	Trp	Trp	Trp	Trp	

L6A

Possible alternatives based on energetics

dStability < 0									
Rank	51y92	5Gn92	5Gn95	5Gn97	5Gn99	5Gn01	5Gn03	5Gn05	5Gn07
1	Trp	Leu	Asp	Asp	Asp	Asp	Asp	Asp	Asp
2	Tyr	Phe	Val	Leu	Leu	Leu	Leu	Leu	Leu
3	Phe	Tyr	Val	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr
4	Leu	Tyr	Leu	Phe	Phe	Phe	Phe	Phe	Phe
5	Arg	Asp	Val	Val	Val	Val	Val	Val	Val
6	Met	Val	Trp	Trp	Trp	Trp	Trp	Trp	Trp
7	Glu	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu
8	Val	Met	Val	Val	Val	Val	Val	Val	Val
9	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp
10	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
11	Val	Val	Val	Val	Val	Val	Val	Val	Val
12	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu
13	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
14	Val	Val	Val	Val	Val	Val	Val	Val	Val
15	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp
16	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
17	Val	Val	Val	Val	Val	Val	Val	Val	Val
18	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu
19	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Ensemble Count									
	12.7	16.2	16.7	16.3					

dStability and dAffinity < 0									
Rank	51y92	5Gn92	5Gn95	5Gn97	5Gn99	5Gn01	5Gn03	5Gn05	5Gn07
1	Trp	Trp	Glu	Arg	Arg	Arg	Arg	Arg	Arg
2	Phe	Tyr	Val	Leu	Leu	Leu	Leu	Leu	Leu
3	Tyr	Phe	Val	Leu	Leu	Leu	Leu	Leu	Leu
4	Leu	Arg	Tyr	Phe	Phe	Phe	Phe	Phe	Phe
5	Glu	Met	Leu	Val	Val	Val	Val	Val	Val
6	Glu	Lys	Phe	Tyr	Tyr	Tyr	Tyr	Tyr	Tyr
7	Arg	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu
8	Met	Lys	Lys	Met	Met	Met	Met	Met	Met
9	Trp	Trp	Arg	Lys	Lys	Lys	Lys	Lys	Lys
10	Arg	Trp	Glu	Arg	Arg	Arg	Arg	Arg	Arg
11	Tyr	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
12	Tyr	Glu	Glu	Trp	Trp	Trp	Trp	Trp	Trp
13	Val	Val	Val	Trp	Trp	Trp	Trp	Trp	Trp
14	Lys	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
15	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp	Asp
16	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg
17	Phe	Asp	Lys	Glu	Glu	Glu	Glu	Glu	Glu
18	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
19	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg
20	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
Ensemble Count									
	9.84	13.7	16.2	16.3					

dStability and dASA vdw < 0									
Rank	51y92	5Gn92	5Gn95	5Gn97	5Gn99	5Gn01	5Gn03	5Gn05	5Gn07
1	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp	Trp
2	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu
3	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg
4	Trp	Trp	Trp	Trp	Tr				

Note: Solutions are highlighted in box

FIGURE 49

Possible alternatives based on energetics

SN3H	dStability < 0																			
	Rank	5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
	5-Tyr82	5-Gln95	5-Arg86	5-Gln87	5-Tyr82	5-Gln95	5-Arg86	5-Gln87	5-Tyr82	5-Gln95	5-Arg86	5-Gln87	5-Tyr82	5-Gln95	5-Arg86	5-Gln87	5-Tyr82	5-Gln95	5-Arg86	5-Gln87
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	Pro	Tyr	Pro	Arg	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	2	Tyr	Pro	Val	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	3	Tyr	Pro	Val	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	4	Met	Met	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	5	Met	Met	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	6	His	Leu	Tyr	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	7	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	8	Leu	Arg	Met	Val	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	9	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	10	Leu	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	11	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	12	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	13	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	14	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	15	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	16	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	17	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	18	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	19	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	20	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro
	Enthalpy	12.7	15.7	14.6	14.9	12.2	13.6	14.6	12.2	13.6	14.6	12.2	13.6	14.6	12.2	13.6	14.6	12.2	13.6	14.6
	Count	12.7	15.7	14.6	14.9	12.2	13.6	14.6	12.2	13.6	14.6	12.2	13.6	14.6	12.2	13.6	14.6	12.2	13.6	14.6

