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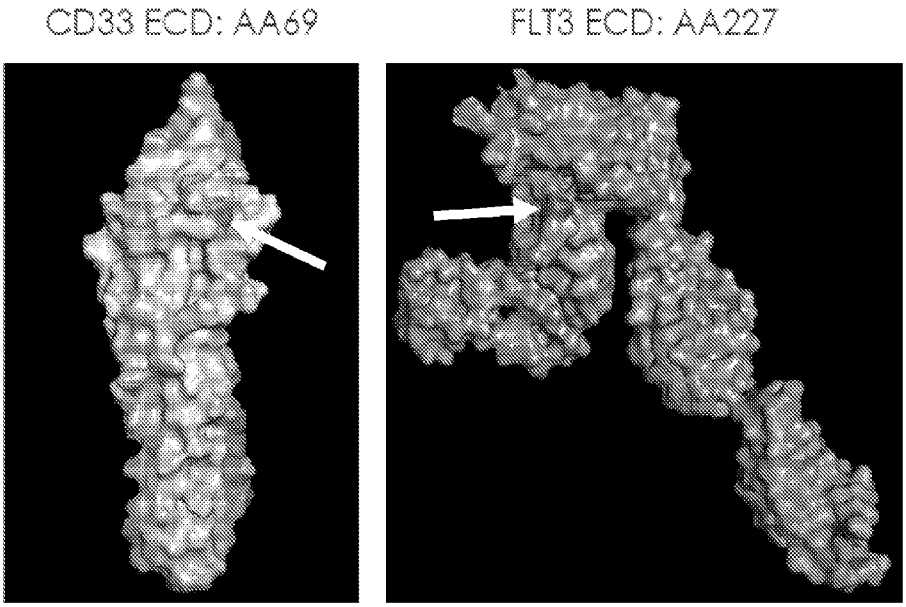
(54) **Title:** POLYPEPTIDES AND THEIR USE IN TREATMENT OF DISEASE

FIG. 1



(57) **Abstract:** Disclosed herein are polypeptides, such as monoclonal antibodies (mAbs) and functional fragments thereof, synthetic antigen-binding proteins such as single-chain variable fragments (scFvs), and chimeric antigen receptors (CARs), that can specifically recognize tumor-associated antigens (TAAs) on cancer cells, for example those that express CD33, FLT3, and CLL-1, useful in the treatment of diseases such as cancer.

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POLYPEPTIDES AND THEIR USE IN TREATMENT OF DISEASE

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to, and the benefit of, U.S. Provisional Pat. Appl. No. 63/148,012, filed February 10, 2021, the entirety of which is incorporated herein by reference.

[0002] Targeted immunotherapies are based on the recognition of antigens, defined structures on diseased cells or pathogens, by immune receptors that are either soluble, i.e., antibodies, or present on the surface of immune cells, such as chimeric antigen receptors (CARs) in CAR-bearing immune effector cells such as CAR-T cells. Recognition and binding of the antigen by the immune receptor usually triggers effector functions that eventually lead to the destruction of the respective pathogen or cell. Soluble immune receptors include natural or synthetic antibodies, antibody derived molecules and other structures, which upon binding to an antigen trigger the complement system or recruit and in most cases activate effector cells. Alternatively, antigen-targeting cells can be generated through the genetic insertion of engineered immune receptors, such as transgenic T-cell receptors (TCRs) or CARs into T cells or other immune effector cells including natural killer (NK) cells. Commonly, CARs comprise a single chain fragment variable (scFv) derived from an antibody specific for a certain target antigen coupled via hinge and transmembrane regions to cytoplasmic domains of T-cell signaling molecules. The CAR-mediated adoptive immunotherapy allows CAR-grafted cells to directly recognize the desired antigen on target cells in a non-HLA-restricted manner.

[0003] One common application of these immunotherapies, though not the only application, is the treatment of cancer. Cancer is a broad group of diseases involving deregulated cell growth. In cancer, cells divide and grow uncontrollably, forming malignant tumors, and invading nearby parts of the body. The cancer may also spread to more distant parts of the body through the lymphatic system or bloodstream. There are over 200 different known cancers that affect humans. Whereas good treatment options are available for many cancer types, others still represent unmet medical need.

[0004] Amongst these are hematologic cancers. Cancers of the hematopoietic system can be roughly divided into different subtypes. Leukemias generally affect the primary lymphatic organs, which are the bone marrow as well as the thymus, and arise from hematopoietic progenitor populations, such as, for example, acute myeloid leukemia

(AML). Lymphomas on the other hand are usually derived from mature lymphocytes and originate from secondary lymphatic organs.

[0005] The current first line treatment for most hematopoietic cancers involves the administration of chemotherapeutic agents (either broad-spectrum or targeted therapies), radiation therapy or a combination of both. In many cases such therapies are combined with or followed by hematopoietic stem cell transfer (HSCT), where the graft versus leukemia (GvL) effect mediated by donor-derived lymphocytes, especially T cells, can lead to the eradication of cancer cells that survived pre-conditioning chemo- or radiotherapies and result in complete remission (CR). Depending on the type of hematological malignancy, the patients' condition, and the availability of hematopoietic stem cell grafts, various versions of HSCT are regularly performed in the clinics. The desired GvL effect is, at present, only achieved in allogeneic HSCT, which at the same time is often accompanied by the occurrence of graft versus host disease (GvHD), a serious and sometimes fatal complication. Moreover, in all cases, persisting cancer stem cells often lead to disease relapse.

[0006] In recent years there has been strong progress in the development of targeted immunotherapies, such as CAR-T cells, for the treatment of cancer. However, most broadly target antigens which are expressed on malignant as well as healthy cells, and do so using polypeptides which target antigens in a polymorphically nonselective manner. Additionally, relapse of hematologic cancer in patients transplanted with HSCT remains a problem to be solved. Therefore, there is a need for the development of novel therapies for the treatment of diseases, such as cancer, that enable the utilization of alternative target molecules, and reduce or avoid the side-effects often associated with current targeted immunotherapies in general, and CAR T cell therapies in particular.

SUMMARY

[0007] Provided herein are polymorphically selective polypeptides, including single-chain variable fragments, monoclonal antibodies and antigen-binding fragments thereof, antibody-drug conjugates, and chimeric antigen receptors and engineered immune effector cells comprising them, useful in the treatment of diseases such as cancer, and in some embodiments, in combination with polymorphically mismatched hematopoietic cell transplant in a manner that permits selective killing of the patient's diseased cells while sparing transplanted hematopoietic cells.

BRIEF DESCRIPTION OF THE SEQUENCES

[0008] SEQ ID NOs:1-200: sequences of CDRs and VH and VL chains of polymorphically selective anti-CD33 polypeptides 1-25.

[0009] SEQ ID NOs:201-336: sequences of CDRs and VH and VL chains of polymorphically selective anti-CD33 polypeptides 26-42.

[0010] SEQ ID NOs:337-528: sequences of CDRs and VH and VL chains of polymorphically selective anti-CLL-1 polypeptides 43-66.

[0011] SEQ ID NOs:529-704: sequences of CDRs and VH and VL chains of polymorphically selective anti-CLL-1 polypeptides 67-88.

[0012] SEQ ID NOs:705-1144 and 1979-2002: sequences of CDRs and VH and VL chains of polymorphically nonselective anti-CD33 polypeptides 89-143 and 191-193.

[0013] SEQ ID NOs:1145-1520 and 2003-2058: sequences of CDRs and VH and VL chains of polymorphically nonselective anti-CLL-1 polypeptides 144-190 and 194-200.

[0014] SEQ ID NOs: 1521-1538: amino acid sequences of selected CAR components.

[0015] SEQ ID NOs:1539-1598: sequences of exemplary CARs which may be made using the polypeptides disclosed herein.

[0016] SEQ ID NOs:1599-1626: Human antibody Fc components which may be combined with polypeptides disclosed herein to form diagnostic or therapeutic antibodies.

[0017] SEQ ID NOs: 1627-1802 sequences of exemplary anti-CD33 and anti-CLL-1 IgG1 antibodies comprising Polypeptides 1-88.

[0018] SEQ ID NOs: 1803-1978: sequences of exemplary anti-CD33 and anti-CLL-1 IgG4 antibodies comprising Polypeptides 1-88.

[0019] SEQ ID NOs:2059-2810: sequences of CDRs and VH and VL chains of polymorphically nonselective anti-FLT3 polypeptides 201-294.

BRIEF DESCRIPTION OF THE DRAWINGS

[0020] Fig. 1 shows the CD33 extracellular domain (ECD) with amino acid (AA) 69 in the left panel, and FLT3 ECD AA267 in the right panel, each in a relatively solvent-accessible position.

[0021] Fig. 2 shows control (C) parental Jurkat cells, Jurkat cells expressing CD33-R69 (R69), and Jurkat cells expressing CD33-G69 (G69), and treated with:

- **A**: PD-L1 scFv as a negative control, yielding a mean fold intensity change in R69 and G69 over parental cells of 0.73 and 0.66, respectively;

- **B**: CD33 nonselective scFv as a positive control, yielding a MFI change in R69 and G69 over parental cells of 78.9 and 74.6, respectively;
- **C**: CD33-R69 selective scFv, yielding a MFI change in R69 and G69 over parental cells of 20.3 and 0.58, respectively; and
- **D**: CD33-G69 selective scFv, yielding a MFI change in R69 and G69 over parental cells of 0.59 and 45.9, respectively.

[0022] Fig. 3 shows the fold selectivity of polypeptides 1-42 against huCD33-R69 or huCD33-G69 stably expressed in Jurkat cells.

[0023] Fig. 4 shows the results of an vitro cytotoxicity assay wherein a culture of $CD33^{GLY69}$ cell targets are treated with $CART33^{ARG69}$, $CART33^{GLY69}$ or CART33. $CART33^{GLY69}$ and CART33, but not $CART33^{ARG69}$, effectively kill $CD33^{GLY69}$-expressing cells.

[0024] Fig. 5 shows the results of an vitro cytotoxicity assay wherein a culture of $CD33^{ARG69}$ cell targets are treated with $CART33^{ARG69}$, $CART33^{GLY69}$ or CART33. $CART33^{ARG69}$ and CART33, but not $CART33^{GLY69}$, effectively kill $CD33^{ARG69}$-expressing cells.

DETAILED DESCRIPTION

[0025] Provided herein are polymorphically selective polypeptides, including single-chain variable fragments, monoclonal antibodies and antigen-binding fragments thereof, antibody-drug conjugates, and chimeric antigen receptors and engineered immune effector cells comprising them, useful in the treatment of diseases such as cancer, and in some embodiments, in combination with polymorphically mismatched hematopoietic cell transplant in a manner that permits selective killing of the patient's diseased cells while sparing transplanted hematopoietic cells.

Embodiments

[0026] Accordingly, although other embodiments may be found throughout the disclosure, provided herein are the following embodiments:

[0027] Embodiment 1. A polypeptide which selectively binds a first polymorphic variant of a human cancer cell antigen over a second polymorphic variant of the human cancer cell antigen; or selectively binds the second polymorphic variant of the antigen over the first polymorphic variant of the antigen.

[0028] Embodiment 2. The polypeptide of embodiment 1, wherein the antigen is chosen from CD33, CLL-1, and FLT3.

[0029] Embodiment 3. The polypeptide of embodiment 2, wherein the antigen is CD33.

[0030] Embodiment 4. A polypeptide which selectively binds a first polymorphic variant of CD33 over a second polymorphic variant of CD33; or selectively binds the second polymorphic variant of CD33 over the first polymorphic variant of CD33; wherein the binding is at least 2-fold selective.

[0031] Embodiment 5. The polypeptide of embodiment 4, wherein the binding is at least 10-fold selective.

[0032] Embodiment 6. The polypeptide of embodiment 5, wherein the binding is at least 30-fold selective.

[0033] Embodiment 7. The polypeptide of any of embodiments 3-6, wherein the first polymorphic variant of CD33 is R69 and the second polymorphic variant of CD33 is G69; or the first polymorphic variant of CD33 is G69 and the second polymorphic variant of CD33 is R69.

[0034] Embodiment 8. The polypeptide of embodiment 7, comprising six complementarity-determining regions (CDRs).

[0035] Embodiment 9. The polypeptide of embodiment 8, comprising:

three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and

three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3.

[0036] Embodiment 10. The polypeptide of any of embodiments 7-9, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:1-25 and 201-217,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:26-50 and 218-234,

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:51-75 and 235-251.

[0037] Embodiment 11. The polypeptide of any of embodiments 7-9, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:1-25,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:26-50, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:51-75.

[0038] Embodiment 12. The polypeptide of any of embodiments 7-9, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 201-217,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 218-234, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 235-251.

[0039] Embodiment 13. The polypeptide of any of embodiments 10-12, wherein the HCDR1, HCDR2, and HCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0040] Embodiment 14. The polypeptide of any of embodiments 10-12, wherein the HCDR1, HCDR2, and HCDR3 have the recited amino acid sequences.

[0041] Embodiment 15. The polypeptide of any of embodiments any of embodiments 7-9 and 8-14, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:76-100 and 252-268,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:101-125 and 269-285, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:126-150 and 286-302.

[0042] Embodiment 16. The polypeptide of any of embodiments any of embodiments 7-9 and 8-14, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 76-100,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:101-125, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:126-150.

[0043] Embodiment 17. The polypeptide of any of embodiments any of embodiments 7-9 and 8-14, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 252-268,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 269-285, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 286-302.

[0044] Embodiment 18. The polypeptide of any of embodiments 15-17, wherein the LCDR1, LCDR2, and LCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0045] Embodiment 19. The polypeptide of any of embodiments 15-17, wherein the LCDR1, LCDR2, and LCDR3 have the recited amino acid sequences.

[0046] Embodiment 20. The polypeptide of embodiment 7, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175 and 303-319.

[0047] Embodiment 21. The polypeptide of embodiment 7, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175.

[0048] Embodiment 22. The polypeptide of embodiment 7, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 303-319.

[0049] Embodiment 23. The polypeptide of any of embodiments 20-22, wherein the V_H domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0050] Embodiment 24. The polypeptide of any of embodiments 20-22, wherein the V_H domain has one of the recited amino acid sequences.

[0051] Embodiment 25. The polypeptide of any of embodiments 7 and 20-24, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200 and 320-336.

[0052] Embodiment 26. The polypeptide of any of embodiments 7 and 20-24, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200.

[0053] Embodiment 27. The polypeptide of any of embodiments 7 and 20-24, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 320-336.

[0054] Embodiment 28. The polypeptide of any of embodiments 25-27, wherein the V_L domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0055] Embodiment 29. The polypeptide of any of embodiments 25-27, wherein the V_L domain has one of the recited amino acid sequences.

[0056] Embodiment 30. The polypeptide of any of embodiments 20-29, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 1-42.

[0057] Embodiment 31. The polypeptide of any of embodiments 20-29, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 1-25.

[0058] Embodiment 32. The polypeptide of any of embodiments 20-29, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 26-42.

[0059] Embodiment 33. The polypeptide of any of embodiments 30-33, wherein the V_H and V_L domains have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequence pairs.

[0060] Embodiment 34. The polypeptide of embodiment 2, wherein the antigen is FLT3.

[0061] Embodiment 35. A polypeptide which selectively binds a first polymorphic variant of FLT3 over a second polymorphic variant of FLT3; or selectively binds the second polymorphic variant of FLT3 over the first polymorphic variant; wherein the binding is at least 2-fold selective.

[0062] Embodiment 36. The polypeptide of embodiment 35, wherein the binding is at least 10-fold selective.

[0063] Embodiment 37. The polypeptide of embodiment 36, wherein the binding is at least 30-fold selective.

[0064] Embodiment 38. The polypeptide of any of embodiments 34-37, wherein the first polymorphic variant of FLT3 is T227 and the second polymorphic variant of FLT3 is M227; or first polymorphic variant of FLT3 is M227 and the second polymorphic variant of FLT3 is T227.

[0065] Embodiment 39. The polypeptide of embodiment 2, wherein the antigen is CLL-1.

[0066] Embodiment 40. A polypeptide which selectively binds a first polymorphic variant of CLL-1 over a second polymorphic variant of CLL-1; or selectively binds the second polymorphic variant of CLL-1 over the first polymorphic variant; wherein the binding is at least 2-fold selective.

[0067] Embodiment 41. The polypeptide of embodiment 40, wherein the binding is at least 10-fold selective.

[0068] Embodiment 42. The polypeptide of embodiment 40, wherein the binding is at least 30-fold selective.

[0069] Embodiment 43. The polypeptide of any of embodiments 39-42, wherein the first polymorphic variant of CLL-1 is K224 and the second polymorphic variant of CLL-1 is Q244; or first polymorphic variant of CLL-1 is Q224 and the second polymorphic variant of CLL-1 is K244.

[0070] Embodiment 44 The polypeptide of claim 43, comprising six complementarity-determining regions (CDRs).

[0071] Embodiment 45. The polypeptide of Embodiment 44, comprising:

three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and

three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3.

[0072] Embodiment 46. The polypeptide of any of Embodiments 43-45, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:337-360- and 529-550,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:361-384 and 551-572, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:385-408 and 573-594.

[0073] Embodiment 47. The polypeptide of any of Embodiments 43-45, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 337-360,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 361-384, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 385-408.

[0074] Embodiment 48. The polypeptide of any of Embodiments 43-45, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 529-550,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 551-572, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 573-594.

[0075] Embodiment 49. The polypeptide of any of Embodiments 46-48, wherein the HCDR1, HCDR2, and HCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0076] Embodiment 50. The polypeptide of any of Embodiments 46-48, wherein the HCDR1, HCDR2, and HCDR3 have the recited amino acid sequences.

[0077] Embodiment 51. The polypeptide of any of Embodiments 43-50, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:409-432 and 595-616,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:433-456 and 617-638, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:457-480 and 639-660.

[0078] Embodiment 52. The polypeptide of any of Embodiments 43-50, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 409-432,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 433-456, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 457-480.

[0079] Embodiment 53. The polypeptide of any of Embodiments 43-50, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 595-616,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 617-638, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 639-660.

[0080] Embodiment 54. The polypeptide of any of Embodiments 51-53, wherein the LCDR1, LCDR2, and LCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0081] Embodiment 55. The polypeptide of any of Embodiments 51-53, wherein the LCDR1, LCDR2, and LCDR3 have the recited amino acid sequences.

[0082] Embodiment 56. The polypeptide of Embodiment 44, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175 and 303-319.

[0083] Embodiment 57. The polypeptide of Embodiment 44, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175.

[0084] Embodiment 58. The polypeptide of Embodiment 44, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 303-319.

[0085] Embodiment 59. The polypeptide of any of Embodiments 56-58, wherein the V_H domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0086] Embodiment 60. The polypeptide of any of Embodiments 56-58, wherein the V_H domain has one of the recited amino acid sequences.

[0087] Embodiment 61. The polypeptide of any of Embodiments 44 and 56-60, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200 and 320-336.

[0088] Embodiment 62. The polypeptide of any of Embodiments 44 and 56-60, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200.

[0089] Embodiment 63. The polypeptide of any of Embodiments 44 and 56-60, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 320-336.

[0090] Embodiment 64. The polypeptide of any of Embodiments 61-63, wherein the V_L domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[0091] Embodiment 65. The polypeptide of any of Embodiments 61-63, wherein the V_L domain has one of the recited amino acid sequences.

[0092] Embodiment 66. The polypeptide of any of Embodiments 56-65, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 43-88.

[0093] Embodiment 67. The polypeptide of any of Embodiments 56-65, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 43-66.

[0094] Embodiment 68. The polypeptide of any of Embodiments 56-65, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 67-88.

[0095] Embodiment 69. The polypeptide of any of Embodiments 66-68, wherein the V_H and V_L domains have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequence pairs.

[0096] Embodiment 70. A single-chain variable fragment (scFv) comprising the polypeptide of any of Embodiments 1-69.

[0097] Embodiment 71. A monoclonal antibody (mAb), or an antigen-binding fragment thereof, comprising the polypeptide of any of Embodiments 1-69.

[0098] Embodiment 72. The mAb, or antigen-binding fragment thereof, of Embodiment 71, wherein the mAb is of the IgG, IgM, or IgA isotype.

[0099] Embodiment 73. The mAb, or antigen-binding fragment thereof, of Embodiment 72, wherein the mAb is of the IgG1 isotype.

[00100] Embodiment 74. The mAb, or antigen-binding fragment thereof, of Embodiment 72, wherein the mAb is of the IgG3 isotype.

[00101] Embodiment 75. The mAb, or antigen-binding fragment thereof, of Embodiment 72, wherein the mAb is of the IgG4 isotype.

[00102] Embodiment 76. The mAb, or antigen-binding fragment thereof, of Embodiment 72, wherein the mAb is human or humanized.

[00103] Embodiment 77. The mAb, or antigen-binding fragment thereof, of any of Embodiments 71-76, wherein the mAb comprises a sequence chosen from SEQ ID NOs: 1201-1368.

[00104] Embodiment 78. An antibody-drug conjugate (ADC) comprising the mAb, or antigen-binding fragment thereof, of any of Embodiments 71-77.

[00105] Embodiment 79. The ADC of Embodiment 52, having Formula I:

$$Ab\text{-}(L\text{-}D)_p$$

(I)

wherein:

Ab is an antibody comprising the polypeptide of any of Embodiments 1-43, or the antibody of any of Embodiments 45-51, or an antigen-binding fragment of either of the foregoing;

L is a linker;

D is a drug; and

p is about 1 to about 20.

[00106] Embodiment 80. The ADC of Embodiment 79, wherein D is chosen from saporin, MMAE, MMAF, DM1, and DM4.

[00107] **Embodiment 81.** A chimeric antigen receptor (CAR) comprising an extracellular ligand binding domain comprising a polypeptide of any one of Embodiments 1-69.

[00108] **Embodiment 82.** The CAR of Embodiment 81, additionally comprising:

a hinge domain;

a transmembrane domain;

optionally, one or more co-stimulatory domains; and

a cytoplasmic signaling domain.

[00109] **Embodiment 83.** The CAR of Embodiment 82, wherein the hinge domain is chosen from FcεRIIIa, CD8α, CD28 and IgG1.

[00110] **Embodiment 84.** The CAR of Embodiment 83, wherein the hinge domain is CD8α.

[00111] **Embodiment 85** The CAR of any of Embodiments 82-84, wherein the transmembrane domain is chosen from alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CDS0, CD86, CD134, CD137 and CD154.

[00112] **Embodiment 86.** The CAR of Embodiment 85, wherein the transmembrane domain is CD28.

[00113] **Embodiment 87.** The CAR of any of Embodiments 82-86, wherein the cytoplasmic signaling domain is chosen from CD8, CD3ζ, CD3δ, CD3γ, CD3ε, CD22, CD32, DAP10, DAP12, CD66d, CD79a, CD79b, FcγRIγ, FcγRIIIγ, FcεRIβ, FcεRIγ, FcRγ, FcRβ, and FcRε.

[00114] **Embodiment 88.** The CAR of Embodiment 87, wherein the cytoplasmic signaling domain is CD3ζ.

[00115] **Embodiment 89.** The CAR of any of Embodiments 82-88, wherein one co-stimulatory domain is chosen from 4-1BB, CD28, and ICOS.

[00116] **Embodiment 90.** The CAR of Embodiment 89, wherein the costimulatory domain is CD28.

[00117] **Embodiment 91.** The CAR of Embodiment 89, wherein the costimulatory domain is 4-1BB.

[00118] **Embodiment 92.** The CAR of Embodiment 89, comprising two or more costimulatory domains.

[00119] **Embodiment 93.** The CAR of Embodiment 89, wherein two of the costimulatory domains are CD28 and 4-1BB.

[00120] **Embodiment 94.** The CAR of Embodiment 82, comprising a sequence chosen from SEQ ID NOs: 1539-1598.

[00121] **Embodiment 95.** A nucleotide sequence encoding any of the polypeptides, scFvs, mAbs, or CARs of any of Embodiments 1-94.

[00122] **Embodiment 96.** A vector comprising the nucleotide sequence of Embodiment 95.

[00123] **Embodiment 97.** The vector of Embodiment 96, wherein the vector is a lentiviral vector.

[00124] **Embodiment 98.** The vector of Embodiment 97, wherein the lentiviral vector comprises a VSVG domain.

[00125] **Embodiment 99.** An engineered immune effector cell expressing at the cell surface a CAR of any one of Embodiment 81-94.

[00126] **Embodiment 100.** The engineered immune effector cell of Embodiment 99, wherein the engineered immune effector cell expresses at the cell surface:

a first polymorphic variant of a human cancer cell antigen; and

a CAR that is selective for a second polymorphic over the first polymorphic variant of the antigen.

[00127] **Embodiment 101.** The engineered immune effector cell of Embodiment 99, wherein the cell is a primary cell.

[00128] **Embodiment 102.** The engineered immune effector cell of Embodiment 99, wherein the cell is derived from:

an induced pluripotent stem cell (iPSC);

cord blood;

peripheral blood; or

an immortalized cell line.

[00129] **Embodiment 103.** The engineered immune effector cell of Embodiment 102, wherein the immortalized cell line is NK-92.

[00130] **Embodiment 104.** The engineered immune cell of any of Embodiments 99-103, wherein the cell is chosen from a T cell, an natural killer (NK) cell, an invariant natural killer T (iNKT) cell, a macrophage, and a dendritic cell.

[00131] **Embodiment 105.** The engineered immune effector cell of Embodiment 104, wherein the cell is a T cell.

[00132] **Embodiment 106.** The engineered immune effector cell of Embodiment 105, wherein the T cell is chosen from an inflammatory T-lymphocyte, a cytotoxic T-lymphocyte, a regulatory T-lymphocyte, or a helper T-lymphocyte.

[00133] **Embodiment 107.** The engineered immune effector cell of Embodiment 105, wherein the engineered immune effector cell is deficient in a subunit of the T cell receptor complex.

[00134] **Embodiment 108.** The engineered immune effector cell of Embodiment 107, wherein the subunit of the T cell receptor complex is chosen from TCRα (TRAC), TCRβ, TCRδ, TCRγ, CD3ε, CD3γ, CD3δ, and CD3ζ.

[00135] **Embodiment 109.** The engineered immune effector cell of any of Embodiments 99-108, wherein the engineered immune effector cell is deficient in a cell surface protein that is the target of the CAR.

[00136] **Embodiment 110.** The engineered immune effector cell of Embodiment 104, wherein the engineered immune effector cell is an NK cell.

[00137] **Embodiment 111.** The engineered immune effector cell of Embodiment 110 wherein the engineered immune effector cell is a memory-like (ML) NK cell.

[00138] **Embodiment 112.** The engineered immune effector cell of Embodiment 111, wherein the engineered immune effector cell is a cytokine-induced memory-like (CIML) NK cell.

[00139] **Embodiment 113.** The engineered immune effector cell of Embodiment 104, wherein the engineered immune effector cell is an iNKT cell.

[00140] **Embodiment 114.** A method of treatment of a subject in need thereof, who has a first polymorphic variant of an antigen on the surface of a target cell, comprising:

a. optionally, treating the subject with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen;
b. administering to the subject either:
   - a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
   - a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or

- an antibody-drug conjugate (ADC) comprising monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; and

c. administering to the subject a population of donor hematopoietic cells, a plurality of which comprise a second polymorphic variant of the antigen;

wherein the administering of the hematopoietic cells, and the administering of the CAR-expressing cells, mAb, or ADC, may be done concurrently, or sequentially in either order.

[00141] Embodiment 115. A method of immunotherapy of a human subject in need thereof, who has a first polymorphic variant of an antigen on the surface of a target cell, comprising:

a. optionally, treating the subject with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen;

b. administering to the subject a population of donor hematopoietic cells, a plurality of which comprise a second polymorphic variant of the antigen; and

c. administering to the subject:

- a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that specifically binds the first polymorphic variant of an antigen on the surface of a target cell; or
- a monoclonal antibody (mAb) or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
- an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

[00142] Embodiment 116. A method of treatment of a subject in need thereof, who has a first polymorphic variant of an antigen on the surface of a target cell, comprising:

a. administering to the subject:

- a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) which binds the antigen on the surface of the target cell; or
- a monoclonal antibody (mAb) which binds the antigen on the surface of the target cell; or
- an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb) which binds the antigen on the surface of the target cell; and

b. optionally, treating the subject with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen;
c. administering to the subject either:
   - a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
   - a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
   - an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; and
d. administering to the subject a population of donor hematopoietic cells, a plurality of which comprise a second polymorphic variant of the antigen;

wherein the administering of the hematopoietic cells, and the administering of the CAR-expressing cells, mAb, or ADC, may be done concurrently, or sequentially in either order.

[00143] **Embodiment 117.** The method of any of Embodiments 114-116, wherein the subject is a human.

[00144] **Embodiment 118.** The method of any of Embodiments 114-117, wherein the binding is at least 2-fold selective.

[00145] **Embodiment 119.** The method of Embodiment 118, wherein the binding is at east 10-fold selective.

[00146] **Embodiment 120.** The method of Embodiment 119, wherein the binding is at least 30-fold selective.

[00147] **Embodiment 121.** The method of any of Embodiments 114-120, wherein the antigen is chosen from CD33, CLL-1, and FLT3.

[00148] **Embodiment 122.** The method of Embodiment 121, wherein the antigen is CD33.

[00149] **Embodiment 123.** The method of Embodiment 122, wherein the first polymorphic variant of CD33 is R69 and the second polymorphic variant of CD33 is G69; or the first polymorphic variant of CD33 is G69 and the second polymorphic variant of CD33 is R69.

[00150] **Embodiment 124.** The method of Embodiment 121, wherein the antigen is FLT3.

[00151] **Embodiment 125.** The method of Embodiment 124, wherein the first polymorphic variant of FLT3 is T227 and the second polymorphic variant of FLT3 is M227; or first polymorphic variant of FLT3 is M227 and the second polymorphic variant of FLT3 is T227.

[00152] **Embodiment 126.** The method of Embodiment 121, wherein the antigen is CLL-1.

[00153] **Embodiment 127.** The method of Embodiment 126, wherein the first polymorphic variant of CLL-1 is K224 and the second polymorphic variant of CLL-1 is Q244; or first polymorphic variant of CLL-1 is Q224 and the second polymorphic variant of CLL-1 is K244.

[00154] **Embodiment 128.** The method of any of Embodiments 114-127, wherein the subject is concurrently administered both the population of engineered immune effector cells and the population of hematopoietic cells.

[00155] **Embodiment 128.** The method of any of Embodiments 114-127, wherein the subject is sequentially administered the population of hematopoietic cells, and the population of engineered immune effector cells, mAb, or ADC.

[00156] **Embodiment 130.** The method of any of Embodiments 114-127, wherein the subject is sequentially administered the population of engineered immune effector cells, mAb, or ADC, and the population of hematopoietic cells.

[00157] **Embodiment 131.** The method of any of Embodiments 114-130, wherein the subject is treated with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen before administering of the hematopoietic cells.

[00158] **Embodiment 132.** The method of any of Embodiments 114-130, wherein the subject has already been conditioned with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen.

[00159] **Embodiment 133.** The method of any of Embodiments 114-12, wherein the hematopoietic cells are hematopoietic stem cells and/or hematopoietic progenitor cells.

[00160] **Embodiment 134.** The method of any of Embodiments 114-133, wherein the subject is administered a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

[00161] **Embodiment 135.** The method of Embodiment 134, wherein the engineered immune effector cells are derived from the subject (i.e., autologous) and the hematopoietic cells are derived from a donor (i.e., allogeneic).

[00162] **Embodiment 136.** The method of Embodiment 134, wherein the engineered immune effector cells and hematopoietic cells are derived from a single donor.

[00163] **Embodiment 137.** The method of Embodiment 134, wherein the engineered immune cells are derived from a first donor and hematopoietic cells are derived from a second donor.

[00164] **Embodiment 138.** The method of any of Embodiments 134-137, wherein the chimeric antigen receptor (CAR) comprises a polypeptide of any of Embodiments 1-69.

[00165] **Embodiment 139.** The method of Embodiment any of Embodiments 134-137, wherein the chimeric antigen receptor (CAR) comprises the scFv of Embodiment 70.

[00166] **Embodiment 140.** The method of any of Embodiments 134-137, wherein the chimeric antigen receptor (CAR) is a CAR of any of Embodiments 81-94.

[00167] **Embodiment 141.** The method of any of Embodiments 134-137, wherein the engineered immune effector cell is one of any of any of Embodiments 99-113.

[00168] **Embodiment 142.** The method of any of Embodiments 114-133, wherein the subject is administered a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

[00169] **Embodiment 143.** The method of Embodiment 142, wherein the monoclonal antibody (mAb) comprises a polypeptide of any of Embodiments 1-69.

[00170] **Embodiment 144.** The method of Embodiment 116, wherein the monoclonal antibody (mAb) is a mAb of any of Embodiments 71-77.

[00171] **Embodiment 145.** The method of any of Embodiments 114-133, wherein the subject is administered an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

[00172] **Embodiment 146.** The method of any of Embodiments 142-145, wherein the mAb or ADC is administered prophylactically after transplant to prevent relapse.

[00173] **Embodiment 147.** The method of any of Embodiments 114-146, additionally comprising genotyping the subject and donor to ensure the HSC donor and patient express different variants of the target antigen.

[00174] Embodiment 148. The method of Embodiment 147, wherein the genotyping is done using either a protein- (FACS) or DNA- (PCR) based assay.

[00175] Embodiment 149. The method of Embodiment 147, wherein the patient is genotyped after relapse from transplant.

[00176] Embodiment 150. The method of Embodiment 147, wherein the patient is genotyped before transplant.

[00177] Embodiment 151. The method of Embodiment 147, wherein the hematopoietic cell donor is genotyped before hematopoietic cell transplant.

[00178] Embodiment 152. The method of any of Embodiments 137-147, wherein the immune effector cell donor is genotyped before transplant of the population of engineered immune effector cells that express the CAR .

[00179] Embodiment 153. The method of any of Embodiments 137-147, wherein the immune effector cell donor is genotyped before hematopoietic cell transplant.

[00180] Embodiment 154. A polypeptide which binds CD33, comprising:

three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and/or

three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3; wherein

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 705-7559 and 1979-1981;

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 760-814 and 1982-1984;

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 815-869 and 1985-1987;

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 870-924 and 1988-1990;

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 925-979 and 1991-1993; and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 980-1034 and 1994-1996.

[00181] Embodiment 155. The polypeptide of Embodiment 154, comprising a combination of HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, respectively, chosen from:

SEQ ID NO.s: 705, 760, 815, 870, 925, and 980;

SEQ ID NO.s: 706, 761, 816, 871, 926, and 981;

SEQ ID NO.s: 707, 762, 817, 872, 927, and 982;

SEQ ID NO.s: 708, 763, 818, 873, 928, and 983;
SEQ ID NO.s: 709, 764, 819, 874, 929, and 984;
SEQ ID NO.s: 710, 765, 820, 875, 930, and 985;
SEQ ID NO.s: 711, 766, 821, 876, 931, and 986;
SEQ ID NO.s: 712, 767, 822, 877, 932, and 987;
SEQ ID NO.s: 713, 768, 823, 878, 933, and 988;
SEQ ID NO.s: 714, 769, 824, 879, 934, and 989;
SEQ ID NO.s: 715, 770, 825, 880, 935, and 990;
SEQ ID NO.s: 716, 771, 826, 881, 936, and 991;
SEQ ID NO.s: 717, 772, 827, 882, 937, and 992;
SEQ ID NO.s: 718, 773, 828, 883, 938, and 993;
SEQ ID NO.s: 719, 774, 829, 884, 939, and 994;
SEQ ID NO.s: 720, 775, 830, 885, 940, and 995;
SEQ ID NO.s: 721, 776, 831, 886, 941, and 996;
SEQ ID NO.s: 722, 777, 832, 887, 942, and 997;
SEQ ID NO.s: 723, 778, 833, 888, 943, and 998;
SEQ ID NO.s: 724, 779, 834, 889, 944, and 999;
SEQ ID NO.s: 725, 780, 835, 890, 945, and 1000;
SEQ ID NO.s: 726, 781, 836, 891, 946, and 1001;
SEQ ID NO.s: 727, 782, 837, 892, 947, and 1002;
SEQ ID NO.s: 728, 783, 838, 893, 948, and 1003;
SEQ ID NO.s: 729, 784, 839, 894, 949, and 1004;
SEQ ID NO.s: 730, 785, 840, 895, 950, and 1005;
SEQ ID NO.s: 731, 786, 841, 896, 951, and 1006;
SEQ ID NO.s: 732, 787, 842, 897, 952, and 1007;
SEQ ID NO.s: 733, 788, 843, 898, 953, and 1008;
SEQ ID NO.s: 734, 789, 844, 899, 954, and 1009;
SEQ ID NO.s: 735, 790, 845, 900, 955, and 1010;
SEQ ID NO.s: 736, 791, 846, 901, 956, and 1011;
SEQ ID NO.s: 737, 792, 847, 902, 957, and 1012;
SEQ ID NO.s: 738, 793, 848, 903, 958, and 1013;
SEQ ID NO.s: 739, 794, 849, 904, 959, and 1014;
SEQ ID NO.s: 740, 795, 850, 905, 960, and 1015;
SEQ ID NO.s: 741, 796, 851, 906, 961, and 1016;

SEQ ID NO.s: 742, 797, 852, 907, 962, and 1017;

SEQ ID NO.s: 743, 798, 853, 908, 963, and 1018;

SEQ ID NO.s: 744, 799, 854, 909, 964, and 1019;

SEQ ID NO.s: 745, 800, 855, 910, 965, and 1020;

SEQ ID NO.s: 746, 801, 856, 911, 966, and 1021;

SEQ ID NO.s: 747, 802, 857, 912, 967, and 1022;

SEQ ID NO.s: 748, 803, 858, 913, 968, and 1023;

SEQ ID NO.s: 749, 804, 859, 914, 969, and 1024;

SEQ ID NO.s: 750, 805, 860, 915, 970, and 1025;

SEQ ID NO.s: 751, 806, 861, 916, 971, and 1026;

SEQ ID NO.s: 752, 807, 862, 917, 972, and 1027;

SEQ ID NO.s: 753, 808, 863, 918, 973, and 1028;

SEQ ID NO.s: 754, 809, 864, 919, 974, and 1029;

SEQ ID NO.s: 755, 810, 865, 920, 975, and 1030;

SEQ ID NO.s: 756, 811, 866, 921, 976, and 1031;

SEQ ID NO.s: 757, 812, 867, 922, 977, and 1032;

SEQ ID NO.s: 758, 813, 868, 923, 978, and 1033;

SEQ ID NO.s: 759, 814, 869, 924, 979, and 1034;

SEQ ID NO.s: 1979, 1982, 1985, 1988, 1991, and 1994;

SEQ ID NO.s: 1980, 1983, 1986, 1989, 1992, and 1995; and

SEQ ID NO.s: 1981, 1984, 1987, 1990, 1993, and 1996;

or a combination of HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 with at least 95% sequence identity to the foregoing.

[00182] **Embodiment 156.** The polypeptide of Embodiment 154, comprising a V_H domain and V_L domain, wherein:

the V_H domain comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1035-1089 and 1997-1999; and/or

the V_L domain comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1090-1144 and 2000-2002.

[00183] **Embodiment 157.** The polypeptide of Embodiment 156, comprising a combination of V_H and V_L domains chosen from:

SEQ ID NO.s: 1035 and 1090;

SEQ ID NO.s: 1036 and 1091;

SEQ ID NO.s: 1037 and 1092;

SEQ ID NO.s: 1038 and 1093;
SEQ ID NO.s: 1039 and 1094;
SEQ ID NO.s: 1040 and 1095;
SEQ ID NO.s: 1041 and 1096;
SEQ ID NO.s: 1042 and 1097;
SEQ ID NO.s: 1043 and 1098;
SEQ ID NO.s: 1044 and 1099;
SEQ ID NO.s: 1045 and 1100;
SEQ ID NO.s: 1046 and 1101;
SEQ ID NO.s: 1047 and 1102;
SEQ ID NO.s: 1048 and 1103;
SEQ ID NO.s: 1049 and 1104;
SEQ ID NO.s: 1050 and 1105;
SEQ ID NO.s: 1051 and 1106;
SEQ ID NO.s: 1052 and 1107;
SEQ ID NO.s: 1053 and 1108;
SEQ ID NO.s: 1054 and 1109;
SEQ ID NO.s: 1055 and 1110;
SEQ ID NO.s: 1056 and 1111;
SEQ ID NO.s: 1057 and 1112;
SEQ ID NO.s: 1058 and 1113;
SEQ ID NO.s: 1059 and 1114;
SEQ ID NO.s: 1060 and 1115;
SEQ ID NO.s: 1061 and 1116;
SEQ ID NO.s: 1062 and 1117;
SEQ ID NO.s: 1063 and 1118;
SEQ ID NO.s: 1064 and 1119;
SEQ ID NO.s: 1065 and 1120;
SEQ ID NO.s: 1066 and 1121;
SEQ ID NO.s: 1067 and 1122;
SEQ ID NO.s: 1068 and 1123;
SEQ ID NO.s: 1069 and 1124;
SEQ ID NO.s: 1070 and 1125;
SEQ ID NO.s: 1071 and 1126;

SEQ ID NO.s: 1072 and 1127;
SEQ ID NO.s: 1073 and 1128;
SEQ ID NO.s: 1074 and 1129;
SEQ ID NO.s: 1075 and 1130;
SEQ ID NO.s: 1076 and 1131;
SEQ ID NO.s: 1077 and 1132;
SEQ ID NO.s: 1078 and 1133;
SEQ ID NO.s: 1079 and 1134;
SEQ ID NO.s: 1080 and 1135;
SEQ ID NO.s: 1081 and 1136;
SEQ ID NO.s: 1082 and 1137;
SEQ ID NO.s: 1083 and 1138;
SEQ ID NO.s: 1084 and 1139;
SEQ ID NO.s: 1085 and 1140;
SEQ ID NO.s: 1086 and 1141;
SEQ ID NO.s: 1087 and 1142;
SEQ ID NO.s: 1088 and 1143;
SEQ ID NO.s: 1089 and 1144;
SEQ ID NO.s: 1997 and 2000;
SEQ ID NO.s: 1998 and 2001; and
SEQ ID NO.s: 1999 and 2002;

or a combination of V_H and V_L domains with at least 95% sequence identity to the foregoing.

[00184] Embodiment 158. A polypeptide which binds CLL-1, comprising:

three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and/or

three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3; wherein

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1145-1191 and 2003-2009;

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1192-1238 and 2010-2016;

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1239-1285 and 2017-2023;

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1286-1332 and 2024-2030;

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1333-1379 and 2031-2037; and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1380-1426 and 2038-2044.