Note: Solutions are highlighted in box

FIGURE 50

Possible alternatives based on energetics

Y8P

dStability < 0

Rank	5-Tyros	5-Leu	5-Arg	5-His	5-His
1	Tyr	Leu	Arg	His	His
2	Tyr	Leu	Leu	Arg	Arg
3	His	Arg	His	Tyr	Tyr
4	Leu	Arg	Leu	His	His
5	His	Tyr	Leu	Arg	Arg
6	His	Arg	Leu	His	His
7	His	Arg	Leu	His	His
8	His	Arg	Leu	His	His
9	His	Arg	Leu	His	His
10	His	Arg	Leu	His	His
11	His	Arg	Leu	His	His
12	His	Arg	Leu	His	His
13	His	Arg	Leu	His	His
14	His	Arg	Leu	His	His
15	His	Arg	Leu	His	His
16	His	Arg	Leu	His	His
17	His	Arg	Leu	His	His
18	His	Arg	Leu	His	His
19	His	Arg	Leu	His	His
20	His	Arg	Leu	His	His
Estimate	10.1	14.9	10.8	14.9	14.9

dStability and dAffinity < 0

Rank	5-Tyros	5-Leu	5-Arg	5-His	5-His
1	Tyr	Leu	Arg	His	His
2	Tyr	Leu	Leu	Arg	Arg
3	His	Arg	His	Tyr	Tyr
4	Leu	Arg	Leu	His	His
5	His	Tyr	Leu	Arg	Arg
6	His	Arg	Leu	His	His
7	His	Arg	Leu	His	His
8	His	Arg	Leu	His	His
9	His	Arg	Leu	His	His
10	His	Arg	Leu	His	His
11	His	Arg	Leu	His	His
12	His	Arg	Leu	His	His
13	His	Arg	Leu	His	His
14	His	Arg	Leu	His	His
15	His	Arg	Leu	His	His
16	His	Arg	Leu	His	His
17	His	Arg	Leu	His	His
18	His	Arg	Leu	His	His
19	His	Arg	Leu	His	His
20	His	Arg	Leu	His	His
Estimate	8.77	11.7	17.0	10.3	10.3

dStability and dSASA vdW < 0

Rank	5-Tyros	5-Leu	5-Arg	5-His	5-His
1	Tyr	Leu	Arg	His	His
2	Tyr	Leu	Leu	Arg	Arg
3	His	Arg	His	Tyr	Tyr
4	Leu	Arg	Leu	His	His
5	His	Tyr	Leu	Arg	Arg
6	His	Arg	Leu	His	His
7	His	Arg	Leu	His	His
8	His	Arg	Leu	His	His
9	His	Arg	Leu	His	His
10	His	Arg	Leu	His	His
11	His	Arg	Leu	His	His
12	His	Arg	Leu	His	His
13	His	Arg	Leu	His	His
14	His	Arg	Leu	His	His
15	His	Arg	Leu	His	His
16	His	Arg	Leu	His	His
17	His	Arg	Leu	His	His
18	His	Arg	Leu	His	His
19	His	Arg	Leu	His	His
20	His	Arg	Leu	His	His
Estimate	8.44	8.51	1.02	8.74	8.74

Note: Solutions are highlighted in box

FIGURE 51A

Induction of Cytokines and Granzyme B in PDX-Organoid models

CR5088 model

ID	HLA-A Alleles		HLA-A LOG2(FPKM)	MAGEB2 LOG2(FPKM)	MAGEA4 LOG2(FPKM)	MAGEA8 LOG2(FPKM)	EGFR LOG2(FPKM)	Cancer Type
CR5088-P0	A*02:01	A*02:01	8.73	3.80	-2.00	-2.00	5.61	Colorectal