[00185] Embodiment 159. The polypeptide of Embodiment 158, comprising a combination of HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, respectively, chosen from:

SEQ ID NO.s: 1145, 1192, 1239, 1286, 1333, and 1380;
SEQ ID NO.s: 1146, 1193, 1240, 1287, 1334, and 1381;
SEQ ID NO.s: 1147, 1194, 1241, 1288, 1335, and 1382;
SEQ ID NO.s: 1148, 1195, 1242, 1289, 1336, and 1383;
SEQ ID NO.s: 1149, 1196, 1243, 1290, 1337, and 1384;
SEQ ID NO.s: 1150, 1197, 1244, 1291, 1338, and 1385;
SEQ ID NO.s: 1151, 1198, 1245, 1292, 1339, and 1386;
SEQ ID NO.s: 1152, 1199, 1246, 1293, 1340, and 1387;
SEQ ID NO.s: 1153, 1200, 1247, 1294, 1341, and 1388;
SEQ ID NO.s: 1154, 1201, 1248, 1295, 1342, and 1389;
SEQ ID NO.s: 1155, 1202, 1249, 1296, 1343, and 1390;
SEQ ID NO.s: 1156, 1203, 1250, 1297, 1344, and 1391;
SEQ ID NO.s: 1157, 1204, 1251, 1298, 1345, and 1392;
SEQ ID NO.s: 1158, 1205, 1252, 1299, 1346, and 1393;
SEQ ID NO.s: 1159, 1206, 1253, 1300, 1347, and 1394;
SEQ ID NO.s: 1160, 1207, 1254, 1301, 1348, and 1395;
SEQ ID NO.s: 1161, 1208, 1255, 1302, 1349, and 1396;
SEQ ID NO.s: 1162, 1209, 1256, 1303, 1350, and 1397;
SEQ ID NO.s: 1163, 1210, 1257, 1304, 1351, and 1398;
SEQ ID NO.s: 1164, 1211, 1258, 1305, 1352, and 1399;
SEQ ID NO.s: 1165, 1212, 1259, 1306, 1353, and 1400;
SEQ ID NO.s: 1166, 1213, 1260, 1307, 1354, and 1401;
SEQ ID NO.s: 1167, 1214, 1261, 1308, 1355, and 1402;
SEQ ID NO.s: 1168, 1215, 1262, 1309, 1356, and 1403;
SEQ ID NO.s: 1169, 1216, 1263, 1310, 1357, and 1404;
SEQ ID NO.s: 1170, 1217, 1264, 1311, 1358, and 1405;
SEQ ID NO.s: 1171, 1218, 1265, 1312, 1359, and 1406;

SEQ ID NO.s: 1172, 1219, 1266, 1313, 1360, and 1407;
SEQ ID NO.s: 1173, 1220, 1267, 1314, 1361, and 1408;
SEQ ID NO.s: 1174, 1221, 1268, 1315, 1362, and 1409;
SEQ ID NO.s: 1175, 1222, 1269, 1316, 1363, and 1410;
SEQ ID NO.s: 1176, 1223, 1270, 1317, 1364, and 1411;
SEQ ID NO.s: 1177, 1224, 1271, 1318, 1365, and 1412;
SEQ ID NO.s: 1178, 1225, 1272, 1319, 1366, and 1413;
SEQ ID NO.s: 1179, 1226, 1273, 1320, 1367, and 1414;
SEQ ID NO.s: 1180, 1227, 1274, 1321, 1368, and 1415;
SEQ ID NO.s: 1181, 1228, 1275, 1322, 1369, and 1416;
SEQ ID NO.s: 1182, 1229, 1276, 1323, 1370, and 1417;
SEQ ID NO.s: 1183, 1230, 1277, 1324, 1371, and 1418;
SEQ ID NO.s: 1184, 1231, 1278, 1325, 1372, and 1419;
SEQ ID NO.s: 1185, 1232, 1279, 1326, 1373, and 1420;
SEQ ID NO.s: 1186, 1233, 1280, 1327, 1374, and 1421;
SEQ ID NO.s: 1187, 1234, 1281, 1328, 1375, and 1422;
SEQ ID NO.s: 1188, 1235, 1282, 1329, 1376, and 1423;
SEQ ID NO.s: 1189, 1236, 1283, 1330, 1377, and 1424;
SEQ ID NO.s: 1190, 1237, 1284, 1331, 1378, and 1425;
SEQ ID NO.s: 1191, 1238, 1285, 1332, 1379, and 1426;
SEQ ID NO.s: 2003, 2010, 2017, 2024, 2031, and 2038;
SEQ ID NO.s: 2004, 2011, 2018, 2025, 2032, and 2039;
SEQ ID NO.s: 2005, 2012, 2019, 2026, 2033, and 2040;
SEQ ID NO.s: 2006, 2013, 2020, 2027, 2034, and 2041;
SEQ ID NO.s: 2007, 2014, 2021, 2028, 2035, and 2042;
SEQ ID NO.s: 2008, 2015, 2022, 2029, 2036, and 2043; and
SEQ ID NO.s: 2009, 2016, 2023, 2030, 2037, and 2044;

or a combination of HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 with at least 95% sequence identity to the foregoing.

[00186] Embodiment 160. The polypeptide of Embodiment 158, comprising a V_H domain and V_L domain, wherein:

the V_H domain comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1427-1473 and 2045-2051; and/or

the V_L domain comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 1474-1520 and 2052-2058.

[00187] Embodiment 161. The polypeptide of Embodiment 160, comprising a combination of V_H and V_L domains chosen from:

SEQ ID NO.s: 1427 and 1474;
SEQ ID NO.s: 1428 and 1475;
SEQ ID NO.s: 1429 and 1476;
SEQ ID NO.s: 1430 and 1477;
SEQ ID NO.s: 1431 and 1478;
SEQ ID NO.s: 1432 and 1479;
SEQ ID NO.s: 1433 and 1480;
SEQ ID NO.s: 1434 and 1481;
SEQ ID NO.s: 1435 and 1482;
SEQ ID NO.s: 1436 and 1483;
SEQ ID NO.s: 1437 and 1484;
SEQ ID NO.s: 1438 and 1485;
SEQ ID NO.s: 1439 and 1486;
SEQ ID NO.s: 1440 and 1487;
SEQ ID NO.s: 1441 and 1488;
SEQ ID NO.s: 1442 and 1489;
SEQ ID NO.s: 1443 and 1490;
SEQ ID NO.s: 1444 and 1491;
SEQ ID NO.s: 1445 and 1492;
SEQ ID NO.s: 1446 and 1493;
SEQ ID NO.s: 1447 and 1494;
SEQ ID NO.s: 1448 and 1495;
SEQ ID NO.s: 1449 and 1496;
SEQ ID NO.s: 1450 and 1497;
SEQ ID NO.s: 1451 and 1498;
SEQ ID NO.s: 1452 and 1499;
SEQ ID NO.s: 1453 and 1500;
SEQ ID NO.s: 1454 and 1501;
SEQ ID NO.s: 1455 and 1502;
SEQ ID NO.s: 1456 and 1503;

SEQ ID NO.s: 1457 and 1504;
SEQ ID NO.s: 1458 and 1505;
SEQ ID NO.s: 1459 and 1506;
SEQ ID NO.s: 1460 and 1507;
SEQ ID NO.s: 1461 and 1508;
SEQ ID NO.s: 1462 and 1509;
SEQ ID NO.s: 1463 and 1510;
SEQ ID NO.s: 1464 and 1511;
SEQ ID NO.s: 1465 and 1512;
SEQ ID NO.s: 1466 and 1513;
SEQ ID NO.s: 1467 and 1514;
SEQ ID NO.s: 1468 and 1515;
SEQ ID NO.s: 1469 and 1516;
SEQ ID NO.s: 1470 and 1517;
SEQ ID NO.s: 1471 and 1518;
SEQ ID NO.s: 1472 and 1519;
SEQ ID NO.s: 1473 and 1520;
SEQ ID NO.s: 2045 and 2052;
SEQ ID NO.s: 2046 and 2053;
SEQ ID NO.s: 2047 and 2054;
SEQ ID NO.s: 2048 and 2055;
SEQ ID NO.s: 2049 and 2056;
SEQ ID NO.s: 2050 and 2057; and
SEQ ID NO.s: 2051 and 2058;

or a combination of V_H and V_L domains with at least 95% sequence identity to the foregoing.

[00188] **Embodiment 162.** A polypeptide which binds FLT3, comprising:

three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and/or

three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3; wherein

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2059-2152 ;

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2153-2246;

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2247-2340;

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2341-2434;

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2435-2528; and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2529-2622.

[00189] Embodiment 163. The polypeptide of Embodiment 162, comprising a combination of HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3, respectively, chosen from:

SEQ ID NO.s: 2059, 2153, 2247, 2341, 2435, and 2529;
SEQ ID NO.s: 2060, 2154, 2248, 2342, 2436, and 2530;
SEQ ID NO.s: 2061, 2155, 2249, 2343, 2437, and 2531;
SEQ ID NO.s: 2062, 2156, 2250, 2344, 2438, and 2532;
SEQ ID NO.s: 2063, 2157, 2251, 2345, 2439, and 2533;
SEQ ID NO.s: 2064, 2158, 2252, 2346, 2440, and 2534;
SEQ ID NO.s: 2065, 2159, 2253, 2347, 2441, and 2535;
SEQ ID NO.s: 2066, 2160, 2254, 2348, 2442, and 2536;
SEQ ID NO.s: 2067, 2161, 2255, 2349, 2443, and 2537;
SEQ ID NO.s: 2068, 2162, 2256, 2350, 2444, and 2538;
SEQ ID NO.s: 2069, 2163, 2257, 2351, 2445, and 2539;
SEQ ID NO.s: 2070, 2164, 2258, 2352, 2446, and 2540;
SEQ ID NO.s: 2071, 2165, 2259, 2353, 2447, and 2541;
SEQ ID NO.s: 2072, 2166, 2260, 2354, 2448, and 2542;
SEQ ID NO.s: 2073, 2167, 2261, 2355, 2449, and 2543;
SEQ ID NO.s: 2074, 2168, 2262, 2356, 2450, and 2544;
SEQ ID NO.s: 2075, 2169, 2263, 2357, 2451, and 2545;
SEQ ID NO.s: 2076, 2170, 2264, 2358, 2452, and 2546;
SEQ ID NO.s: 2077, 2171, 2265, 2359, 2453, and 2547;
SEQ ID NO.s: 2078, 2172, 2266, 2360, 2454, and 2548;
SEQ ID NO.s: 2079, 2173, 2267, 2361, 2455, and 2549;
SEQ ID NO.s: 2080, 2174, 2268, 2362, 2456, and 2550;
SEQ ID NO.s: 2081, 2175, 2269, 2363, 2457, and 2551;

SEQ ID NO.s: 2082, 2176, 2270, 2364, 2458, and 2552;
SEQ ID NO.s: 2083, 2177, 2271, 2365, 2459, and 2553;
SEQ ID NO.s: 2084, 2178, 2272, 2366, 2460, and 2554;
SEQ ID NO.s: 2085, 2179, 2273, 2367, 2461, and 2555;
SEQ ID NO.s: 2086, 2180, 2274, 2368, 2462, and 2556;
SEQ ID NO.s: 2087, 2181, 2275, 2369, 2463, and 2557;
SEQ ID NO.s: 2088, 2182, 2276, 2370, 2464, and 2558;
SEQ ID NO.s: 2089, 2183, 2277, 2371, 2465, and 2559;
SEQ ID NO.s: 2090, 2184, 2278, 2372, 2466, and 2560;
SEQ ID NO.s: 2091, 2185, 2279, 2373, 2467, and 2561;
SEQ ID NO.s: 2092, 2186, 2280, 2374, 2468, and 2562;
SEQ ID NO.s: 2093, 2187, 2281, 2375, 2469, and 2563;
SEQ ID NO.s: 2094, 2188, 2282, 2376, 2470, and 2564;
SEQ ID NO.s: 2095, 2189, 2283, 2377, 2471, and 2565;
SEQ ID NO.s: 2096, 2190, 2284, 2378, 2472, and 2566;
SEQ ID NO.s: 2097, 2191, 2285, 2379, 2473, and 2567;
SEQ ID NO.s: 2098, 2192, 2286, 2380, 2474, and 2568;
SEQ ID NO.s: 2099, 2193, 2287, 2381, 2475, and 2569;
SEQ ID NO.s: 2100, 2194, 2288, 2382, 2476, and 2570;
SEQ ID NO.s: 2101, 2195, 2289, 2383, 2477, and 2571;
SEQ ID NO.s: 2102, 2196, 2290, 2384, 2478, and 2572;
SEQ ID NO.s: 2103, 2197, 2291, 2385, 2479, and 2573;
SEQ ID NO.s: 2104, 2198, 2292, 2386, 2480, and 2574;
SEQ ID NO.s: 2105, 2199, 2293, 2387, 2481, and 2575;
SEQ ID NO.s: 2106, 2200, 2294, 2388, 2482, and 2576;
SEQ ID NO.s: 2107, 2201, 2295, 2389, 2483, and 2577;
SEQ ID NO.s: 2108, 2202, 2296, 2390, 2484, and 2578;
SEQ ID NO.s: 2109, 2203, 2297, 2391, 2485, and 2579;
SEQ ID NO.s: 2110, 2204, 2298, 2392, 2486, and 2580;
SEQ ID NO.s: 2111, 2205, 2299, 2393, 2487, and 2581;
SEQ ID NO.s: 2112, 2206, 2300, 2394, 2488, and 2582;
SEQ ID NO.s: 2113, 2207, 2301, 2395, 2489, and 2583;
SEQ ID NO.s: 2114, 2208, 2302, 2396, 2490, and 2584;
SEQ ID NO.s: 2115, 2209, 2303, 2397, 2491, and 2585;

SEQ ID NO.s: 2116, 2210, 2304, 2398, 2492, and 2586;
SEQ ID NO.s: 2117, 2211, 2305, 2399, 2493, and 2587;
SEQ ID NO.s: 2118, 2212, 2306, 2400, 2494, and 2588;
SEQ ID NO.s: 2119, 2213, 2307, 2401, 2495, and 2589;
SEQ ID NO.s: 2120, 2214, 2308, 2402, 2496, and 2590;
SEQ ID NO.s: 2121, 2215, 2309, 2403, 2497, and 2591;
SEQ ID NO.s: 2122, 2216, 2310, 2404, 2498, and 2592;
SEQ ID NO.s: 2123, 2217, 2311, 2405, 2499, and 2593;
SEQ ID NO.s: 2124, 2218, 2312, 2406, 2500, and 2594;
SEQ ID NO.s: 2125, 2219, 2313, 2407, 2501, and 2595;
SEQ ID NO.s: 2126, 2220, 2314, 2408, 2502, and 2596;
SEQ ID NO.s: 2127, 2221, 2315, 2409, 2503, and 2597;
SEQ ID NO.s: 2128, 2222, 2316, 2410, 2504, and 2598;
SEQ ID NO.s: 2129, 2223, 2317, 2411, 2505, and 2599;
SEQ ID NO.s: 2130, 2224, 2318, 2412, 2506, and 2600;
SEQ ID NO.s: 2131, 2225, 2319, 2413, 2507, and 2601;
SEQ ID NO.s: 2132, 2226, 2320, 2414, 2508, and 2602;
SEQ ID NO.s: 2133, 2227, 2321, 2415, 2509, and 2603;
SEQ ID NO.s: 2134, 2228, 2322, 2416, 2510, and 2604;
SEQ ID NO.s: 2135, 2229, 2323, 2417, 2511, and 2605;
SEQ ID NO.s: 2136, 2230, 2324, 2418, 2512, and 2606;
SEQ ID NO.s: 2137, 2231, 2325, 2419, 2513, and 2607;
SEQ ID NO.s: 2138, 2232, 2326, 2420, 2514, and 2608;
SEQ ID NO.s: 2139, 2233, 2327, 2421, 2515, and 2609;
SEQ ID NO.s: 2140, 2234, 2328, 2422, 2516, and 2610;
SEQ ID NO.s: 2141, 2235, 2329, 2423, 2517, and 2611;
SEQ ID NO.s: 2142, 2236, 2330, 2424, 2518, and 2612;
SEQ ID NO.s: 2143, 2237, 2331, 2425, 2519, and 2613;
SEQ ID NO.s: 2144, 2238, 2332, 2426, 2520, and 2614;
SEQ ID NO.s: 2145, 2239, 2333, 2427, 2521, and 2615;
SEQ ID NO.s: 2146, 2240, 2334, 2428, 2522, and 2616;
SEQ ID NO.s: 2147, 2241, 2335, 2429, 2523, and 2617;
SEQ ID NO.s: 2148, 2242, 2336, 2430, 2524, and 2618;
SEQ ID NO.s: 2149, 2243, 2337, 2431, 2525, and 2619;

SEQ ID NO.s: 2150, 2244, 2338, 2432, 2526, and 2620;

SEQ ID NO.s: 2151, 2245, 2339, 2433, 2527, and 2621; and

SEQ ID NO.s: 2152, 2246, 2340, 2434, 2528, and 2622;

or a combination of HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3 with at least 95% sequence identity to the foregoing.

[00190] **Embodiment 164.** The polypeptide of Embodiment 162, comprising a V_H domain and V_L domain, wherein:

the V_H domain comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2623-2716; and/or

the V_L domain comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 2717-2810.

[00191] **Embodiment 165.** The polypeptide of Embodiment 164, comprising a combination of V_H and V_L domains chosen from:

SEQ ID NO.s: 2623 and 2717;

SEQ ID NO.s: 2624 and 2718;

SEQ ID NO.s: 2625 and 2719;

SEQ ID NO.s: 2626 and 2720;

SEQ ID NO.s: 2627 and 2721;

SEQ ID NO.s: 2628 and 2722;

SEQ ID NO.s: 2629 and 2723;

SEQ ID NO.s: 2630 and 2724;

SEQ ID NO.s: 2631 and 2725;

SEQ ID NO.s: 2632 and 2726;

SEQ ID NO.s: 2633 and 2727;

SEQ ID NO.s: 2634 and 2728;

SEQ ID NO.s: 2635 and 2729;

SEQ ID NO.s: 2636 and 2730;

SEQ ID NO.s: 2637 and 2731;

SEQ ID NO.s: 2638 and 2732;

SEQ ID NO.s: 2639 and 2733;

SEQ ID NO.s: 2640 and 2734;

SEQ ID NO.s: 2641 and 2735;

SEQ ID NO.s: 2642 and 2736;

SEQ ID NO.s: 2643 and 2737;

SEQ ID NO.s: 2644 and 2738;
SEQ ID NO.s: 2645 and 2739;
SEQ ID NO.s: 2646 and 2740;
SEQ ID NO.s: 2647 and 2741;
SEQ ID NO.s: 2648 and 2742;
SEQ ID NO.s: 2649 and 2743;
SEQ ID NO.s: 2650 and 2744;
SEQ ID NO.s: 2651 and 2745;
SEQ ID NO.s: 2652 and 2746;
SEQ ID NO.s: 2653 and 2747;
SEQ ID NO.s: 2654 and 2748;
SEQ ID NO.s: 2655 and 2749;
SEQ ID NO.s: 2656 and 2750;
SEQ ID NO.s: 2657 and 2751;
SEQ ID NO.s: 2658 and 2752;
SEQ ID NO.s: 2659 and 2753;
SEQ ID NO.s: 2660 and 2754;
SEQ ID NO.s: 2661 and 2755;
SEQ ID NO.s: 2662 and 2756;
SEQ ID NO.s: 2663 and 2757;
SEQ ID NO.s: 2664 and 2758;
SEQ ID NO.s: 2665 and 2759;
SEQ ID NO.s: 2666 and 2760;
SEQ ID NO.s: 2667 and 2761;
SEQ ID NO.s: 2668 and 2762;
SEQ ID NO.s: 2669 and 2763;
SEQ ID NO.s: 2670 and 2764;
SEQ ID NO.s: 2671 and 2765;
SEQ ID NO.s: 2672 and 2766;
SEQ ID NO.s: 2673 and 2767;
SEQ ID NO.s: 2674 and 2768;
SEQ ID NO.s: 2675 and 2769;
SEQ ID NO.s: 2676 and 2770;
SEQ ID NO.s: 2677 and 2771;

SEQ ID NO.s: 2678 and 2772;
SEQ ID NO.s: 2679 and 2773;
SEQ ID NO.s: 2680 and 2774;
SEQ ID NO.s: 2681 and 2775;
SEQ ID NO.s: 2682 and 2776;
SEQ ID NO.s: 2683 and 2777;
SEQ ID NO.s: 2684 and 2778;
SEQ ID NO.s: 2685 and 2779;
SEQ ID NO.s: 2686 and 2780;
SEQ ID NO.s: 2687 and 2781;
SEQ ID NO.s: 2688 and 2782;
SEQ ID NO.s: 2689 and 2783;
SEQ ID NO.s: 2690 and 2784;
SEQ ID NO.s: 2691 and 2785;
SEQ ID NO.s: 2692 and 2786;
SEQ ID NO.s: 2693 and 2787;
SEQ ID NO.s: 2694 and 2788;
SEQ ID NO.s: 2695 and 2789;
SEQ ID NO.s: 2696 and 2790;
SEQ ID NO.s: 2697 and 2791;
SEQ ID NO.s: 2698 and 2792;
SEQ ID NO.s: 2699 and 2793;
SEQ ID NO.s: 2700 and 2794;
SEQ ID NO.s: 2701 and 2795;
SEQ ID NO.s: 2702 and 2796;
SEQ ID NO.s: 2703 and 2797;
SEQ ID NO.s: 2704 and 2798;
SEQ ID NO.s: 2705 and 2799;
SEQ ID NO.s: 2706 and 2800;
SEQ ID NO.s: 2707 and 2801;
SEQ ID NO.s: 2708 and 2802;
SEQ ID NO.s: 2709 and 2803;
SEQ ID NO.s: 2710 and 2804;
SEQ ID NO.s: 2711 and 2805;

SEQ ID NO.s: 2712 and 2806;

SEQ ID NO.s: 2713 and 2807;

SEQ ID NO.s: 2714 and 2808;

SEQ ID NO.s: 2715 and 2809; and

SEQ ID NO.s: 2716 and 2810;

or a combination of V_H and V_L domains with at least 95% sequence identity to the foregoing.

[00192] **Embodiment 165.** The polypeptide of any of Embodiments 154-164, wherein

- the HCDR1, HCDR2, and HCDR3 and/or the LCDR1, LCDR2, and LCDR3, or
- the V_H and/0r V_L domains,

have at least 97%, 98% or 99% sequence identity to the recited amino acid sequences.

[00193] **Embodiment 166.** A single-chain variable fragment (scFv) comprising the polypeptide of any of Embodiments 154-164.

[00194] **Embodiment 167.** A monoclonal antibody (mAb), or an antigen-binding fragment thereof, comprising the polypeptide of any of Embodiments 154-164.

[00195] **Embodiment 168.** The mAb, or antigen-binding fragment thereof, of Embodiment 167, wherein the mAb is of the IgG, IgM, or IgA isotype.

[00196] **Embodiment 169.** The mAb, or antigen-binding fragment thereof, of Embodiment 170, wherein the mAb is of the IgG1 isotype.

[00197] **Embodiment 170.** The mAb, or antigen-binding fragment thereof, of Embodiment 170, wherein the mAb is of the IgG3 isotype.

[00198] **Embodiment 171.** The mAb, or antigen-binding fragment thereof, of Embodiment 170, wherein the mAb is of the IgG4 isotype.

[00199] **Embodiment 172.** The mAb, or antigen-binding fragment thereof, of Embodiment 170, wherein the mAb is human or humanized.

[00200] **Embodiment 173.** An antibody-drug conjugate (ADC) comprising the mAb, or antigen-binding fragment thereof, of any of Embodiments 167-172.

[00201] **Embodiment 174.** The ADC of Embodiment 173, having Formula I:

$$Ab\text{-}(L\text{-}D)_p$$

(I)

wherein:

Ab is an antibody comprising the polypeptide of any of Embodiments 1-43, or the antibody of any of Embodiments 45-51, or an antigen-binding fragment of either of the foregoing;

L is a linker;

D is a drug; and

p is about 1 to about 20.

[00202] Embodiment 175. The ADC of Embodiment 174, wherein D is chosen from saporin, MMAE, MMAF, DM1, and DM4.

[00203] Embodiment 176. A chimeric antigen receptor (CAR) comprising an extracellular ligand binding domain comprising a polypeptide of any one of Embodiments 1-69.

[00204] Embodiment 177. The CAR of Embodiment 176, additionally comprising:

a hinge domain;

a transmembrane domain;

optionally, one or more co-stimulatory domains; and

a cytoplasmic signaling domain.

[00205] Embodiment 178. The CAR of Embodiment 177, wherein the hinge domain is chosen from FcεRIIIa, CD8α, CD28 and IgG1.

[00206] Embodiment 179. The CAR of Embodiment 178, wherein the hinge domain is CD8α.

[00207] Embodiment 180. The CAR of any of Embodiments 177-179, wherein the transmembrane domain is chosen from alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CDS0, CD86, CD134, CD137 and CD154.

[00208] Embodiment 181. The CAR of Embodiment 180, wherein the transmembrane domain is CD28.

[00209] Embodiment 182. The CAR of any of Embodiments 177-181, wherein the cytoplasmic signaling domain is chosen from CD8, CD3ζ, CD3δ, CD3γ, CD3ε, CD22, CD32, DAP10, DAP12, CD66d, CD79a, CD79b, FcγRIγ, FcγRIIIγ, FcεRIβ, FcεRIγ, FcRγ, FcRβ, and FcRε.

[00210] Embodiment 183. The CAR of Embodiment 182, wherein the cytoplasmic signaling domain is CD3ζ.

[00211] Embodiment 184. The CAR of any of Embodiments 177-183, wherein one co-stimulatory domain is chosen from 4-1BB, CD28, and ICOS.

[00212] **Embodiment 185.** The CAR of Embodiment 184, wherein the costimulatory domain is CD28.

[00213] **Embodiment 186.** The CAR of Embodiment 184, wherein the costimulatory domain is 4-1BB.

[00214] **Embodiment 187.** The CAR of Embodiment 184, comprising two or more costimulatory domains.

[00215] **Embodiment 188.** The CAR of Embodiment 184, wherein two of the costimulatory domains are CD28 and 4-1BB.

[00216] **Embodiment 189.** A nucleotide sequence encoding any of the polypeptides, scFvs, mAbs, or CARs of any of Embodiments 154-188.

[00217] **Embodiment 190.** A vector comprising the nucleotide sequence of Embodiment 189.

[00218] **Embodiment 191.** The vector of Embodiment 190, wherein the vector is a lentiviral vector.

[00219] **Embodiment 192.** The vector of Embodiment 191, wherein the lentiviral vector comprises a VSVG domain.

[00220] **Embodiment 193.** An engineered immune effector cell expressing at the cell surface a CAR of any one of Embodiment 176-188.

[00221] **Embodiment 194.** The engineered immune effector cell of Embodiment 193, wherein the engineered immune effector cell expresses at the cell surface:

a first polymorphic variant of a human cancer cell antigen; and

a CAR that is selective for a second polymorphic over the first polymorphic variant of the antigen.

[00222] **Embodiment 195.** The engineered immune effector cell of Embodiment 193, wherein the cell is a primary cell.

[00223] **Embodiment 196.** The engineered immune effector cell of Embodiment 193, wherein the cell is derived from:

an induced pluripotent stem cell (iPSC);

cord blood;

peripheral blood; or

an immortalized cell line.

[00224] **Embodiment 197.** The engineered immune effector cell of Embodiment 196, wherein the immortalized cell line is NK-92.

[00225] **Embodiment 198.** The engineered immune cell of any of Embodiments 193-197, wherein the cell is chosen from a T cell, an natural killer (NK) cell, an invariant natural killer T (iNKT) cell, a macrophage, and a dendritic cell.

[00226] **Embodiment 199.** The engineered immune effector cell of Embodiment 198, wherein the cell is a T cell.

[00227] **Embodiment 200.** The engineered immune effector cell of Embodiment 199, wherein the T cell is chosen from an inflammatory T-lymphocyte, a cytotoxic T-lymphocyte, a regulatory T-lymphocyte, or a helper T-lymphocyte.

[00228] **Embodiment 201.** The engineered immune effector cell of Embodiment 199, wherein the engineered immune effector cell is deficient in a subunit of the T cell receptor complex.

[00229] **Embodiment 202.** The engineered immune effector cell of Embodiment 201, wherein the subunit of the T cell receptor complex is chosen from TCRα (TRAC), TCRβ, TCRδ, TCRγ, CD3ε, CD3γ, CD3δ, and CD3ζ.

[00230] **Embodiment 203.** The engineered immune effector cell of any of Embodiments 193-202, wherein the engineered immune effector cell is deficient in a cell surface protein that is the target of the CAR.

[00231] **Embodiment 204.** The engineered immune effector cell of Embodiment 198, wherein the engineered immune effector cell is an NK cell.

[00232] **Embodiment 205.** The engineered immune effector cell of Embodiment 204 wherein the engineered immune effector cell is a memory-like (ML) NK cell.

[00233] **Embodiment 206.** The engineered immune effector cell of Embodiment 205, wherein the engineered immune effector cell is a cytokine-induced memory-like (CIML) NK cell.

[00234] **Embodiment 207.** The engineered immune effector cell of Embodiment 198, wherein the engineered immune effector cell is an iNKT cell.

[00235] **Embodiment 208.** A method for treatment of cancer in a patient comprising administering to a cancer patient, a therapeutically effective amount of:

a monoclonal antibody (mAb), or an antigen-binding fragment thereof, of any of Embodiments 167-170;

an antibody-drug conjugate (ADC) of any of Embodiments 173-175; or

an engineered immune effector cell of any of Embodiments 193-207.

[00236] **Embodiment 209.** The method of Embodiment 208, wherein the cancer is a hematologic malignancy.

[00237] **Embodiment 210.** The method of Embodiment 209, wherein the hematologic malignancy is multiple myeloma.

[00238] **Embodiment 211.** The method of Embodiment 210, wherein the hematologic malignancy is acute myeloid leukemia (AML).

Polypeptides

[00239] Disclosed herein are polypeptides, such as monoclonal antibodies (mAbs) and functional fragments thereof, synthetic antigen-binding proteins such as single-chain variable fragments (scFvs), and chimeric antigen receptors (CARs), that can specifically recognize tumor-associated antigens (TAAs) on cancer cells, for example those that express CD33, FLT3, and CLL-1. In some embodiments, the mAbs, scFvs, or CARs recognize polymorphic variants of CD33, FLT3, and CLL-1 expressed on cancer cells; in some embodiments, they are selective for one polymorphic variant over other polymorphic variants. Also disclosed are immune effector cells, such as T cells, natural killer (NK) cells, and invariant natural killer T (iNKT) cells that are engineered to express CARs that specifically recognize the tumor-associated antigens (TAAs) CD33, FLT3, and CLL-1 or polymorphic variants of CD33, FLT3, and CLL-1. Also disclosed are methods for providing an anti-tumor immunity in a subject with CD33, FLT3, and CLL-1-expressing cancers using the disclosed monoclonal antibodies and immune effector cells which express CARs.

[00240] Antibodies that can be used in the disclosed compositions and methods include whole immunoglobulin (i.e., an intact antibody) of any class, fragments thereof, and, using the term more loosely, synthetic proteins containing at least the antigen binding variable domain of an antibody (e.g., single-chain variable fragments, scFvs). The variable domains differ in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not usually evenly distributed through the variable domains of antibodies. It is typically concentrated in three segments called complementarity determining regions (CDRs) or hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of the variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a beta-sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the beta-sheet structure.

The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen binding site of antibodies.

[00241] Transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production can be employed. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region (J(H)) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. Human antibodies can also be produced in phage display libraries. The techniques of Cote et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies.

[00242] Optionally, the antibodies are generated in other species and "humanized" for administration in humans. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2, or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementarity determining region (CDR) of the recipient antibody are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

[00243] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often

referred to as "import" residues, which are typically taken from an "import" variable domain. Antibody humanization techniques generally involve the use of recombinant DNA technology to manipulate the DNA sequence encoding one or more polypeptide chains of an antibody molecule. Humanization can be essentially performed following the method of Winter and co-workers (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, a humanized form of a non-human antibody (or an antigen-binding fragment thereof) is a chimeric antibody or fragment (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[00244] The embodiments of the disclosure include polypeptides, specifically monoclonal antibodies (mAbs), antigen-binding fragments thereof, synthetic antigen-binding proteins such as scFvs, and chimeric antigen receptors (CARs), which are defined by reference to structural characteristics, i.e., specific amino acid sequences of either the Complementarity-Determining Regions (CDRs), heavy chain or light chain variable domains (V_H or V_L), or full length heavy or light chains (HC or LC). The monoclonal antibodies or antigen binding fragments thereof of the disclosure bind to, e.g., CD33, FLT3, or CLL-1 or polymorphic variants thereof.

[00245] Also disclosed are fragments of antibodies which have bioactivity. The fragments, whether attached to other sequences or not, include insertions, deletions, substitutions, or other selected modifications of particular regions or specific amino acids residues, provided the activity of the fragment is not significantly altered or impaired compared to the non-modified antibody or antibody fragment.

[00246] Techniques can also be adapted for the production of synthetic single-chain antibodies (actually antibody-like fusion proteins) specific to an antigenic protein of the present disclosure. Methods for the production of single-chain antibodies are well known to those of skill in the art. A single-chain antibody can be created by fusing together the variable domains of the heavy and light chains using a short peptide linker, thereby reconstituting an antigen binding site on a single molecule. Single-chain antibody variable fragments (scFvs) in which the C-terminus of one variable domain is

tethered to the N-terminus of the other variable domain via a 15 to 25 amino acid peptide or linker have been developed without significantly disrupting antigen binding or specificity of the binding. The linker is chosen to permit the heavy chain and light chain to bind together in their proper conformational orientation.

[00247] The monoclonal antibodies or antigen binding fragments thereof of the disclosure, comprise at least one, usually at least three CDR sequences, in combination with framework sequences from a human variable region or as an isolated CDR peptide. In some embodiments, an antibody comprises at least one heavy chain comprising three heavy chain CDR sequences situated in a variable region framework, which may be a human or murine variable region framework, and at least one light chain comprising the three light chain CDR sequences provided herein situated in a variable region framework, which may be a murine or human variable region framework.

Anti-CD33 Polypeptides

[00248] In some embodiments of the disclosure are provided anti-CD33 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs), comprising one or more complementarity-determining regions (CDRs) which recognize and bind CD33. In some embodiments, the anti- CD33 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs) selectively bind a first polymorphic variant of CD33 over a second polymorphic variant of CD33; or selectively binds the second polymorphic variant of CD33 over the first polymorphic variant. In some embodiments, the binding is at least 2-fold, 10-fold, or 30-fold selective.

[00249] In some embodiments, the first polymorphic variant of CD33 is R69 and the second polymorphic variant of CD33 is G69; or first polymorphic variant of CD33 is G69 and the second polymorphic variant of CD33 is R69.

[00250] In some embodiments of the disclosure are provided anti-CD33 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs), comprising one or more complementarity-determining regions (CDRs) which recognize and bind CD33. Sequences of the CDRs and V_H and V_L domains for the anti-CD33 polypeptides described herein for binding CD33 are provided in Tables and Examples below.

[00251] Provided herein therefore, are a heavy chain variable (V_H) domain CDR1 (HCDR1), a V_H domain CDR2 (HCDR2), and a V_H domain CDR3 (HCDR3), and polypeptides comprising them, wherein the HCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 1-25 and 201-217; HCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 26-50 and 218-234; and HCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 51-75 and 235-251. Also provided are a HCDR1, a HCDR2, and a HCDR3, and polypeptides comprising them, wherein the HCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 1-25; HCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 26-50; and HCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 51-75. Also provided are HCDR1, a HCDR2, and a HCDR3, and polypeptides comprising them, wherein the HCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 201-217; HCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 218-234; and HCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 235-251.

[00252] Also provided is a V_H domain comprising one or more of these CDRs. The V_H domain of the anti-CD33 mAb or antigen binding fragment thereof may comprise any one of the listed HCDR1 sequences in combination with any one of the HCDR2 sequences, and in combination with any one of the HCDR3 sequences. However, in certain embodiments, the provided HCDR1, HCDR2, and HCDR3 sequences are derived from a single common V_H domain, the examples of which are described herein.

[00253] The anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs may additionally comprise a light chain variable (V_L) domain, which is paired with the V_H domain to form an CD33 antigen binding domain.

[00254] Provided herein therefore, are a light chain variable (V_L) domain CDR1 (LCDR1), a V_L domain CDR2 (LCDR2), and a V_L domain CDR3 (LCDR3), and polypeptides comprising them, wherein the LCDR1 comprises an amino acid sequence chosen from: SEQ ID NOs 76-100 and 252-268; LCDR2 comprises an amino acid sequence chosen from: SEQ ID NOs 101-125 and 269-285; and LCDR3 comprises an amino acid sequence chosen from: SEQ ID NOs 126-150 and 286-302. Also provided are a LCDR1, a LCDR2, and a LCDR3, and polypeptides comprising them, wherein the LCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 76-100; LCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 101-125;

and LCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 125-150. Also provided are a LCDR1, a LCDR2, and a LCDR3, and polypeptides comprising them, wherein the LCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 252-268; LCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 269-285; and LCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 286-302.

[00255] Also provided is a V_L domain comprising one or more of these CDRs. The V_L domain of the anti-CD33 mAb, antigen binding fragment thereof, or synthetic antigen-binding protein such as an scFv may comprise any one of the listed LCDR1 sequences in combination with any one of the LCDR2 sequences, and in combination with any one of the LCDR3 sequences. However, in certain embodiments, the LCDR1, LCDR2, and LCDR3 sequences are derived from a single common V_L domain, examples of which are described herein.

[00256] Also provided are mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprising the CDRs, V_H domains, and/or V_L domain disclosed herein. Any given anti-CD33 mAb (and certain antigen-binding fragments thereof) or scFv comprising a V_H domain paired with a V_L domain will comprise a combination of six (6) CDRs: a V_H domain CDR1 (HCDR1), a V_H domain CDR2 (HCDR2), and a V_H domain CDR3 (HCDR3), a V_L domain CDR1 (LCDR1), a V_L domain CDR2 (LCDR2), and a V_L domain CDR3 (LCDR3). Although all combinations of six (6) CDRs chosen from the CDR amino acid sequences described above are permissible and within the scope of the disclosure, certain combinations of the six (6) CDRs are provided herein.

[00257] In some embodiments, the combination of the six (6) CDRs is chosen from the combinations recited in each of Polypeptide No.s 1-42. In some embodiments, the combination of the six (6) CDRs is chosen from the combinations recited in each of Polypeptide No.s 1-25. In some embodiments, the combination of the six (6) CDRs is chosen from the combinations recited in each of Polypeptide No.s 26-42.

[00258] In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_H domain chosen from any of SEQ ID NOs 151-175 and 303-319, with amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding

proteins such as scFvs comprise a V_H domain chosen from any of SEQ ID NOs 151-175, with amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_H domain chosen from any of SEQ ID NOs 303-319, with amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[00259] Alternatively, or in addition, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_L domain having an amino acid sequence chosen from any of SEQ ID NOs 176-200 and 320-336, and amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_L domain having an amino acid sequence chosen from any of SEQ ID NOs 176-200, and amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_L domain having an amino acid sequence chosen from any of SEQ ID NOs 320-336, and amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[00260] Although all possible pairing of V_H domains and V_L domains chosen from the V_H and V_L domain amino acid sequences listed above are permissible and within the scope of the disclosure, some embodiments provide certain combinations of V_H and V_L domains. Accordingly, in some embodiments, anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 1-42, e.g.:

SEQ ID NO: 151 and SEQ ID NO: 176;

SEQ ID NO: 152 and SEQ ID NO: 177;

SEQ ID NO: 153 and SEQ ID NO: 178;

SEQ ID NO: 154 and SEQ ID NO: 179;

SEQ ID NO: 155 and SEQ ID NO: 180;
SEQ ID NO: 156 and SEQ ID NO: 181;
SEQ ID NO: 157 and SEQ ID NO: 182;
SEQ ID NO: 158 and SEQ ID NO: 183;
SEQ ID NO: 159 and SEQ ID NO: 184;
SEQ ID NO: 160 and SEQ ID NO: 185;
SEQ ID NO: 161 and SEQ ID NO: 186;
SEQ ID NO: 162 and SEQ ID NO: 187;
SEQ ID NO: 163 and SEQ ID NO: 188;
SEQ ID NO: 164 and SEQ ID NO: 189;
SEQ ID NO: 165 and SEQ ID NO: 190;
SEQ ID NO: 166 and SEQ ID NO: 191;
SEQ ID NO: 167 and SEQ ID NO: 192;
SEQ ID NO: 168 and SEQ ID NO: 193;
SEQ ID NO: 169 and SEQ ID NO: 194;
SEQ ID NO: 170 and SEQ ID NO: 195;
SEQ ID NO: 171 and SEQ ID NO: 196;
SEQ ID NO: 172 and SEQ ID NO: 197;
SEQ ID NO: 173 and SEQ ID NO: 198;
SEQ ID NO: 174 and SEQ ID NO: 199;
SEQ ID NO: 175 and SEQ ID NO: 200;
SEQ ID NO: 303 and SEQ ID NO: 320;
SEQ ID NO: 304 and SEQ ID NO: 321;
SEQ ID NO: 305 and SEQ ID NO: 322;
SEQ ID NO: 306 and SEQ ID NO: 323;
SEQ ID NO: 307 and SEQ ID NO: 324;
SEQ ID NO: 308 and SEQ ID NO: 325;
SEQ ID NO: 309 and SEQ ID NO: 326;
SEQ ID NO: 310 and SEQ ID NO: 327;
SEQ ID NO: 311 and SEQ ID NO: 328;
SEQ ID NO: 312 and SEQ ID NO: 329;
SEQ ID NO: 313 and SEQ ID NO: 330;
SEQ ID NO: 314 and SEQ ID NO: 331;
SEQ ID NO: 315 and SEQ ID NO: 332;

SEQ ID NO: 316 and SEQ ID NO: 333;
SEQ ID NO: 317 and SEQ ID NO: 334;
SEQ ID NO: 318 and SEQ ID NO: 335;
and
SEQ ID NO: 319 and SEQ ID NO: 336.

[00261] In some embodiments, anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 1-25, e.g.:

SEQ ID NO: 151 and SEQ ID NO: 176;
SEQ ID NO: 152 and SEQ ID NO: 177;
SEQ ID NO: 153 and SEQ ID NO: 178;
SEQ ID NO: 154 and SEQ ID NO: 179;
SEQ ID NO: 155 and SEQ ID NO: 180;
SEQ ID NO: 156 and SEQ ID NO: 181;
SEQ ID NO: 157 and SEQ ID NO: 182;
SEQ ID NO: 158 and SEQ ID NO: 183;
SEQ ID NO: 159 and SEQ ID NO: 184;
SEQ ID NO: 160 and SEQ ID NO: 185;
SEQ ID NO: 161 and SEQ ID NO: 186;
SEQ ID NO: 162 and SEQ ID NO: 187;
SEQ ID NO: 163 and SEQ ID NO: 188;
SEQ ID NO: 164 and SEQ ID NO: 189;
SEQ ID NO: 165 and SEQ ID NO: 190;
SEQ ID NO: 166 and SEQ ID NO: 191;
SEQ ID NO: 167 and SEQ ID NO: 192;
SEQ ID NO: 168 and SEQ ID NO: 193;
SEQ ID NO: 169 and SEQ ID NO: 194;
SEQ ID NO: 170 and SEQ ID NO: 195;
SEQ ID NO: 171 and SEQ ID NO: 196;
SEQ ID NO: 172 and SEQ ID NO: 197;
SEQ ID NO: 173 and SEQ ID NO: 198;
SEQ ID NO: 174 and SEQ ID NO: 199;

and

SEQ ID NO: 175 and SEQ ID NO: 200.

[00262] In some embodiments, anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 26-42, e.g.:

SEQ ID NO: 303 and SEQ ID NO: 320;

SEQ ID NO: 304 and SEQ ID NO: 321;

SEQ ID NO: 305 and SEQ ID NO: 322;

SEQ ID NO: 306 and SEQ ID NO: 323;

SEQ ID NO: 307 and SEQ ID NO: 324;

SEQ ID NO: 308 and SEQ ID NO: 325;

SEQ ID NO: 309 and SEQ ID NO: 326;

SEQ ID NO: 310 and SEQ ID NO: 327;

SEQ ID NO: 311 and SEQ ID NO: 328;

SEQ ID NO: 312 and SEQ ID NO: 329;

SEQ ID NO: 313 and SEQ ID NO: 330;

SEQ ID NO: 314 and SEQ ID NO: 331;

SEQ ID NO: 315 and SEQ ID NO: 332;

SEQ ID NO: 316 and SEQ ID NO: 333;

SEQ ID NO: 317 and SEQ ID NO: 334;

SEQ ID NO: 318 and SEQ ID NO: 335;

and

SEQ ID NO: 319 and SEQ ID NO: 336.

[00263] In some embodiments, anti-CD33 antibodies, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs may also comprise a combination of a variable heavy chain domain and a variable light chain domain wherein the variable heavy chain domain comprises a V_H sequence with at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity, to the variable heavy chain amino acid sequences shown above and/or wherein the variable light chain domain comprises a V_L sequence with at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity, to the variable light chain domain amino acid sequences shown above. The specific V_H and V_L pairings or combinations above may be preserved for anti-CD33 antibodies, antigen binding fragments thereof, and synthetic antigen-

binding proteins such as scFvs having V_H and V_L domain sequences with a particular amino acid sequence percent identity to these reference sequences disclosed herein.

[00264] For all embodiments wherein the variable heavy chain and/or light chain domains of the antibodies, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs are defined by a particular amino acid sequence percent identity to a reference sequence, the V_H and/or V_L domains may retain identical CDR sequences to those present in the reference sequence such that the variation is present only within the framework regions.

Anti-FLT3 Polypeptides

[00265] In some embodiments of the disclosure are provided anti-FLT3 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs), comprising one or more complementarity-determining regions (CDRs) which recognize and bind FLT3. In some embodiments, the anti-FLT3 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs) selectively bind a first polymorphic variant of FLT3 over a second polymorphic variant of FLT3; or selectively binds the second polymorphic variant of FLT3 over the first polymorphic variant. In some embodiments, the binding is at least 2-fold, 10-fold, or 30-fold selective.

[00266] In some embodiments, the first polymorphic variant of FLT3 is T227 and the second polymorphic variant of FLT3 is M227; or first polymorphic variant of FLT3 is M227 and the second polymorphic variant of FLT3 is T227.

[00267] Provided herein therefore, are a heavy chain variable (V_H) domain CDR1 (HCDR1), a V_H domain CDR2 (HCDR2), and a V_H domain CDR3 (HCDR3), and polypeptides comprising them.

[00268] Also provided is a V_H domain comprising one or more of these CDRs. The V_H domain of the anti-FLT3 mAb, antigen binding fragment thereof, or synthetic antigen-binding protein such as an scFv may comprise any one of the listed HCDR1 sequences in combination with any one of the HCDR2 sequences, and in combination with any one of the HCDR3 sequences. However, in certain embodiments, the provided HCDR1, HCDR2, and HCDR3 sequences are derived from a single common V_H domain, the examples of which are described herein.