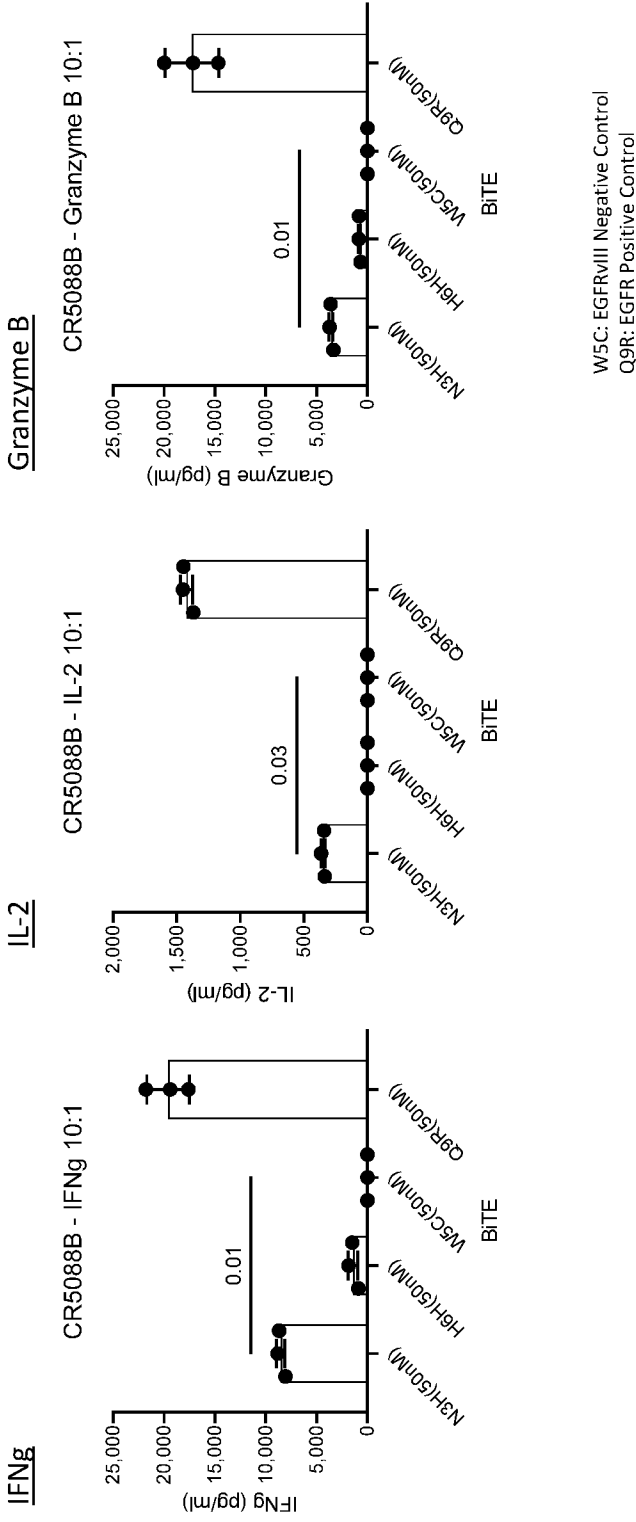
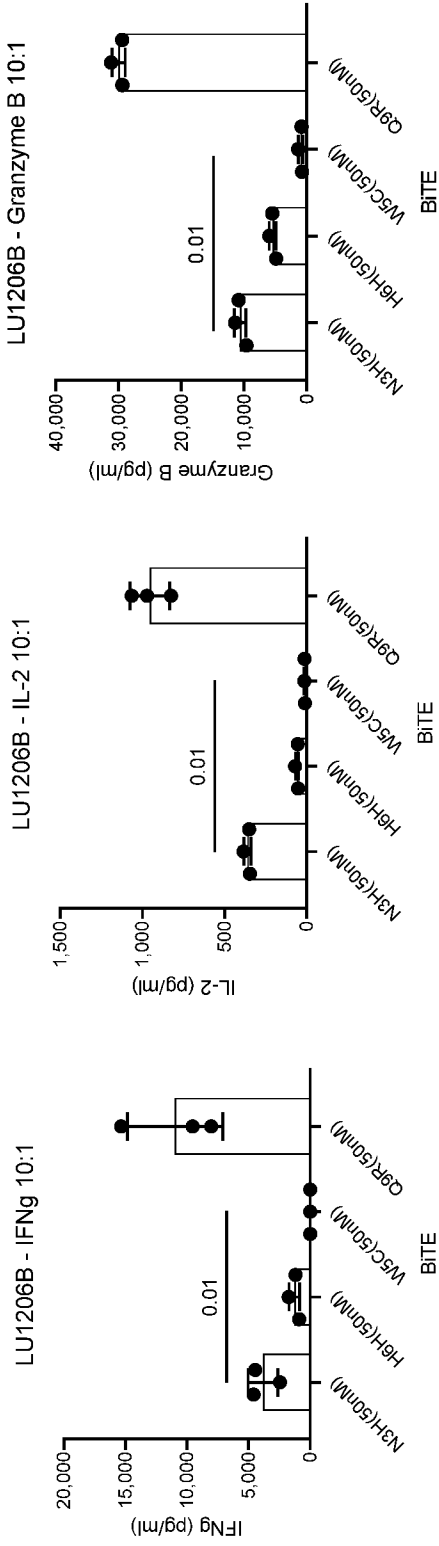