[00269] The anti-FLT3 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs may additionally comprise a light chain variable (V_L) domain, which is paired with the V_H domain to form an FLT3 antigen binding domain.

[00270] Provided herein therefore, are a light chain variable (V_L) domain CDR1 (LCDR1), a V_L domain CDR2 (LCDR2), and a V_L domain CDR3 (LCDR3), and polypeptides comprising them

[00271] Also provided is a V_L domain comprising one or more of these CDRs. The V_L domain of the anti-FLT3 mAb, antigen binding fragments thereof, or synthetic antigen-binding protein such as an scFv may comprise any one of the listed LCDR1 sequences in combination with any one of the LCDR2 sequences, and in combination with any one of the LCDR3 sequences. However, in certain embodiments, the LCDR1, LCDR2, and LCDR3 sequences are derived from a single common V_L domain, examples of which are described herein.

[00272] Also provided are mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprising the CDRs, V_H domains, and/or V_L domain disclosed herein. Any given anti-FLT3 mAb (and certain antigen-binding fragments thereof or scFv comprising a V_H domain paired with a V_L domain will comprise a combination of six (6) CDRs: a V_H domain CDR1 (HCDR1), a V_H domain CDR2 (HCDR2), and a V_H domain CDR3 (HCDR3), a V_L domain CDR1 (LCDR1), a V_L domain CDR2 (LCDR2), and a V_L domain CDR3 (LCDR3). Although all combinations of six (6) CDRs chosen from the CDR amino acid sequences described above are permissible and within the scope of the disclosure, certain combinations of the six (6) CDRs are provided herein.

[00273] Although all possible pairing of V_H domains and V_L domains chosen from the V_H and V_L domain amino acid sequences listed above are permissible and within the scope of the disclosure, some embodiments provide certain combinations of V_H and V_L domains.

[00274] In some embodiments, anti-FLT3 antibodies, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs may also comprise a combination of a variable heavy chain domain and a variable light chain domain wherein the variable heavy chain domain comprises a V_H sequence with at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity, to the variable heavy chain amino acid sequences shown above and/or wherein the variable light chain domain

comprises a V_L sequence with at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity, to the variable light chain domain amino acid sequences shown above. The specific V_H and V_L pairings or combinations in parts (i) through may be preserved for anti-FLT3 antibodies having V_H and V_L domain sequences with a particular amino acid sequence percent identity to these reference sequences disclosed herein.

[00275] For all embodiments wherein the variable heavy chain and/or light chain domains of the antibodies, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs are defined by a particular amino acid sequence percent identity to a reference sequence, the V_H and/or V_L domains may retain identical CDR sequences to those present in the reference sequence such that the variation is present only within the framework regions.

Anti-CLL-1 Polypeptides

[00276] In some embodiments of the disclosure are provided anti-CLL-1 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs), comprising one or more complementarity-determining regions (CDRs) which recognize and bind CLL-1. In some embodiments, the anti-CLL-1 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs) selectively bind a first polymorphic variant of CLL-1 over a second polymorphic variant of CLL-1; or selectively binds the second polymorphic variant of CLL-1 over the first polymorphic variant. In some embodiments, the binding is at least 2-fold, 10-fold, or 30-fold selective.

[00277] In some embodiments, the first polymorphic variant of CLL-1 is K224 and the second polymorphic variant of CLL-1 is Q244; or first polymorphic variant of CLL-1 is Q224 and the second polymorphic variant of CLL-1 is K244.

[00278] In some embodiments of the disclosure are provided anti-CLL-1 polypeptides, including mAbs, antigen binding fragments thereof, and synthetic fusion proteins such as single-chain variable fragments (scFvs), comprising one or more complementarity-determining regions (CDRs) which recognize and bind CLL-1. Sequences of the CDRs and V_H and V_L domains for the anti-CD33 polypeptides described herein for binding CLL-1 are provided in Tables and Examples below.

[00279] Provided herein therefore, are a heavy chain variable (V_H) domain CDR1 (HCDR1), a V_H domain CDR2 (HCDR2), and a V_H domain CDR3 (HCDR3), and polypeptides comprising them, wherein the HCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 337-360 and 529-550; HCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 361-384 and 551-572; and HCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 385-408 and 573-594. Also provided are a HCDR1, a HCDR2, and a HCDR3, and polypeptides comprising them, wherein the HCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 337-360; HCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 361-384; and HCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 361-384. Also provided are HCDR1, a HCDR2, and a HCDR3, and polypeptides comprising them, wherein the HCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 529-550; HCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 551-572; and HCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 573-594.

[00280] Also provided is a V_H domain comprising one or more of these CDRs. The V_H domain of the anti-CLL-1 mAb, antigen binding fragment thereof, or synthetic antigen-binding protein such as an scFv may comprise any one of the listed HCDR1 sequences in combination with any one of the HCDR2 sequences, and in combination with any one of the HCDR3 sequences. However, in certain embodiments, the provided HCDR1, HCDR2, and HCDR3 sequences are derived from a single common V_H domain, the examples of which are described herein.

[00281] The anti-CLL-1 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs may additionally comprise a light chain variable (V_L) domain, which is paired with the V_H domain to form an CLL-1 antigen binding domain.

[00282] Provided herein therefore, are a light chain variable (V_L) domain CDR1 (LCDR1), a V_L domain CDR2 (LCDR2), and a V_L domain CDR3 (LCDR3), and polypeptides comprising them, wherein the LCDR1 comprises an amino acid sequence chosen from: SEQ ID NOs 409-432 and 595-616; LCDR2 comprises an amino acid sequence chosen from: SEQ ID NOs 433-456 and 617-638; and LCDR3 comprises an amino acid sequence chosen from: SEQ ID NOs 457-480 and 639-660. Also provided are a LCDR1, a LCDR2, and a LCDR3, and polypeptides comprising them, wherein the LCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 409-432;

LCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 433-456; and LCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 433-456. Also provided are a LCDR1, a LCDR2, and a LCDR3, and polypeptides comprising them, wherein the LCDR1 comprises an amino acid sequence chosen from any of SEQ ID NOs 595-616; LCDR2 comprises an amino acid sequence chosen from any of SEQ ID NOs 617-638; and LCDR3 comprises an amino acid sequence chosen from any of SEQ ID NOs 639-660.

[00283] Also provided is a V_L domain comprising one or more of these CDRs. The V_L domain of the anti-CLL-1 mAb, antigen binding fragments thereof, or synthetic antigen-binding protein such as an scFv may comprise any one of the listed LCDR1 sequences in combination with any one of the LCDR2 sequences, and in combination with any one of the LCDR3 sequences. However, in certain embodiments, the LCDR1, LCDR2, and LCDR3 sequences are derived from a single common V_L domain, examples of which are described herein.

[00284] Also provided are mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprising the CDRs, V_H domains, and/or V_L domain disclosed herein. Any given anti-CLL-1 mAb (and certain antigen-binding fragments thereof or scFv comprising a V_H domain paired with a V_L domain will comprise a combination of six (6) CDRs: a V_H domain CDR1 (HCDR1), a V_H domain CDR2 (HCDR2), and a V_H domain CDR3 (HCDR3), a V_L domain CDR1 (LCDR1), a V_L domain CDR2 (LCDR2), and a V_L domain CDR3 (LCDR3). Although all combinations of six (6) CDRs chosen from the CDR amino acid sequences described above are permissible and within the scope of the disclosure, certain combinations of the six (6) CDRs are provided herein.

[00285] In some embodiments, the combination of the six (6) CDRs is chosen from the combinations recited in each of Polypeptide No.s 43-88. In some embodiments, the combination of the six (6) CDRs is chosen from the combinations recited in each of Polypeptide No.s 43-66. In some embodiments, the combination of the six (6) CDRs is chosen from the combinations recited in each of Polypeptide No.s 67-88.

[00286] In some embodiments, the anti-CLL-1 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_H domain chosen from any of SEQ ID NOs 481-504 and 661-682, with amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the

anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_H domain chosen from any of SEQ ID NOs 481-504, with amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_H domain chosen from any of SEQ ID NOs 661-682, with amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[00287] Alternatively, or in addition, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_L domain having an amino acid sequence chosen from any of SEQ ID NOs 505-528 and 683-704, and amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_L domain having an amino acid sequence chosen from any of SEQ ID NOs 505-528, and amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences. In some embodiments, the anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a V_L domain having an amino acid sequence chosen from any of SEQ ID NOs 683-704, and amino acid sequences exhibiting at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

[00288] Although all possible pairing of V_H domains and V_L domains chosen from the V_H and V_L domain amino acid sequences listed above are permissible and within the scope of the disclosure, some embodiments provide certain combinations of V_H and V_L domains. Accordingly, in some embodiments, anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 43-88, e.g.:

SEQ ID NO: 481 and SEQ ID NO: 505;

SEQ ID NO: 482 and SEQ ID NO: 506;

SEQ ID NO: 483 and SEQ ID NO: 507;

SEQ ID NO: 484 and SEQ ID NO: 508;
SEQ ID NO: 485 and SEQ ID NO: 509;
SEQ ID NO: 486 and SEQ ID NO: 510;
SEQ ID NO: 487 and SEQ ID NO: 511;
SEQ ID NO: 488 and SEQ ID NO: 512;
SEQ ID NO: 489 and SEQ ID NO: 513;
SEQ ID NO: 490 and SEQ ID NO: 514;
SEQ ID NO: 491 and SEQ ID NO: 515;
SEQ ID NO: 492 and SEQ ID NO: 516;
SEQ ID NO: 493 and SEQ ID NO: 517;
SEQ ID NO: 494 and SEQ ID NO: 518;
SEQ ID NO: 495 and SEQ ID NO: 519;
SEQ ID NO: 496 and SEQ ID NO: 520;
SEQ ID NO: 497 and SEQ ID NO: 521;
SEQ ID NO: 498 and SEQ ID NO: 522;
SEQ ID NO: 499 and SEQ ID NO: 523;
SEQ ID NO: 500 and SEQ ID NO: 524;
SEQ ID NO: 501 and SEQ ID NO: 525;
SEQ ID NO: 502 and SEQ ID NO: 526;
SEQ ID NO: 503 and SEQ ID NO: 527;
SEQ ID NO: 504 and SEQ ID NO: 528;
SEQ ID NO: 661 and SEQ ID NO: 683;
SEQ ID NO: 662 and SEQ ID NO: 684;
SEQ ID NO: 663 and SEQ ID NO: 685;
SEQ ID NO: 664 and SEQ ID NO: 686;
SEQ ID NO: 665 and SEQ ID NO: 687;
SEQ ID NO: 666 and SEQ ID NO: 688;
SEQ ID NO: 667 and SEQ ID NO: 689;
SEQ ID NO: 668 and SEQ ID NO: 690;
SEQ ID NO: 669 and SEQ ID NO: 691;
SEQ ID NO: 670 and SEQ ID NO: 692;
SEQ ID NO: 671 and SEQ ID NO: 693;
SEQ ID NO: 672 and SEQ ID NO: 694;
SEQ ID NO: 673 and SEQ ID NO: 695;

SEQ ID NO: 674 and SEQ ID NO: 696;
SEQ ID NO: 675 and SEQ ID NO: 697;
SEQ ID NO: 676 and SEQ ID NO: 698;
SEQ ID NO: 677 and SEQ ID NO: 699;
SEQ ID NO: 678 and SEQ ID NO: 700;
SEQ ID NO: 679 and SEQ ID NO: 701;
SEQ ID NO: 680 and SEQ ID NO: 702;
SEQ ID NO: 681 and SEQ ID NO: 703;
and
SEQ ID NO: 682 and SEQ ID NO: 704.

[00289] In some embodiments, anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 43-66, e.g.:

SEQ ID NO: 481 and SEQ ID NO: 505;
SEQ ID NO: 482 and SEQ ID NO: 506;
SEQ ID NO: 483 and SEQ ID NO: 507;
SEQ ID NO: 484 and SEQ ID NO: 508;
SEQ ID NO: 485 and SEQ ID NO: 509;
SEQ ID NO: 486 and SEQ ID NO: 510;
SEQ ID NO: 487 and SEQ ID NO: 511;
SEQ ID NO: 488 and SEQ ID NO: 512;
SEQ ID NO: 489 and SEQ ID NO: 513;
SEQ ID NO: 490 and SEQ ID NO: 514;
SEQ ID NO: 491 and SEQ ID NO: 515;
SEQ ID NO: 492 and SEQ ID NO: 516;
SEQ ID NO: 493 and SEQ ID NO: 517;
SEQ ID NO: 494 and SEQ ID NO: 518;
SEQ ID NO: 495 and SEQ ID NO: 519;
SEQ ID NO: 496 and SEQ ID NO: 520;
SEQ ID NO: 497 and SEQ ID NO: 521;
SEQ ID NO: 498 and SEQ ID NO: 522;
SEQ ID NO: 499 and SEQ ID NO: 523;
SEQ ID NO: 500 and SEQ ID NO: 524;

SEQ ID NO: 501 and SEQ ID NO: 525;
SEQ ID NO: 502 and SEQ ID NO: 526;
SEQ ID NO: 503 and SEQ ID NO: 527;
and
SEQ ID NO: 504 and SEQ ID NO: 528.

[00290] In some embodiments, anti-CD33 mAbs, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs comprise a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 67-88, e.g.:
SEQ ID NO: 661 and SEQ ID NO: 683;
SEQ ID NO: 662 and SEQ ID NO: 684;
SEQ ID NO: 663 and SEQ ID NO: 685;
SEQ ID NO: 664 and SEQ ID NO: 686;
SEQ ID NO: 665 and SEQ ID NO: 687;
SEQ ID NO: 666 and SEQ ID NO: 688;
SEQ ID NO: 667 and SEQ ID NO: 689;
SEQ ID NO: 668 and SEQ ID NO: 690;
SEQ ID NO: 669 and SEQ ID NO: 691;
SEQ ID NO: 670 and SEQ ID NO: 692;
SEQ ID NO: 671 and SEQ ID NO: 693;
SEQ ID NO: 672 and SEQ ID NO: 694;
SEQ ID NO: 673 and SEQ ID NO: 695;
SEQ ID NO: 674 and SEQ ID NO: 696;
SEQ ID NO: 675 and SEQ ID NO: 697;
SEQ ID NO: 676 and SEQ ID NO: 698;
SEQ ID NO: 677 and SEQ ID NO: 699;
SEQ ID NO: 678 and SEQ ID NO: 700;
SEQ ID NO: 679 and SEQ ID NO: 701;
SEQ ID NO: 680 and SEQ ID NO: 702;
SEQ ID NO: 681 and SEQ ID NO: 703;
and
SEQ ID NO: 682 and SEQ ID NO: 704.

[00291] In some embodiments, anti-CLL-1 antibodies, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs may also comprise a

combination of a variable heavy chain domain and a variable light chain domain wherein the variable heavy chain domain comprises a V_H sequence with at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity, to the variable heavy chain amino acid sequences shown above and/or wherein the variable light chain domain comprises a V_L sequence with at least 90% sequence identity, or at least 95%, 96% 97%, 98% or 99% sequence identity, to the variable light chain domain amino acid sequences shown above. The specific V_H and V_L pairings or combinations in parts (i) through may be preserved for anti-CLL-1 antibodies having V_H and V_L domain sequences with a particular amino acid sequence percent identity to these reference sequences disclosed herein.

[00292] For all embodiments wherein the variable heavy chain and/or light chain domains of the antibodies, antigen binding fragments thereof, and synthetic antigen-binding proteins such as scFvs are defined by a particular amino acid sequence percent identity to a reference sequence, the V_H and/or V_L domains may retain identical CDR sequences to those present in the reference sequence such that the variation is present only within the framework regions.

Chimeric Antigen Receptors (CARs) and CAR-Bearing Immune Effector Cells

[00293] Also provided herein are chimeric antigen receptors (CARs; and transgenic T-cell receptors, TCRs) comprising polypeptides as disclosed herein, e.g. as disclosed in Tables 2, 3, 12 and 13, and immune effector cells expressing them. A CAR is a recombinant fusion protein comprising: 1) an extracellular ligand-binding domain, i.e., an antigen-recognition domain, 2) a hinge domain, 3) a transmembrane domain, and 4) a cytoplasmic signaling domain, 5) and optionally, a co-stimulatory domain.

[00294] Methods for CAR design, delivery and expression, and the manufacturing of clinical-grade CAR-T cell populations are known in the art. CAR designs are generally tailored to each cell type.

[00295] The extracellular ligand-binding domain of a chimeric antigen receptor recognizes and specifically binds an antigen, typically a surface-expressed antigen of a malignant cell. The extracellular ligand-binding domain specifically binds an antigen when, for example, it binds the antigen with an affinity constant or affinity of interaction (K_D) between about 0.1 pM to about 10 μM, or about 0.1 pM to about 1 μM, or about 0.1 pM to about 100 nM. Methods for determining the affinity of interaction are known in the art. An extracellular ligand-binding domain can also be said to specifically bind a

first polymorphic variant of an antigen when it binds it selectively over a second polymorphic variant of the same antigen.

[00296] An extracellular ligand-binding domain suitable for use in a CAR may be any antigen-binding polypeptide, a wide variety of which are known in the art. In some instances, the extracellular ligand-binding domain is a single chain Fv (scFv). Other antibody based recognition domains (cAb VHH (camelid antibody variable domains) and humanized versions thereof, lgNAR VH (shark antibody variable domains) and humanized versions thereof, sdAb VH (single domain antibody variable domains) and "camelized" antibody variable domains are suitable for use. In some instances, T-cell receptor (TCR) based recognition domains such as single chain TCR (scTv, single chain two-domain TCR containing VαVβ) are also suitable for use. In some embodiments, the extracellular ligand-binding domain is constructed from a natural binding partner, or a functional fragment thereof, to a target antigen. For example, CARs in general may be constructed with a portion of the APRIL protein, targeting the ligand for the B-Cell Maturation Antigen (BCMA) and Transmembrane Activator and CAML Interactor (TACI), effectively co-targeting both BCMA and TACI for the treatment of multiple myeloma.

[00297] The targeted antigen to which the CAR binds via its extracellular ligand-binding domain may be an antigen that is expressed on a malignant myeloid (AML) cell, T cell or other cell. Antigens expressed on a malignant myeloid (AML) cells include CD33, FLT3, CD123, and CLL-1. Antigens expressed on T cells include CD2, CD3, CD4, CD5, CD7, TCRα (TRAC), and TCRβ. Antigens expressed on malignant plasma cells include BCMA, CS1, CD38, CD79A, CD79B, CD138, and CD19. Antigens expressed on malignant B cells include CD19, CD20, CD21, CD22, CD23, CD24, CD25, CD27, CD38, and CD45.

[00298] Typically, the extracellular ligand-binding domain is linked to the intracellular domain of the chimeric antigen receptor by a transmembrane (TM) domain. A peptide hinge connects the extracellular ligand-binding domain to the transmembrane domain. A transmembrane domain traverses the cell membrane, anchors the CAR to the T cell surface, and connects the extracellular ligand-binding to the cytoplasmic signaling domain, thus impacting expression of the CAR on the T cell surface.

[00299] The transmembrane domain may be derived either from a natural or from a synthetic source. Where the source is natural, the domain may be derived from any membrane-bound or transmembrane protein. For example, the transmembrane region may be derived from (i.e. comprise at least the transmembrane region(s) of) the alpha,

beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD8 (e.g., CD8 alpha, CD8 beta), CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, CD134, CD154, KIRDS2, OX40, CD2, CD27, LFA-1 (CD11a, CD18), ICOS (CD278), 4-1BB (CD137), GITR, CD40, BAFFR, HVEM (LIGHTR), SLAMF7, NKp80 (KLRF1), CD160, CD19, IL2R beta, IL2R gamma, IL7R α, ITGA1, VLA1, CD49a, ITGA4, IA4, CD49D, ITGA6, VLA-6, CD49f, ITGAD, CD11d, ITGAE, CD103, ITGAL, CD11a, LFA-1, ITGAM, CD11b, ITGAX, CD11c, ITGB1, CD29, ITGB2, CD18, LFA-1, ITGB7, TNFR2, DNAM1 (CD226), SLAMF4 (CD244, 2B4), CD84, CD96 (Tactile), CEACAM1, CRTAM, Ly9 (CD229), CD160 (BY55), PSGL1, CD100 (SEMA4D), SLAMF6 (NTB-A, Ly108), SLAM (SLAMF1, CD150, IPO-3), BLAME (SLAMF8), SELPLG (CD162), LTBR, and PAG/Cbp. Alternatively, the transmembrane domain can be synthetic and comprise predominantly hydrophobic amino acid residues (e.g., leucine and valine). In some cases, a triplet of phenylalanine, tryptophan and valine will be found at each end of a synthetic transmembrane domain. In some embodiments, the transmembrane domain is derived from the T-cell surface glycoprotein CD8 alpha chain isoform 1 precursor (NP_001139345.1) or CD28. A short oligo- or polypeptide linker, such as between 2 and 10 amino acids in length, may form the linkage between the transmembrane domain and the endoplasmic domain of the CAR. In some embodiments, the CAR has more than one transmembrane domain, which can be a repeat of the same transmembrane domain, or can be different transmembrane domains.

[00300] NK cells express a number of transmembrane (TM) adapters that signal activation, that are triggered via association with activating receptors. This provides an NK cell specific signal enhancement via engineering the TM domains from activating receptors, and thereby harness endogenous adapters. The TM adapter can be any endogenous TM adapter capable of signaling activation. In some embodiments, the TM adapter may be chosen from FceR1γ (ITAMx1), CD3ζ (ITAMx3), DAP12 (ITAMx1), or DAP10 (YxxM/YINM), NKG2D, FcγRIIIa, NKp44, NKp30, NKp46, actKIR, NKG2C, CD8α, and IL15Rb.

[00301] The CAR can further comprise a hinge region between extracellular ligand-binding domain and said transmembrane domain. The term "hinge region" (equivalently, "hinge" or "spacer") generally means any oligo- or polypeptide that functions to link the transmembrane domain to the extracellular ligand-binding domain. In particular, hinge region is used to provide more flexibility and accessibility for the extracellular ligand binding domain, and can confer stability for efficient CAR expression and activity. A hinge region

may comprise up to 300 amino acids, preferably 10 to 100 amino acids and most preferably 25 to 50 amino acids. Hinge region may be derived from all or parts of naturally-occurring molecules such as CD28, 4-1BB (CD137), OX-40 (CD134), CD3ζ, the T cell receptor α or β chain, CD45, CD4, CD5, CD8, CD8α, CD9, CD16, CD22, CD33, CD37, CD64, CD80, CD86, ICOS, CD154 or from all or parts of an antibody constant region. In some embodiments, for example, the hinge sequence is derived from a CD8a molecule or a CD28 molecule. Alternatively, the hinge region may be a synthetic sequence that corresponds to a naturally-occurring hinge sequence or the hinge region may be an entirely synthetic hinge sequence. In one embodiment, the hinge domain comprises a part of human CD8α, FcγRIIIα receptor, or IgGl, and have at least 80%, 90%, 95%, 97%, or 99% sequence identity thereto.

[00302] After antigen recognition, the cytoplasmic signaling domain transmits a signal to the immune effector cell, activating at least one of the normal effector functions of the immune effector cell. Effector function of a T cell, for example, may be cytolytic activity or helper activity including the secretion of cytokines. While usually the entire cytoplasmic signaling domain can be employed, in many cases it is not necessary to use the entire chain. To the extent that a truncated portion of the cytoplasmic signaling domain is used, such truncated portion may be used in place of the intact chain as long as it transduces the effector function

[00303] Cytoplasmic signaling sequences that regulate primary activation of the TCR complex that act in a stimulatory manner may contain signaling motifs which are known as immunoreceptor tyrosine-based activation motifs (ITAMs). Examples of ITAM containing cytoplasmic signaling sequences include those derived from CD8, CD3ζ, CD3δ, CD3γ, CD3ε, CD32 (Fc gamma RIIa), DAP10, DAP12, CD79a, CD79b, FcγRIγ, FcγRIIIγ, FcεRIβ (FCERIB), and FcεRIγ (FCERIG).

[00304] First-generation CARs typically have the cytoplasmic signaling domain from the CD3 chain, which is the primary transmitter of signals from endogenous TCRs. Second-generation CARs add cytoplasmic signaling domains from various co-stimulatory protein receptors (e.g., CD28, 4-1BB, ICOS) to the cytoplasmic signaling domain of the CAR to provide additional signals to the T cell.

[00305] A "costimulatory domain" is derived from the intracellular signaling domains of costimulatory proteins that enhance cytokine production, proliferation, cytotoxicity, and/or persistence in vivo. Preclinical studies have indicated that the second generation of CAR designs improves the antitumor activity of T cells. More

recent, third-generation, and later generation, CARs combine multiple costimulatory domains to further augment potency. T cells grafted with these CARs have demonstrated improved expansion, activation, persistence, and tumor-eradicating efficiency independent of costimulatory receptor/ligand interaction.

[00306] For example, the cytoplasmic signaling domain of the CAR can be designed to comprise the signaling domain (e.g., CD3ζ) by itself or combined with any other desired cytoplasmic domain(s) useful in the context of the CAR. For example, the cytoplasmic domain of the CAR can comprise a signaling domain (e.g., CD3ζ) chain portion and a costimulatory signaling region. The co-stimulatory signaling region refers to a portion of the CAR comprising the intracellular domain of a co-stimulatory molecule. Examples of such molecules include CD27, CD28, 4-1BB (CD137), OX40, CD30, CD40, ICOS, LFA-1, CD2, CD7, LIGHT, NKG2C, B7-H3, and a ligand that specifically binds with CD83, CD8, CD4, b2c, CD80, CD86, DAP10, DAP12, MyD88, BTNL3, and NKG2D.

[00307] In some embodiments, the cytoplasmic signaling domain is a CD3 zeta (CD3ζ) signaling domain. In some embodiments, the co-stimulatory domain comprises the cytoplasmic domain of CD28, 4-1BB, or a combination thereof. In some cases, the co-stimulatory signaling region contains 1, 2, 3, or 4 cytoplasmic domains of one or more intracellular signaling and/or co-stimulatory molecules.

[00308] The co-stimulatory signaling domain(s) may contain one or more mutations in the cytoplasmic domains of CD28 and/or 4-1BB that enhance signaling. In some embodiments, the disclosed CARs comprises a co-stimulatory signaling region comprising a mutated form of the cytoplasmic domain of CD28 with altered phosphorylation at Y206 and/or Y218. In some embodiments, the disclosed CAR comprises an attenuating mutation at Y206, which will reduce the activity of the CAR. In some embodiments, the disclosed CAR comprises an attenuating mutation at Y218, which will reduce expression of the CAR. Any amino acid residue, such as alanine or phenylalanine, can be substituted for the tyrosine to achieve attenuation. In some embodiments, the tyrosine at Y206 and/or Y218 is substituted with a phosphomimetic residue. In some embodiments, the disclosed CAR substitution of Y206 with a phosphomimetic residue, which will increase the activity of the CAR. In some embodiments, the disclosed CAR comprises substitution of Y218 with a phosphomimetic residue, which will increase expression of the CAR. For example, the phosphomimetic residue can be phosphotyrosine. In some embodiments, a CAR may contain a

combination of phosphomimetic amino acids and substitution(s) with non-phosphorylatable amino acids in different residues of the same CAR. For instance, a CAR may contain an alanine or phenylalanine substitution in Y209 and/or Y191 plus a phosphomimetic substitution in Y206 and/or Y218.

[00309] In some embodiments, the disclosed CARs comprises one or more 4-1BB domains with mutations that enhance binding to specific TRAF proteins, such as TRAF1, TRAF2, TRAF3, TRAF4, TRAF5, TRAF6, or any combination thereof. In some cases, the 41BB mutation enhances TRAF1- and/or TRAF2-dependent proliferation and survival of the T-cell, e.g. through NF-kB. In some cases, the 4-1BB mutation enhances TRAF3-dependent antitumor efficacy, e.g. through IRF7/INFβ. Therefore, the disclosed CARs can comprise cytoplasmic domain(s) of 4-1BB having at least one mutation in these sequences that enhance TRAF-binding and/or enhance NFκB signaling.-

[00310] Also as disclosed herein, TRAF proteins can in some cases enhance CAR T cell function independent of NFκB and 4-1BB. For example, TRAF proteins can in some cases enhance CD28 co-stimulation in T cells. Therefore, also disclosed herein are immune effector cells co-expressing CARs with one or more TRAF proteins, such as TRAF1, TRAF2, TRAF3, TRAF4, TRAF5, TRAF6, or any combination thereof. In some cases, the CAR is any CAR that targets a tumor antigen. For example, first-generation CARs typically had the intracellular domain from the CD3 chain, while second-generation CARs added intracellular signaling domains from various costimulatory protein receptors (e.g., CD28, 4-1BB, ICOS) to the cytoplasmic signaling domain of the CAR to provide additional signals to the T cell. In some cases, the CAR is the disclosed CAR with enhanced 4-1BB activation.

[00311] Variations on CAR components may be advantageous, depending upon the type of cell in which the CAR is expressed.

[00312] For example, in NK cells, in some embodiments, the transmembrane domain can be a sequence associated with NKG2D, FcγRIIIa, NKp44, NKp30, NKp46, actKIR, NKG2C, or CD8α. In certain embodiments, the NK cell is a ML-NK or CIML-NK cell and the TM domain is CD8 α. Certain TM domains that do not work well in NK cells generally may work in a subset; CD8α, for example, works in ML-NKs but not NK cells generally.

[00313] Similarly, in NK cells, in some embodiments, the intracellular signaling domain(s) can be any co-activating receptor(s) capable of functioning in an NK cell, such

as, for example, CD28, CD137/41BB (TRAF, NFkB), CD134/OX40, CD278/ICOS, DNAM-1 (Y-motif), NKp80 (Y-motif), 2B4 (SLAMF) :: ITSM, CRACC (CS1/SLAMF7) :: ITSM, CD2 (Y-motifs, MAPK/Erk), CD27 (TRAF, NFkB), or integrins (e.g., multiple integrins).

[00314] Similarly, in NK cells, in some embodiments, an intracellular signaling domain can be a cytokine receptor capable of functioning in an NK cell. For example, a cytokine receptor can be a cytokine receptor associated with persistence, survival, or metabolism, such as IL-2/15Rbyc :: Jak1/3, STAT3/5, PI3K/mTOR, MAPK/ERK. As another example, a cytokine receptor can be a cytokine receptor associated with activation, such as IL-18R :: NFkB. As another example, a cytokine receptor can be a cytokine receptor associated with IFN-γ production, such as IL-12R :: STAT4. As another example, a cytokine receptor can be a cytokine receptor associated with cytotoxicity or persistence, such as IL-21R :: Jak3/Tyk2, or STAT3. As another example, an intracellular signaling domain can be a TM adapter, such as FceR1γ (ITAMx1), CD3ζ (ITAMx3), DAP12 (ITAMx1), or DAP10 (YxxM/YINM). As another example, CAR intracellular signaling domains (also known as endodomains) can be derived from costimulatory molecules from the CD28 family (such as CD28 and ICOS) or the tumor necrosis factor receptor (TNFR) family of genes (such as 4-1BB, OX40, or CD27). The TNFR family members signal through recruitment of TRAF proteins and are associated with cellular activation, differentiation and survival. Certain signaling domains that may not work well in all NK cells generally may work in a subset; CD28 or 4-1BB, for example, work in ML-NKs.

Methods of Making CARs and CAR-Bearing Cells

[00315] The chimeric antigen receptor (CAR) construct, which encodes the chimeric receptor can be prepared in conventional ways. Since, for the most part, natural sequences are employed, the natural genes are isolated and manipulated, as appropriate (e.g., when employing a Type II receptor, the immune signaling receptor component may have to be inverted), so as to allow for the proper joining of the various components. Thus, the nucleic acid sequences encoding for the N-terminal and C-terminal proteins of the chimeric receptor can be isolated by employing the polymerase chain reaction (PCR), using appropriate primers which result in deletion of the undesired portions of the gene. Alternatively, restriction digests of cloned genes can be used to generate the chimeric

construct. In either case, the sequences can be selected to provide for restriction sites which are blunt-ended, or have complementary overlaps.

[00316] The various manipulations for preparing the chimeric construct can be carried out in vitro and in particular embodiments the chimeric construct is introduced into vectors for cloning and expression in an appropriate host using standard transformation or transfection methods. Thus, after each manipulation, the resulting construct from joining of the DNA sequences is cloned, the vector isolated, and the sequence screened to ensure that the sequence encodes the desired chimeric receptor. The sequence can be screened by restriction analysis, sequencing, or the like.

[00317] A chimeric construct can be introduced into immune effector cells as naked DNA or in a suitable vector. Methods of stably transfecting immune effector cells by electroporation using naked DNA are known in the art. Naked DNA generally refers to the DNA encoding a chimeric receptor contained in a plasmid expression vector in proper orientation for expression.

[00318] Alternatively, a viral vector (e.g., a retroviral vector, adenoviral vector, adeno-associated viral vector, or lentiviral vector) can be used to introduce the chimeric construct into immune cell, e.g., T cells. Suitable vectors are non-replicating in the immune effector cells of the subject. A large number of vectors are known which are based on viruses, where the copy number of the virus maintained in the cell is low enough to maintain the viability of the cell. Illustrative vectors include the pFB-neo vectors (STRATAGENE™) as well as vectors based on HIV, SV40, EBV, HSV or BPV. Once it is established that the transfected or transduced immune effector cell is capable of expressing the chimeric receptor as a surface membrane protein with the desired regulation and at a desired level, it can be determined whether the chimeric receptor is functional in the host cell to provide for the desired signal induction (e.g., production of Rantes, Mip1-alpha, GM-CSF upon stimulation with the appropriate ligand).

[00319] Engineered CARs may be introduced into CAR-bearing immune effector cells using retroviruses, which efficiently and stably integrate a nucleic acid sequence encoding the chimeric antigen receptor into the target cell genome. Other methods known in the art include, but are not limited to, lentiviral transduction, transposon-based systems, direct RNA transfection, and CRISPR/Cas systems (e.g., type I, type II, or type Ill systems using a suitable Cas protein such Cas3, Cas4, Cas5, Cas5e (or CasD), Cash, Cas6e, Cas6f, Cas7, Cas8a1, Cas8a2, Cas8b, Cas8c, Cas9, Cas10, Cas1 Od, CasF, CasG, CasH, Csy1, Csy2, Csy3, Cse1 (or CasA), Cse2 (or CasB), Cse3 (or CasE), Cse4 (or

CasC), Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3,Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csz1, Csx15, Csf1, Csf2, Csf3, Csf4, and Cu1966, etc.). Zinc finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs) may also be used. See, e.g., Shearer RF and Saunders DN, "Experimental design for stable genetic manipulation in mammalian cell lines: lentivirus and alternatives," *Genes Cells* 2015 January; 20(1):1-10.

[00320] Amino acid sequences for selected components which may be used to construct a CAR are disclosed below in Table 1.

Table 1. Amino acid sequences of selected CAR components.

Functional domains	SEQ ID NO:	Amino acid sequence
CD8α signal peptide (variant 1)	1521	MALPVTALLLPLALLLHAARP
CD8α signal peptide (variant 2)	1522	MALPVTALLLPLALLLHAA
CD8α signal peptide (variant 3)	1523	MALPVTALLLP
CD8α signal peptide (variant 4)	1524	PVTALLLPLALL
CD8α signal peptide (variant 5)	1525	LLLPLALLLHAARP
CD8α hinge	1526	TTTPAPRPPTPAPTIASQPLSLRPEACRPA AGGAVHTRGLDFACD
CD28 Transmembrane (T_m) domain	1527	FWVLVVVGGVLACYSLLVTVAFIIFWV
Surface glycoprotein CD8 alpha chain isoform 1 precursor (NP_001139345.1)	1528	MALPVTALLLPLALLLHAARPSQFRVSP LDRTWNLGETVELKCQVLLSNPTSGCS WLFQPRGAAASPTFLLYLSQNKPKAAEG LDTQRFSGKRLGDTFVLTLSDFRRENEG YYFCSALSNSIMYFSHFVPVFLPAKPTTT PAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDIYIWAPLAGTCGVLL LSLVITLYCNHRNRRRVCKCPRPVVKSG DKPSLSARYV
4-1BB costimulatory domain	1529	KRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCEL
CD28 costimulatory domain	1530	RSKRSRLLHSDYMNMTPRRPGPTRKHY QPYAPPRDFAAYRS
CD3 zeta (ζ)	1531	RVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNP

		QEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQ ALPPR
P2A peptide	1532	GSGATNFSLLKQAGDVEENPGP
(GGGGS) linker	1533	GGGGS
$(GGGGS)_2$ linker	1534	GGGGSGGGGS
$(GGGGS)_3$ linker	1535	GGGGSGGGGSGGGGS
$(GGGGS)_4$ linker	1536	GGGGSGGGGSGGGGSGGGGS
hCD34	1537	MPRGWTALCLLSLLPSGFMSLDNNGTA TPELPTQGTFSNVSTNVSYQETTTPSTLG STSLHPVSQHGNEATTNITETTVKFTSTS VITSVYGNTNSSVQSQTSVISTVFTTPAN VSTPETTLKPSLSPGNVSDLSTTSTSLATS PTKPYTSSSPILSDIKAEIKCSGIREVKLT QGICLEQNKTSSCAEFKKDRGEGLARVL CGEEQADADAGAQVCSLLLAQSEVRPQ CLLLVLANRTEISSKLQLMKKHQSDLKK LGILDFTEQDVASHQSYSQKTLIALVTSG ALLAVLGITGYFLMNRRSWSPI
Human-Herpes Simplex Virus-1 (HSV) - thymidine kinase (TK)	1538	MPRGWTALCLLSLLPSGFMSLDNNGTA TPELPTQGTFSNVSTNVSYQETTTPSTLG STSLHPVSQHGNEATTNITETTVKFTSTS VITSVYGNTNSSVQSQTSVISTVFTTPAN VSTPETTLKPSLSPGNVSDLSTTSTSLATS PTKPYTSSSPILSDIKAEIKCSGIREVKLT QGICLEQNKTSSCAEFKKDRGEGLARVL CGEEQADADAGAQVCSLLLAQSEVRPQ CLLLVLANRTEISSKLQLMKKHQSDLKK LGILDFTEQDVASHQSYSQKTLIALVTSG ALLAVLGITGYFLMNRRSWSPTGEGGG GGDLGGVKLPHLFGKRLVEARMASYPC HQHASAFDQAARSRGHSNRRTALRPRR QQEATEVRLEQKMPTLLRVYIDGPHGM GKTTTTQLLVALGSRDDIVYVPEPMTY WQVLGASETIANIYTTQHRLDQGEISAG DAAVVMTSAQITMGMPYAVTDAVLAP HVGGEAGSSHAPPPALTLLLDRHPIAVM LCYPAARYLMGSMTPQAVLAFVALIPPT LPGTNIVLGALPEDRHIDRLAKRQRPGE RLDLAMLAAIRRVYGLLANTVRYLQGG GSWWEDWGQLSGTAVPPQGAEPQSNA GPRPHIGDTLFTLFRAPELLAPNGDLYNV FAWALDVLAKRLRPMHVFILDYDQSPA

		GCRDALLQLTSGMVQTHVTTPGSIPTIC DLARTFAREMGEAN

Cell-Specific Variations

[00321] The CAR components and construction methods disclosed above are suitable for use in T cells and other immune effector cells, but are not exhaustive. Certain variations may be useful in subsets of cells, and are known in the art.

[00322] For example, in NK cells, the TM domain may be chosen or adapted from NKG2D, FcγRIIIa, NKp44, NKp30, NKp46, actKIR, NKG2C, or CD8α. NK cells also express a number of transmembrane adapters that are triggered via association with activating receptors, providing an NK cell specific signal enhancement. For example, the TM adapter can be chosen or adapted from FceR1γ (ITAMx1), CD3ζ (ITAMx3), DAP12 (ITAMx1), or DAP10 (YxxM/YINM). In certain embodiments, the TM domains and adapters may be paired, e.g.: NKG2D and DAP10, FcγRIIIa and CD3ζ or FceR1γ, NKp44 and DAP12, NKp30 and CD3ζ or FceR1γ, NKp46 and CD3ζ or FceR1γ, actKIR and DAP12, and NKG2C and DAP12.

[00323] In certain embodiments, in NK cells, the hinge domain may be chosen or adapted from, e.g., NKG2, TMα, or CD8.

[00324] In certain embodiments, in NK cells, the intracellular signaling and/or costimulatory domain may comprise one or more of: CD137/41BB (TRAF, NFkB), DNAM-1 (Y-motif), NKp80 (Y-motif), 2B4 (SLAMF) :: ITSM, CRACC (CS1/SLAMF7) :: ITSM, CD2 (Y-motifs, MAPK/Erk), CD27 (TRAF, NFkB); one or more integrins (e.g., multiple integrins); a cytokine receptor associated with persistence, survival, or metabolism, such as IL-2/15Rbyc :: Jak1/3, STAT3/5, PI3K/mTOR, and MAPK/ERK; a cytokine receptor associated with activation, such as IL-18R :: NFkB. a cytokine receptor associated with IFN-γ production, such as IL-12R :: STAT4; a cytokine receptor associated with cytotoxicity or persistence, such as IL-21R :: Jak3/Tyk2, or STAT3; and a TM adapter, as disclosed above. In some embodiments, the NK cell CAR comprises three signaling domains, a TM domain, and optionally, a TM adapter.

[00325] The choice of costimulatory domain may also depend on the phenotype or subtype of the NK cell; for example, in some experiments, 4-1BB may be effective as a costimulatory domain in memory-like (ML) NK cells (including CIMLs) but less

efficacious in NK cells. Additionally, signaling domains that may be harnessed that are more selectively expressed in ML NK cells include DNAM-1, CD137, and CD2.

Immune Effector Cells

[00326] Immune effector cells as disclosed herein may include T cells, NK cells, iNKT cells, and others, for example macrophages, and subtypes thereof.

[00327] Any of these immune effector cells may be transduced with a CAR using techniques known in the art. The resulting CAR-bearing immune effector cells may be used in the immunotherapy of disease, for example cancer, by adoptive cell transfer (ACT) into a subject in need. CAR-bearing immune effector cells include CAR-T cells, CAR-NK cells (and subtypes thereof, such as CAR-ML NK cells and CAR-CIMLs), CAR-iNKT cells, and CAR-macrophages.

[00328] Immune effector cells for use in ACT may be autologous or allogeneic. In some embodiments, the use of allogeneic cells permits deliberate polymorphic mismatch between donor and recipient, which offers certain advantages discussed below.

T Cells

[00329] T cells are immune cells which express a T cell receptor (TCR) on their surface. Effector T cells include cytotoxic (CD8+) T cells, helper (CD4+) T cells, viral-specific cytotoxic T cells, memory T cells, gamma delta ($\gamma\delta$) T cells.

[00330] T cells may be primary T cells, or may be derived from progenitor cells. T cells can be derived from various sources, including peripheral or cord blood cells, stem cells, or induced pluripotent stem cells (iPSCs), Methods of enriching/isolating, differentiating, and otherwise producing T cells are known in the art.

iNKT Cells

[00331] Invariant natural killer T cells, also called iNKT cells or type-I NKT cells, represent a distinct lymphocyte population, characterized by expression of an invariant T cell receptor α-chain and certain TCR β-chains (Vα24-Jα18 combined with Vβ11). iNKT TCR–mediated responses are restricted by CD1d, a member of the non-polymorphic CD1 antigen presenting protein family, which promotes the presentation of endogenous and pathogen-derived lipid antigens to the TCR. The prototypical ligand for invariant receptor is α-galactosylceramide (αGalCer). Upon binding of the invariant TCR to CD1d-αGalCer, iNKT will expand. The CD1d gene is monomorphic and expressed by only a few cell types, limiting the potential toxicity of NKT cells in the autologous or allogeneic settings.

NK Cells

[00332] Natural killer (NK) cells are traditionally considered innate immune effector lymphocytes which mediate host defense against pathogens and antitumor immune responses by targeting and eliminating abnormal or stressed cells not by antigen recognition or prior sensitization, but through the integration of signals from activating and inhibitory receptors. Natural killer (NK) cells are an alternative to T cells for allogeneic cellular immunotherapy since they have been administered safely without major toxicity, do not cause graft versus host disease (GvHD), naturally recognize and eliminate malignant cells, and are amendable to cellular engineering.

[00333] NK cells may be primary NK cells, or may be derived from progenitor cells. NK cells can be derived from various sources, including peripheral or cord blood cells, stem cells, or induced pluripotent stem cells (iPSCs), Methods of enriching/isolating, differentiating, and otherwise producing NK cells are known in the art.

Memory-Like NK cells

[00334] In addition to their innate cytotoxic and immunostimulatory activity, NK cells constitute a heterogeneous and versatile cell subset, including persistent memory-like NK populations that mount a robust recall response. ML-NK cells can be produced by stimulation by pro-inflammatory cytokines or activating receptor pathways, either naturally or artificially. ML-NK cells produced by cytokine activation have been used clinically in the setting of leukemia immunotherapy.