FIGURE 51B

Induction of Cytokines and Granzyme B in PDX-Organoid models

LU1206 model

ID	HLA-A Alleles		HLA-A LOG2(FPKM)	MAGEB2 LOG2(FPKM)	MAGEA4 LOG2(FPKM)	MAGEA8 LOG2(FPKM)	EGFR LOG2(FPKM)	Cancer Type
LU1206-P6	A*02:01	A*11:01	8.56	5.42	4.99	-2.00	8.68	Lung



One-way ANOVA non-parametric Kruskal-Wallis test
Dunn's multiple comparison test of N3H and H6H vs W5C

FIGURE 52A

N3H TDCC Assays with DAN-G and DAN-G-MAGE-B2-KO cells

Redirected Lysis T-cell Activation

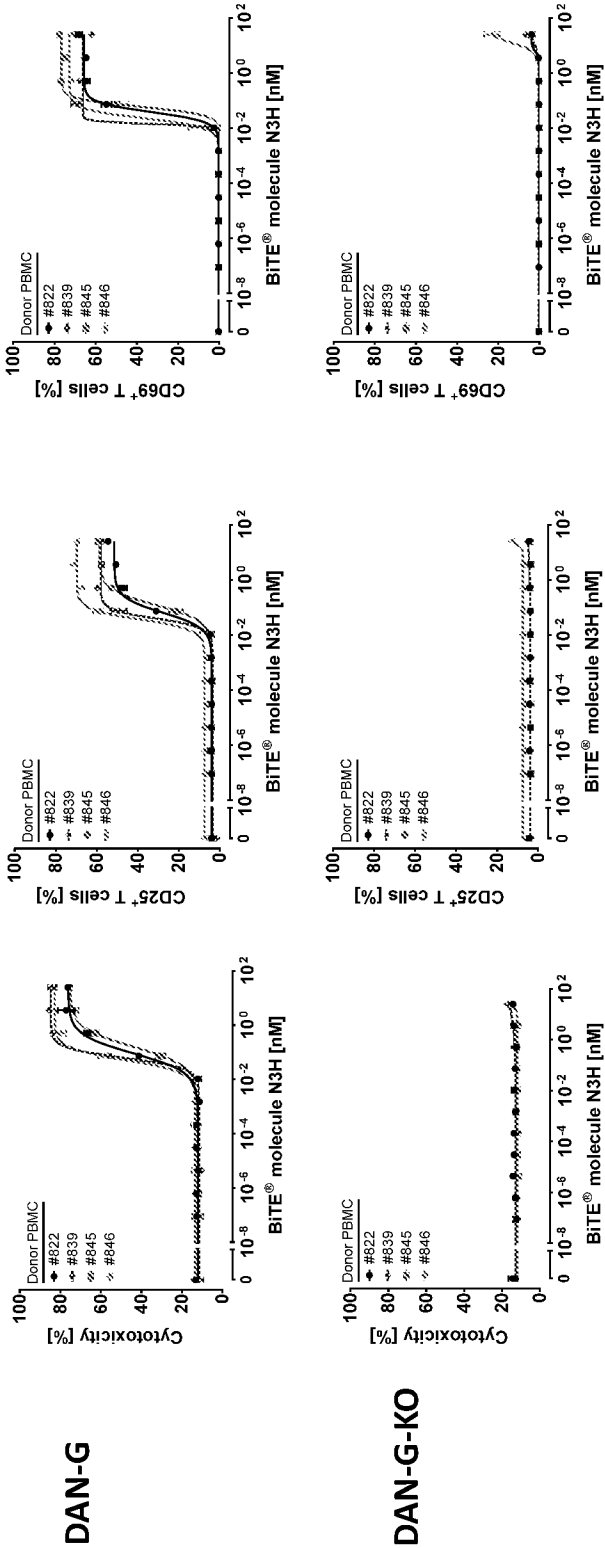
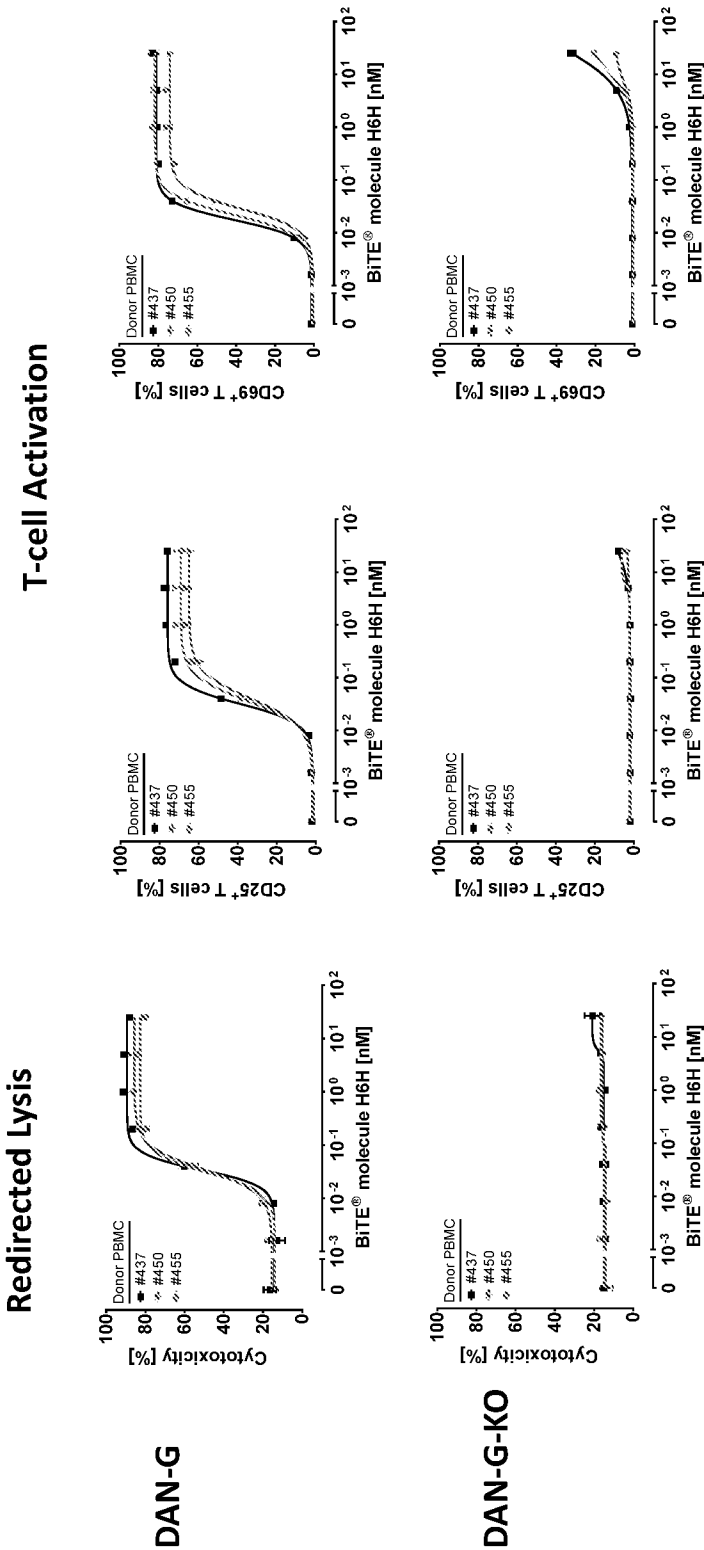