[00335] Increased CD56, Ki-67, NKG2A, and increased activating receptors NKG2D, NKp30, and NKp44 have been observed in *in vivo* differentiated ML NK cells. In addition, *in vivo* differentiation showed modest decreases in the median expression of CD16 and CD11b. Increased frequency of TRAIL, CD69, CD62L, NKG2A, and NKp30-positive NK cells were observed in ML NK cells compared with both ACT and BL NK cells, whereas the frequencies of CD27+ and CD127+ NK cells were reduced. Finally, unlike in vitro differentiated ML NK cells, in vivo differentiated ML NK cells did not express CD25.

Cytokine-Induced Memory-Like Natural Killer Cells (CIML-NKs)

[00336] NK cells may be induced to acquire a memory-like phenotype, for example by preactivation with combinations of cytokines, such as interleukin-12 (IL-12), IL-15, and IL-18. These cytokine-induced memory-like (CIML) NK cells (CIML-NKs

or CIMLs) exhibit enhanced response upon restimulation with the cytokines or triggering via activating receptors. CIML NK cells may be produced by activation with cytokines such as IL-12, IL-15, and IL-18 and their related family members, or functional fragments thereof, or fusion proteins comprising functional fragments thereof.

[00337] CIML NK cells may be identified by their method of production. CIML cells can be produced by differentiated cytokine-activated (i.e., CIML) NK cells.

[00338] CIML NK cells typically exhibit differential cell surface protein expression patterns when compared to traditional NK cells. Such expression patterns are known in the art and may comprise, for example, increased CD56, CD56 subset CD56dim, CD56 subset CD56bright, CD16, CD94, NKG2A, NKG2D, CD62L, CD25, NKp30, NKp44, and NKp46 (compared to control NK cells) in CIML NK cells (see e.g., Romee et al. Sci Transl Med. 2016 Sep 21;8(357):357). Memory-like (ML) and cytokine induced memory-like (CIML) NK cells may also be identified by observed in vitro and in vivo properties, such as enhanced effector functions such as cytotoxicity, improved persistence, increased IFN-γ production, and the like.

[00339] NK cells can be activated using cytokines, such as IL-12/15/18. The NK cells can be incubated in the presence of the cytokines for an amount of time sufficient to form cytokine-induced memory-like (CIML) NK cells. Such techniques are known in the art.

CD33, FTL-3, and CLL-1-Specific Chimeric Antigen Receptors (CARs)

[00340] CARs generally incorporate an antigen recognition domain from the single-chain variable fragments (scFv) of a monoclonal antibody (mAb) with transmembrane signaling motifs involved in lymphocyte activation (Sadelain M, et al. *Nat Rev Cancer* 2003 3:35-45). Disclosed herein are CD33, FTL-3, and CLL-1-specific chimeric antigen receptor (CAR) that can be that can be expressed in immune effector cells to enhance antitumor activity against CD33, FTL-3, and CLL-1-expressing tumor cells.

[00341] As discussed above, the disclosed CAR generally comprises: an extracellular ligand binding domain, a hinge domain, a transmembrane domain, a cytoplasmic signaling domain, and optionally a co-stimulatory domain. The extracellular ligand binding domain comprises the CD33-binding region and is responsible for antigen recognition. In another embodiment, the extracellular ligand binding domain comprises a FLT3-binding region. In yet another embodiment, the extracellular ligand binding

domain comprises a CLL-1 binding region. The transmembrane domain connects the extracellular ligand binding domain to the cytoplasmic signaling domain and resides within the cell membrane when expressed by a cell. The cytoplasmic signaling domain transmits an activation signal to the immune effector cell after antigen recognition. For example, the cytoplasmic signaling domain may optionally contain costimulatory protein domains, such as CD28, 41BB, and ICOS, that are able to enhance T-cell activation by T-cell receptors.

Antibodies

[00342] Provided herein are antibodies comprising the polypeptides disclosed herein. In some embodiments the antibodies comprise the V_H and V_L chains disclosed herein.

[00343] Various forms of antibodies disclosed are contemplated herein. For example, the antibodies can have human frameworks and constant regions of the isotypes, IgA, IgD, IgE, IgG, and IgM, more particularly, IgG1, IgG2, IgG3, IgG4, and in some cases with various mutations to alter Fc receptor function or prevent Fab arm exchange or an antibody fragment, e.g., a F(ab')2 fragment, a F(ab) fragment, a single chain Fv fragment (scFv), etc.

[00344] In certain embodiments, an antibody provided herein is a human antibody. Human antibodies can be produced using various techniques known in the art. For example, human antibodies may also be generated by isolating Fv clone variable domain sequences selected from human-derived phage display libraries. Such variable domain sequences may then be combined with a desired human constant domain.

[00345] An antibody as provided herein may be a chimeric antibody, e.g. comprising a non-human variable region (e.g., a variable region derived from a mouse, rat, hamster, rabbit, or non-human primate, such as a monkey) and a human constant region, or a "class switched" antibody in which the class or subclass has been changed from that of the parent antibody.

[00346] An antibody as provided herein may be a humanized antibody. Typically, a non-human antibody is humanized to reduce immunogenicity to humans, while retaining the specificity and affinity of the parental non-human antibody. Generally, a humanized antibody comprises one or more variable domains in which HVRs, e.g., CDRs, (or portions thereof) are derived from a non-human antibody, and FRs (or portions thereof) are derived from human antibody sequences. A humanized antibody optionally will also comprise at least a portion of a human constant region. In some

embodiments, some FR residues in a humanized antibody are substituted with corresponding residues from a non-human antibody (e.g., the antibody from which the HVR residues are derived), e.g., to restore or improve antibody specificity or affinity.

[00347] Antibodies disclosed herein may also be bispecific or trispecific – i.e., that comprise an antigen-recognition domain that comprises one of the polypeptides disclosed herein and one or more other antigen-recognition domains that binds to another antigen. For example, one arm of the antibody may bind a polymorph of an antigen on an AML cell, and the other arm may bind CD3 or another T-cell target to bring T-cells in proximity to tumor cells. In an example of a trispecific antibody, the antibody would also bind another target on T-cell such as CD28 to enhance activity and persistence of recruited T-cells.

[00348] In some embodiments, a humanized antibody comprises, in addition to the variable regions, a human acceptor framework, e.g. a human immunoglobulin framework or a human consensus framework. Human framework regions that may be used for humanization include but are not limited to framework regions selected using the "best-fit" method, framework regions derived from the consensus sequence of human antibodies of a particular subgroup of light or heavy chain variable regions, human mature (somatically mutated) framework regions or human germline framework regions, and framework regions derived from screening FR libraries.

[00349] In certain embodiments, an antibody provided herein is a multispecific antibody, e.g. a bispecific antibody. Multispecific antibodies are monoclonal antibodies that have binding specificities for at least two different sites. For example, one of the binding specificities is for CD33 and the other is for any other antigen. In certain embodiments, bispecific antibodies may bind to two different epitopes of the same antigen. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a target antigen. Bispecific antibodies can be prepared as full length antibodies or antibody fragments. Techniques for making multispecific antibodies include, but are not limited to, recombinant co- expression of two immunoglobulin heavy chain- light chain pairs having different specificities, "knob-in-hole" engineering, engineering electrostatic steering effects for making antibody Fc-heterodimeric molecules, cross-linking two or more antibodies or fragments, using leucine zippers to produce bi-specific antibodies, using "diabody" technology for making bispecific antibody fragments, and using single-chain Fv (sFv) dimers.

[00350] Amino acid sequence variants of the antibodies provided herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of an antibody may be

prepared by introducing appropriate modifications into the nucleotide sequence encoding the antibody, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution can be made to arrive at the final construct, provided that the final construct possesses the desired characteristics, e.g., antigen-binding.

[00351] Sites of interest for substitutional mutagenesis include the variable regions and framework regions. Amino acids may be grouped according to common side-chain properties:

(1) hydrophobic: Norleucine, Met, Ala, Val, Leu, He;

(2) neutral hydrophilic: Cys, Ser, Thr, Asn, Gln;

(3) acidic: Asp, Glu;

(4) basic: His, Lys, Arg;

(5) residues that influence chain orientation: Gly, Pro;

(6) aromatic: Trp, Tyr, Phe.

[00352] Amino acid substitutions may be introduced into an antibody of interest and the products screened for a desired activity, e.g., retained/improved antigen binding, decreased immunogenicity, or improved ADCC or CDC. Conservative substitutions are known in the art and are preferred. Non-conservative substitutions will entail exchanging a member of one of these classes for another class.

[00353] Antibodies may also comprise modifications to glycan chains substituting certain residues such as Asn 297. For example, antibodies may be engineered or treated to be afucosylated to improve ADCC.

[00354] Antibodies comprising the CDRs, variable heavy and light chains disclosed herein may be made by methods known in the art.

[00355] For example, variable antibody domains may be cloned into IgG expression vectors (IgG conversion). PCR-amplified DNA fragments of heavy and light chain V-domains may be inserted in frame into, e.g., a human IgG1 constant heavy chain containing recipient mammalian expression vector. Antibody expression may be driven by an MPSV promoter and transcription terminated by a synthetic polyA signal sequence located downstream of the CDS.

[00356] Antibodies may be produced using recombinant methods and compositions. Nucleic acids encoding the antibodies described herein are provided. Such a nucleic acid may encode an amino acid sequence comprising the VL and/or an

amino acid sequence comprising the VH of the antibody (e.g. , the light and/or heavy chains of the antibody). Expression vectors comprising (i.e., transformed with) such nucleic acids are provided, as are host cells comprising such nucleic acids. In one such embodiment, a host cell comprises (1) a vector comprising a nucleic acid that encodes an amino acid sequence comprising the VL and an amino acid sequence comprising the VH, or (2) a first vector comprising a nucleic acid that encodes an amino acid sequence comprising the VL of the antibody and a second vector comprising a nucleic acid that encodes an amino acid sequence comprising the VH of the antibody.

[00357] The host cell may be eukaryotic, e.g. a Chinese Hamster Ovary (CHO) cell or lymphoid cell (e.g. , Y0, NS0, Sp20 cell). Host cells comprising a nucleic acid encoding the antibody may be cultured under conditions suitable for expression, and the antibody recovered from the host cell or culture medium.

[00358] Suitable host cells for cloning or expression of antibody-encoding vectors include other prokaryotic or eukaryotic cells described herein. For example, antibodies may be produced in bacteria (e.g., E. coli), in particular when glycosylation and Fc effector function are not needed. In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for antibody-encoding vectors, including fungi and yeast strains whose glycosylation pathways have been "humanized," resulting in the production of an antibody with a partially or fully human glycosylation pattern. Additional suitable host cells for the expression of glycosylated antibody are also derived from multicellular organisms (invertebrates and vertebrates). Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains have been identified which may be used in conjunction with insect cells, particularly for transfection of Spodoptera frugiperda cells. Plant cell cultures can also be utilized as hosts.

[00359] In some embodiments, an antibody provided herein has a dissociation constant (Kd) of < 1μM, < 100 nM, < 50 nM, < 10 nM, < 5 nM, < 1 nM, < 0.1 nM, < 0.01 nM, or < 0.001 nM, and optionally is > 10^{-13} M. (e.g. 10^{-8} M or less, e.g. from 10^{-8} M to 10^{-13} M, e.g. , from 10^{-9} M to 10^{-13} M). In one embodiment, Kd is measured by a radiolabeled antigen binding assay (RIA) performed with the Fab version of an antibody of interest and its antigen, or using a surface plasmon resonance assay, e.g., WO2015089344.

Antibody-Drug Conjugates

[00360] Also provided herein are immunoconjugates comprising an antibody as disclosed herein, or an antigen-binding fragment thereof, conjugated to one or more drugs (e.g., cytotoxic agents such as chemotherapeutic agents, growth inhibitory agents, toxins, or radioactive isotopes). Immunoconjugates allow for the targeted delivery of a drug or other cytotoxic agent to a tumor, enhancing the therapeutic index by maximizing efficacy and minimizing off-target toxicity. Antibody-drug conjugates (ADCs) disclosed herein include those with anticancer activity. The antibody may be covalently attached to the drug moiety through a linker.

[00361] An exemplary embodiment of an ADC comprises: an antibody (Ab), or an antigen-binding fragment thereof, which targets a tumor cell, a cytotoxic moiety such as a drug (D), and a linker moiety (L) that attaches Ab to D. In some embodiments, the antibody is attached to the linker moiety (L) through one or more amino acid residues, such as lysine and/or cysteine.

[00362] An ADC may have Formula I:

$$Ab\text{-}(L\text{-}D)_p$$

wherein:

Ab is an antibody as disclosed herein, or an antigen-binding fragment thereof;

L is a linker;

D is a drug; and

p is about 1 to about 20.

[00363] The antibody (Ab) may comprise a polypeptide disclosed herein.

[00364] The drug moiety (D) of the ADC may include any compound, moiety or group that has a cytotoxic or cytostatic effect, or may be a diagnostic or detectable agent.

[00365] The linker (L) is a bifunctional or multifunctional moiety that has, e.g., reactive functionalities for attaching to the drug and to the antibody. A linker may have a functionality that is capable of reacting with a free cysteine present on an antibody to form a covalent bond, or a functionality that is capable of reacting with an electrophilic group present on an antibody. Linkers can be susceptible to cleavage (cleavable linker), such as, acid-induced cleavage, photo-induced cleavage, peptidase-induced cleavage, esterase-induced cleavage, and disulfide bond cleavage, at conditions under which the compound or the antibody remains active. Alternatively, linkers can be substantially resistant to cleavage (e.g., stable linker or noncleavable linker). In some aspects, the linker is a procharged linker, a hydrophilic linker, or a dicarboxylic acid based linker.

[00366] Examples of cleavable linkers include acid-labile linkers (e.g. , comprising hydrazone), protease-sensitive (e.g., peptidase-sensitive) linkers, photolabile linkers, or disulfide-containing linkers. The linker may be, for example, any one of N- succinimidyl-4-(2-pyridyldithio)2-sulfo-butanoate (sulfo-SPDB), N-succinimidy1-3-(2-pyridyldithio)propionate (SPDP), N-succinimidyl 4-(2-pyridyldithio)pentanoate (SPP), N-succinimidyl 4-(2-pyridyldithio)butanoate (SPDB), N-succinimidyl iodoacetate (SIA), N-succimmidyl(4-iodoacetyl)aminobenzoate (SIAB), maleimide PEG NHS, N-succinimidyl 4-(maleimidomethyl) cyclohexanecarboxylate (SMCC), N- sulfosuccinimidyl 4-(maleimidomethyl) cyclohexanecarboxylate (sulfo-SMCC) and 2,5-dioxopyrrolidin-l-yl 17-(2,5-dioxo-2,5-dihydro-lH- pyrrol-l-yl)-5,8, 11,14-tetraoxo-4,7, 10,13-tetraazaheptadecan-l-oate (CXl-1).

[00367] The number of drug moieties (e.g., p) that can be conjugated to an antibody may be limited by the number of free cysteine residues (which may be naturally occurring or introduced into the antibody amino acid sequence, or generated using reducing conditions prior to conjugation). In some embodiments, p may be 1 to 10, 2 to 8, or 2 to 5. In some embodiments, p is 3 to 4.

[00368] In some embodiments, the drug moiety (D) may be chosen from an anti-cancer agent, anti-hematological disorder agent, an autoimmune treatment agent, an antiinflammatory agent, an antifungal agent, an antibacterial agent, an anti-parasitic agent, an anti-viral agent, an anesthetic agent, a cytotoxin, or a radiotoxin.

[00369] In some embodiments, D may be a maytansinoid, a V-ATPase inhibitor, a pro-apoptotic agent, a Bcl2 inhibitor, an MCL1 inhibitor, a HSP90 inhibitor, an IAP inhibitor, an mTor inhibitor, a microtubule stabilizer, a microtubule destabilizer, an auristatin, a dolastatin, a MetAP (methionine aminopeptidase), an inhibitor of nuclear export of proteins CRM1, a DPPIV inhibitor, proteasome inhibitors, inhibitors of phosphoryl transfer reactions in mitochondria, a protein synthesis inhibitor, a kinase inhibitor, a CDK2 inhibitor, a CDK9 inhibitor, a kinesin inhibitor, an HDAC inhibitor, a DNA damaging agent, a DNA alkylating agent, a DNA intercalator, a DNA minor groove binder and a DHFR inhibitor.

[00370] In some embodiments, the drug (D) may be an anticancer agent. Anti-cancer agents include, and D may be, for example:

1) inhibitor or modulator of a protein involved in one or more of the DNA damage repair (DDR) pathways such as:
    a. PARP1/2, including, but not limited to: olaparib, niraparib, rucaparib;

b. checkpoint kinase 1 (CHK1), including, but not limited to: UCN-01, AZD7762, PF477736 , SCH900776, MK-8776, LY2603618, V158411, and EXEL-9844;
c. checkpoint kinase 2 (CHK2), including, but not limited to: PV1019, NSC 109555, and VRX0466617;
d. dual CHK1 / CHK2, including, but not limited to: XL-844, AZD7762, and PF-473336;
e. WEE1, including, but not limited to: MK-1775 and PD0166285;
f. ATM, including, but not limited to KU-55933,
g. DNA-dependent protein kinase, including, but not limited to NU7441 and M3814; and
h. Additional proteins involved in DDR;

2) an inhibitor or modulator of one or more immune checkpoints, including, but not limited to:
a. a PD-1 inhibitor such as nivolumab (OPDIVO), pembrolizumab (KEYTRUDA), pidilizumab (CT-011), and AMP-224 (AMPLIMMUNE);
b. a PD-L1 inhibitor such as Atezolizumab (TECENTRIQ), Avelumab (Bavencio), Durvalumab (Imfinzi), MPDL3280A (Tecentriq), BMS-936559, and MEDI4736;
c. an anti-CTLA-4 antibodies such as ipilimumab (YERVOY) and CP-675,206 (TREMELIMUMAB);
d. an inhibitor of T-cell immunoglobulin and mucin domain 3 (Tim-3);
e. an inhibitor of V-domain Ig suppressor of T cell activation (Vista);
f. an inhibitor of band T lymphocyte attenuator (BTLA);
g. an inhibitor of lymphocyte activation gene 3 (LAG3); and
h. an inhibitor of T cell immunoglobulin and immunoreceptor tyrosine-based inhibitory motif domain (TIGIT);

3) a telomerase inhibitor or telomeric DNA binding compound;
4) an alkylating agent, including, but not limited to: chlorambucil (LEUKERAN), oxaliplatin (ELOXATIN), streptozocin (ZANOSAR), dacarbazine, ifosfamide, lomustine (CCNU), procarbazine (MATULAN), temozolomide (TEMODAR), and thiotepa;
5) a DNA crosslinking agent, including, but not limited to: carmustine, chlorambucil (LEUKERAN), carboplatin (PARAPLATIN), cisplatin (PLATIN), busulfan

(MYLERAN), melphalan (ALKERAN), mitomycin (MITOSOL), and cyclophosphamide (ENDOXAN);

6) an anti-metabolite, including, but not limited to: cladribine (LEUSTATIN), cytarbine, (ARA-C), mercaptopurine (PURINETHOL), thioguanine, pentostatin (NIPENT), cytosine arabinoside (cytarabine, ARA-C), gemcitabine (GEMZAR), fluorouracil (5-FU, CARAC), capecitabine (XELODA), leucovorin (FUSILEV), methotrexate (RHEUMATREX), and raltitrexed;
7) an antimitotic, which are often plant alkaloids and terpenoids, or a derivative thereof including but limited to: a taxane such as docetaxel (TAXITERE), paclitaxel (ABRAXANE, TAXOL), a vinca alkaloid such as vincristine (ONCOVIN), vinblastine, vindesine, and vinorelbine (NAVELBINE);
8) a topoisomerase inhibitor, including, but not limited to: amsacrine, camptothecin (CTP), genistein, irinotecan (CAMPTOSAR), topotecan (HYCAMTIN), doxorubicin (ADRIAMYCIN), daunorubicin (CERUBIDINE), epirubicin (ELLENCE), ICRF-193, teniposide (VUMON), mitoxantrone (NOVANTRONE), and etoposide (EPOSIN);
9) a DNA replication inhibitor, including, but not limited to: fludarabine (FLUDARA), aphidicolin, ganciclovir, and cidofovir;
10) a ribonucleoside diphosphate reductase inhibitor, including, but not limited to: hydroxyurea;
11) a transcription inhibitor, including, but not limited to: actinomycin D (dactinomycin, COSMEGEN) and plicamycin (mithramycin);
12) a DNA cleaving agent, including, but not limited to: bleomycin (BLENOXANE) and idarubicin;
13) an aromatase inhibitor, including, but not limited to: aminoglutethimide, anastrozole (ARIMIDEX), letrozole (FEMARA), vorozole (RIVIZOR), and exemestane (AROMASIN);
14) an angiogenesis inhibitor, including, but not limited to: genistein, sunitinib (SUTENT), and bevacizumab (AVASTIN);
15) an anti-steroid or anti-androgen, including, but not limited to: aminoglutethimide (CYTADREN), bicalutamide (CASODEX), cyproterone, flutamide (EULEXIN), nilutamide(NILANDRON);

16) a tyrosine kinase inhibitor, including, but not limited to: imatinib (GLEEVEC), erlotinib (TARCEVA), lapatininb (TYKERB), sorafenib (NEXAVAR), and axitinib (INLYTA);
17) an mTOR inhibitor, including, but not limited to: everolimus, temsirolimus (TORISEL), and sirolimus;
18) an apoptosis inducer such as cordycepin;
19) a protein synthesis inhibitor, including, but not limited to: clindamycin, chloramphenicol, streptomycin, anisomycin, and cycloheximide;
20) an antidiabetic, including, but not limited to: metformin and phenformin;
21) a cytotoxic antibiotic, including, but not limited to:
    a. tetracyclines, including, but not limited to: doxycycline;
    b. erythromycins, including, but not limited to: azithromycin;
    c. glycylglycines, including, but not limited to: tigecyline;
    d. antiparasitics, including, but not limited to: pyrvinium pamoate;
    e. beta-lactams, including, but not limited to the penicillins and cephalosporins;
    f. an anthracycline antibiotic, including, but not limited to: doxorubicin, daunorubicin, epirubicin, idarubicin, pirarubicin, aclarubicin, and mitoxantrone;
    g. a bleomycin such as the classical bleomycin A2 (BLENOXANE) and pingyangmycin (also known as bleomycin A5)
    h. another antibiotic, including, but not limited to: chloramphenicol, mitomycin C and actinomycin D (dactinomycin, COSMEGEN); and
22) another agent, such as Bacillus Calmette–Guérin (B-C-G) vaccine; buserelin (ETILAMIDE); chloroquine (ARALEN); clodronate, pamidronate, or another bisphosphonate; colchicine; demethoxyviridin; dichloroacetate; estramustine; filgrastim (NEUPOGEN); fludrocortisone (FLORINEF); goserelin (ZOLADEX); interferon; leucovorin; leuprolide (LUPRON); levamisole; lonidamine; mesna; metformin; mitotane (o,p'-DDD, LYSODREN); nocodazole; octreotide (SANDOSTATIN); perifosine; porfimer (particularly in combination with photo- and radiotherapy); suramin; tamoxifen; titanocene dichloride; tretinoin; an anabolic steroid such as fluoxymesterone (HALOTESTIN); estrogens such as estradiol, diethylstilbestrol (DES), and dienestrol; a progestin such as medroxyprogesterone acetate (MPA) and megestrol; and testosterone.