FIGURE 52B

H6H TDCC Assays with DAN-G and DAN-G-MAGE-B2-KO cells



INTERNATIONAL SEARCH REPORT

International application No
PCT/US2021/032961

A. CLASSIFICATION OF SUBJECT MATTER

INV. C07K16/30 C07K16/28
ADD. A61K39/00

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K A61P A61K

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

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

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	JUNG-HEE LEE ET AL: "Identification, Expression, and Nuclear Location of Murine Mage-b2 Protein, a Tumor-associated Antigen", MOLECULES AND CELLS, SEOUL, KR, vol. 10, no. 6, 1 January 2001 (2001-01-01), pages 647-653, XP019361382, ISSN: 1016-8478 page 648, right-hand column, last paragraph - page 649, left-hand column, paragraph 1 page 650, left-hand column, paragraph 2; figure 3 ----- -/--	1-21



Further documents are listed in the continuation of Box C.



See patent family annex.

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Date of the actual completion of the international search

25 October 2021

Date of mailing of the international search report

05/11/2021

Name and mailing address of the ISA/

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Authorized officer

Siaterli, Maria

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2021/032961

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2019/036688 A1 (GRITSTONE ONCOLOGY INC [US]; FRANCIS JOSHUA MICHAEL [US] ET AL.) 21 February 2019 (2019-02-21)	3-13, 17-26
A	paragraph [0326] - paragraph [0332]; claims 1(d), 66	1, 2, 14-16
X	----- WO 2017/175006 A1 (IMMUNOCORE LTD [GB]) 12 October 2017 (2017-10-12) claims 1-36; figures 4-9; examples 4, 5; table 11; sequence 1	3-13, 17-26
X	----- US 2018/179283 A1 (PELED KAMAR MIRA [IL] ET AL) 28 June 2018 (2018-06-28) the whole document paragraphs [0503], [0599]; figures 52-54; examples III, IIIB; table 8; sequences 176, 179	3-13, 17-26
X	----- WO 2017/174822 A1 (ADAPTIMMUNE LTD [GB]) 12 October 2017 (2017-10-12) the whole document claim 1; example 3 -----	3-13, 17-26

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2021/032961

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
- a. ☒ forming part of the international application as filed:
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- ☐ on paper or in the form of an image file.
- b. ☐ furnished together with the international application under PCT Rule 13~~ter~~.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.
- c. ☐ furnished subsequent to the international filing date for the purposes of international search only:
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2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2021/032961

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