[00371] In some embodiments, the drug moiety (D) may be a toxin. Plant-derived protein toxins include ribosome inactivating proteins (RIPs) such as shiga toxins, type I (e.g. trichosanthin and luffin) and type II (e.g. ricin, agglutinin, and abrin), as well as saporin, gelonin, and pokeweed antiviral protein; and bacterial toxins include *Pseudomonas* exotoxin and Diphtheria toxin.

[00372] In some embodiments, the drug moiety (D) may be a diagnostic or detectable agent. Such immunoconjugates can be useful for monitoring or prognosing the onset, development, progression and/or severity of a disease or disorder as part of a clinical testing procedure, such as determining the efficacy of a particular therapy. Such diagnosis and detection can be accomplished by coupling the antibody to detectable substances including, but not limited to, various enzymes, such as horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; prosthetic groups, such as, but not limited to, streptavidinfoiotin and avidin/biotin; fluorescent materials, such as, but not limited to, Alexa Fluor 350, Alexa Fluor 405, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 500, Alexa Fluor 514, Alexa Fluor 532, Alexa Fluor 546, Alexa Fluor 555, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 610, Alexa Fluor 633, Alexa Fluor 647, Alexa Fluor 660, Alexa Fluor 680, Alexa Fluor 700, Alexa Fluor 750, umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; luminescent materials, such as, but not limited to, luminol; bioluminescent materials, such as but not limited to, luciferase, luciferin, and aequorin; radioactive materials, such as, but not limited to, iodine (^{131}I, ^{125}I, ^{123}I, and ^{m}I,), carbon (^{14}C), sulfur (^{35}S), tritium, indium (^{115}In, ^{113}In, ^{112}In, and ^{m}In,), technetium (^{99}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, ^{47}Sc, ^{186}Re, ^{188}Re, ^{142}Pr, ^{105}Rh, ^{97}Ru, ^{68}Ge, ^{57}Co, ^{65}Zn, ^{85}Sr, ^{32}P, ^{153}Gd, ^{169}Yb, ^{51}Cr, ^{54}Mn, ^{75}Se, ^{64}Cu, ^{113}Sn, and ^{117}Sn; and positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions.

[00373] In some embodiments the drug moiety D is chosen from saporin, MMAE, MMAF, DM1, DM4. In some embodiments, the drug is saporin.

Treatment Applications

[00374] The polypeptides, including antibodies and functional antigen-binding fragments thereof, CAR-bearing immune effector cells, and compositions described herein, antibody-drug conjugates, and pharmaceutical compositions comprising them can be used in

the treatment or prevention of progression of proliferative diseases such as cancers and myelodysplastic syndromes. The cancer may be a hematologic malignancy or solid tumor. Hematologic malignancies include leukemias, lymphomas, multiple myeloma, and subtypes thereof. Lymphomas can be classified various ways, often based on the underlying type of malignant cell, including Hodgkin's lymphoma (often cancers of Reed-Sternberg cells, but also sometimes originating in B cells; all other lymphomas are non-Hodgkin's lymphomas), non-Hodgkin's lymphomas, B-cell lymphomas, T-cell lymphomas, mantle cell lymphomas, Burkitt's lymphoma, follicular lymphoma, and others as defined herein and known in the art. Myelodysplastic syndromes comprise a group of diseases affecting immature leukocytes and/or hematopoietic stem cells (HSCs); MDS may progress to AML.

[00375] B-cell lymphomas include, but are not limited to, diffuse large B-cell lymphoma (DLBCL), chronic lymphocytic leukemia (CLL) /small lymphocytic lymphoma (SLL) , and others as defined herein and known in the art.

[00376] T-cell lymphomas include T-cell acute lymphoblastic leukemia/lymphoma (T-ALL), peripheral T-cell lymphoma (PTCL), T-cell chronic lymphocytic leukemia (T-CLL), Sezary syndrome, and others as defined herein and known in the art.

[00377] Leukemias include acute myeloid (or myelogenous) leukemia (AML), chronic myeloid (or myelogenous) leukemia (CML), acute lymphocytic (or lymphoblastic) leukemia (ALL), chronic lymphocytic leukemia (CLL) hairy cell leukemia (sometimes classified as a lymphoma) , and others as defined herein and known in the art.

[00378] Plasma cell malignancies include lymphoplasmacytic lymphoma, plasmacytoma, and multiple myeloma.

[00379] Solid tumors include melanomas, neuroblastomas, gliomas or carcinomas such as tumors of the brain, head and neck, breast, lung (e.g., non-small cell lung cancer, NSCLC), reproductive tract (e.g., ovary), upper digestive tract, pancreas, liver, renal system (e.g., kidneys), bladder, prostate and colorectum.

[00380] Methods described herein are generally performed on a subject in need thereof. A subject in need of the therapeutic methods described herein can be a subject having, diagnosed with, suspected of having, or at risk for developing, or at rick of progressing to a later stage of, cancer. A determination of the need for treatment will typically be assessed by a history, physical exam, or diagnostic tests consistent with the disease or condition at issue. Diagnosis of the various conditions treatable by the methods described herein is within the skill of the art. The subject can be an animal subject, including a mammal, such as horses, cows, dogs, cats, sheep, pigs, mice, rats, monkeys, hamsters,

guinea pigs, and humans, or other animals such as chickens. For example, the subject can be a human subject.

[00381] Generally, a safe and effective amount of a therapy, e.g. an antibody or functional antigen-binding fragment thereof, CAR-bearing immune effector cell, or antibody-drug conjugate, is, for example, an amount that would cause the desired therapeutic effect in a subject while minimizing undesired side effects.

[00382] According to the methods described herein, administration can be parenteral, pulmonary, oral, topical, intradermal, intramuscular, intraperitoneal, intravenous, intratumoral, intrathecal, intracranial, intracerebroventricular, subcutaneous, intranasal, epidural, ophthalmic, buccal, or rectal administration. Where the product is, for example, a biologic or cell therapy, the mode of administration will likely be via injection or infusion.

Standards of Care and Conditioning Regimens for Immunotherapy

[00383] Standard of care treatment for cancers, such as AML, can involve anti-cancer pharmaceutical therapy including chemotherapy and targeted therapy, as well as hematopoietic stem cell transplant (HSCT).

[00384] For example, the combination of cytarabine (cytosine arabinoside or ara-C) and an anthracycline such as daunorubicin (daunomycin) or idarubicin is the first-line chemotherapy for AML. Other chemotherapeutics that may be used to treat AML include cladribine (Leustatin, 2-CdA), fludarabine (Fludara), mitoxantrone, Etoposide (VP-16), 6-thioguanine (6-TG), hydroxyurea, corticosteroids such as prednisone or dexamethasone, methotrexate (MTX), 6-mercaptopurine (6-MP), azacitidine (Vidaza), and decitabine (Dacogen). In addition, targeted therapies may be used in appropriate patients, such as midostaurin (Rydapt) or gilteritinib (Xospata) in patients with FLT-3 mutations; gemtuzumab ozogamicin (Mylotarg) in CD33-positive AML; BCL-2 inhibitor such as venetoclax (Venclexta); IDH inhibitors such as ivosidenib (Tibsovo) or enasidenib (Idhifa); and hedgehog pathway inhibitors such as glasdegib (Daurismo). Although the rate of complete remission can be as high as 80% following initial induction chemotherapy, the majority of AML patients will eventually progress to relapsed or refractory (RR) disease, and five-year survival rate are about 35% in people under 60 years old and 10% in people over 60 years old. *See,* Walter RB et al., "Resistance prediction in AML: analysis of 4601 patients from MRC/NCRI, HOVON/SAKK, SWOG *and* MD Anderson Cancer Center," *Leukemia* 29(2):312-20

(2015) and Döhner, Het al., "Acute Myeloid Leukemia," *NEJM* 373 (12): 1136–52 (2015).

[00385] Adoptive cell transfer (ACT) therapy is also possible in the treatment of cancers such as AML, either with or without a conditioning regimen. Currently, hematopoietic stem cell transfer (HSCT) is used; other therapies such as transplant of NK cells, chimeric antigen receptor (CAR) T cells (CAR-T) and other CAR-bearing immune effector cells are in development.

Hematopoietic Stem Cell Transplant (HSCT)

[00386] Hematopoietic stem cell transplantation (HSCT) is a potentially curative therapeutic approach for a variety of malignant and nonmalignant hematopoietic diseases, such as AML, CML, ALL, Hodgkin and non-Hodgkin lymphoma, multiple myeloma, myelodysplastic syndrome, neuroblastoma, Ewing sarcoma, gliomas, and solid tumors. HSCT for AML is typically allogeneic and requires HLA-matching between donor and patient for several reasons. The first is to prevent HvGD, but an additional benefit is the graft-versus-leukemia (GvL) effect wherein donor immune cells recognize patient leukemia cells as being foreign to them and attack them. In some cases, for example where the patient may not be able to tolerate an allogeneic transplant, an autologous transplant may be used, often after careful purging to attempt to remove leukemia cells.

[00387] Typically, when HSCT is performed in patients with malignant disorders, preparative or conditioning regimens are administered as part of the procedure to effect immunoablation to prevent graft rejection, and to reduce tumor burden. Traditionally, these goals have been achieved by using otherwise supralethal doses of total body irradiation (TBI) and chemotherapeutic agents with nonoverlapping toxicities, so-called "high-intensity" pre-HSCT conditioning. However, as it was recognized that immunologic reactions of donor cells against malignant host cells (i.e., graft-versus-tumor effects) substantially contributed to the effectiveness of HSCT, reduced-intensity and nonmyeloablative conditioning regimens have been developed, making HCT applicable to older and medically infirm patients.

[00388] Conditioning regimens are known in the art. See, e.g., Gyurkocza and Sandmaier BM, "Conditioning regimens for hematopoietic cell transplantation: one size does not fit all ," Blood 124(3): 344–353 (2014). Conditioning regimens may be classified as high-dose (myeloablative), reduced-intensity, and nonmyeloablative, following the Reduced-Intensity Conditioning Regimen Workshop, convened by the Center for

International Blood and Marrow Transplant Research (CIBMTR) during the Bone Marrow Transplantation Tandem Meeting in 2006.

Immunotherapy with CAR-Bearing Immune Effector Cells

[00389] CAR-bearing immune effector cells have been used in treatment of AML with varying results. Clinical trials with CAR-T cells targeting AML antigens such as CD33 and CD123 have been registered and are proceeding, but have not to date seen unequivocal success. One problem is the difficulty in targeting a suitable targetable surface antigen that is not also expressed on healthy cells. CAR-engineered cells from the immortalized NK-92 cell line targeting AML antigen CD33 have also been tested.

[00390] There are multiple scenarios where therapy with CAR-bearing immune effector cells would be useful in AML. In one scenario where a patient with AML is treated with CAR cell therapy, the CAR present on the surface of the CAR-bearing immune effector cell recognizes and binds to an AML cell antigen, such as CD33, FLT-3, or CLL-1, and the AML cell is targeted for killing. The CAR cell therapy will also target the same antigens on the patient's own hematopoietic stem cells. Thereafter, the patient receives hematopoietic stem cell transplant (HSCT), optionally undergoing preliminary procedures to extinguish the CAR cells and condition the patient for HSCT beforehand, and the engrafted donor stem cells then attack the remaining AML cells. Although this is an effective therapy for many patients, AML may nevertheless relapse (e.g. in about 50% of cases), and further treatment with the same CAR cell therapy is typically not feasible because the engrafted stem cells and their progeny will recognize the newly-infused CAR cells as foreign and destroy them.

Polymorphic Targeting of Cancer Antigens

[00391] *Polymorphic Targeting.* Another approach to the use of CAR-bearing immune effector cells in the treatment of AML exploits natural variation in AML target antigen polymorphism to solve this problem. Certain AML antigens, such as CD33, FLT-3, and CLL-1 occur as polymorphic variants. For example, in a given population, an AML antigen exists as two predominant polymorphs, e.g. A, in which a given base pair in the genomic sequence of the antigen is A-T, and B, in which the base pair is C-G at the same position. This will lead to a different amino acid residue being translated, and provided that the base pair occurs in a coding region, an antigen with a different amino acid residue and thus a different primary and, thus, tertiary structure. If the change is significant, and the residue is in an solvent-exposed position on the cell surface

that is accessible to an antibody, an antigen-binding fragment thereof, or a synthetic antigen-binding protein such as an scFv, then a CAR may be designed to bind a single polymorph selectively over the other(s). And a CAR-T cell, or other immune effector cell, bearing such a selective CAR, can target and kill AML cells of a single polymorphic form. See, e.g., Table 2 below, setting forth three AML antigens and their common polymorphisms:

Table 2. Polymorphisms in AML Antigens

POLYMORPHISM	A	BB
CD33 ARG69GLY (R69G)	Arg 64.3%	Gly 35.7%
FLT3 THR227MET (T227M)	Thr 40.1%	Met 59.9%
CLL1 LYS244GLN (K244Q)	Lys 26.3%	Gln 73.7%

See also **Figure 1** showing the positions of the CD33 extracellular domain with amino acid 69 in the left panel, and FLT3 ECD AA267 in the right panel, each in a relatively solvent-accessible position.

[00392] *Patient – Donor Mismatch.* When the patient has one polymorphic form of an AML antigen, and a donor of cells for use in HSCT has another polymorphic form of the antigen, creating a "mismatch" of AML antigen polymorphisms, several useful treatment scenarios arise.

[00393] When the donor provides polymorphically "mismatched" stem cells for HSCT, and those cells are engrafted into a recipient patient, CAR-bearing immune effector cell therapy with a CAR selective for the patient's polymorphic variant may be used – even after HSCT transplant – to target and kill any remaining cells bearing the patient's polymorphic form of the antigen. Because the cells selectively target the patient's polymorphism, the donor's engrafted cells will be spared. Treatment may be either prophylactic, or upon signs of relapsing disease. Thus, relapse is prevented or treated, and the patient can achieve disease-free survival.

[00394] The HSC and the T cells or other immune effector cells that will be engineered to express a CAR may both come from the same donor, polymorphically mismatched to the intended recipient. As shown below in Table 3, the donor must be homozygous for either one polymorphism or the other (i.e., cannot be heterozygous), and

the receiving patient can be either homozygous for the other polymorphism or heterozygous.

Table 3. Treatment Options with Anti-CD33 Polymorphic Antibodies and CARs

		Donor Genotype		
	Rs2455069 A>G Arg69Gly	**AA (ARG/ARG)**	**AG (ARG/GLY)**	**GG(GLY/GLY)**
Patient Genotype	**AA(ARG/ARG)**	--	--	CAR-A
	AG (ARG/GLY)	CAR-G	--	CAR-A
	GG (GLY/GLY)	CAR-G	--	--

[00395] In another variation, the HSC may come from one mismatched donor, and the immune effector cells that will be engineered to express a CAR will come from a different donor. If the CAR-bearing immune effector cells are CAR-T cells, these cells may have the T-cell receptor disabled, e.g., by genetic disruption of one or more of its components (such as TRAC), e.g., using CRISPR or another genome editing tool, or a technology such as PEBL.

Pharmaceutical Compositions

[00396] Also disclosed is a pharmaceutical composition comprising a disclosed molecule in a pharmaceutically acceptable carrier. Pharmaceutical carriers are known to those skilled in the art. These most typically would be standard carriers for administration of drugs to humans, including solutions such as sterile water, saline, and buffered solutions at physiological pH. Typically, an appropriate amount of a pharmaceutically-acceptable salt is used in the formulation to render the formulation isotonic. Examples of the pharmaceutically-acceptable carrier include, but are not limited to, saline, Ringer's solution and dextrose solution. The pH of the solution is preferably from about 5 to about 8, and more preferably from about 7 to about 7.5. The solution should be RNAse free. Further carriers include sustained release preparations such as semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, liposomes or microparticles. It will be apparent to those persons skilled in the art that certain carriers may be more preferable depending upon, for instance, the route of administration and concentration of composition being administered.

[00397] Pharmaceutical compositions may include carriers, thickeners, diluents, buffers, preservatives, surface active agents and the like in addition to the molecule of choice. Pharmaceutical compositions may also include one or more active ingredients such as antimicrobial agents, anti-inflammatory agents, anesthetics, and the like.

[00398] Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like.

Definitions

[00399] Unless otherwise defined, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. Generally, nomenclatures utilized in connection with, and techniques of, cell and tissue culture, molecular biology, and protein and oligo or polynucleotide chemistry and hybridization described herein are those well-known and commonly used in the art.

[00400] The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms also apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

[00401] As used herein, the term "antibody" refers to a polypeptide that includes canonical immunoglobulin sequence elements sufficient to confer specific binding, or e.g. immune-reacts and /or is directed to a particular target antigen. As is known in the art, intact antibodies as produced in nature are approximately 150 kD tetrameric agents comprised of two identical heavy chain polypeptides (about 50 kD each) and two identical light chain polypeptides (about 25 kD each) that associate with each other into

what is commonly referred to as a "Y-shaped" structure. Each heavy chain is comprised of at least four domains (each about 110 amino acids long)—an amino-terminal variable (V_H) domain , followed by three constant domains: C_H1, C_H2, and the carboxy-terminal C_H3. A short region, known as the "switch", connects the heavy chain variable and constant regions. The "hinge" connects C_H2 and C_H3 domains to the rest of the antibody. Two disulfide bonds in this hinge region connect the two heavy chain polypeptides to one another in an intact antibody. Each light chain is comprised of two domains—an amino-terminal variable (V_L) domain, followed by a carboxy-terminal constant (C_L) domain, separated from one another by another "switch". Intact antibody tetramers are comprised of two heavy chain-light chain dimers in which the heavy and light chains are linked to one another by a single disulfide bond; two other disulfide bonds connect the heavy chain hinge regions to one another, so that the dimers are connected to one another and the tetramer is formed. Naturally-produced antibodies are also glycosylated, typically on the C_H2 domain. Each domain in a natural antibody has a structure characterized by an "immunoglobulin fold" formed from two beta sheets (e.g., 3-, 4-, or 5-stranded sheets) packed against each other in a compressed antiparallel beta barrel. Each variable domain contains three hypervariable loops known as "Complementarity-Determining Regions" (CDR1, CDR2, and CDR3) and four somewhat invariant "framework" regions (FR1, FR2, FR3, and FR4). When natural antibodies fold, the FR regions form the beta sheets that provide the structural framework for the domains, and the CDR loop regions from both the heavy and light chains are brought together in three-dimensional space so that they create a single hypervariable antigen binding site located at the tip of the Y structure. The Fc region of naturally-occurring antibodies binds to elements of the complement system, and also to receptors on effector cells, including for example effector cells that mediate cytotoxicity.

[00402] The term "antigen" refers to a molecular entity that may be soluble or cell membrane bound in particular but not restricted to molecular entities that can be recognized by means of the adaptive immune system including but not restricted to antibodies or TCRs, or engineered molecules including but not restricted to transgenic TCRs, chimeric antigen receptors (CARs), scFvs or multimers thereof, Fab-fragments or multimers thereof, antibodies or multimers thereof, single chain antibodies or multimers thereof, or any other molecule that can execute binding to a structure with high affinity.

[00403] The terms "specifically binds" or "specific for" or "specifically recognize" with respect to an antigen-recognizing receptor refer to an antigen-binding domain of

said antigen-recognizing receptor which recognizes and binds to a specific polymorphic variant of an antigen, but does not substantially recognize or bind other variants.

[00404] The term "monoclonal antibody" (mAb), as applied to the antibodies described in the present disclosure, are compounds derived from a single copy or a clone from any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced. mAbs of the present disclosure may exist in a homogeneous or substantially homogeneous population.

[00405] As used herein, the term "binding affinity" refers to the strength of binding of one molecule to another at a site on the molecule. If a particular molecule will bind to or specifically associate with another particular molecule, these two molecules are said to exhibit binding affinity for each other. Binding affinity is related to the association constant and dissociation constant for a pair of molecules, but it is not critical to the methods herein that these constants be measured or determined. Rather, affinities as used herein to describe interactions between molecules of the described methods are generally apparent affinities (unless otherwise specified) observed in empirical studies, which can be used to compare the relative strength with which one molecule (e.g., an antibody or other specific binding partner) will bind two other molecules (e.g., two versions or variants of a peptide). The concepts of binding affinity, association constant, and dissociation constant are well known.

[00406] As used herein, the term "sequence identity" means the percentage of identical nucleotide or amino acid residues at corresponding positions in two or more sequences when the sequences are aligned to maximize sequence matching, i.e., taking into account gaps and insertions. Identity can be readily calculated by known methods. Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available computer programs. Optimal alignment of sequences for comparison can be conducted, for example, by the local homology algorithm of Smith & Waterman, by the homology alignment algorithms, by the search for similarity method or, by computerized implementations of these algorithms (GAP, BESTFIT, PASTA, and TFASTA in the GCG Wisconsin Package, available from Accelrys, Inc. See generally, Altschul, S. F. et al., J. Mol. Biol. 215: 403-410 (1990) and Altschul et al. Nucl. Acids Res. 25: 3389-3402 (1997). One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm,

[00407] An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds. Several examples of antibody fragments include but are not limited to

Fv, Fab, Fab', Fab'-SH, $F(ab')_2$, diabodies, linear antibodies, single chain variable fragments (scFvs), and multi-specific antibodies formed from antibody fragments. In some embodiments, the antibody fragment is an antigen-binding fragment.

[00408] Reviews of current methods for antibody engineering and improvement can be found in R. Kontermann and S. Dubel, (2010) Antibody Engineering Vols.1 and 2, Springer Protocols, 2nd Edition and W. Strohl and L. Strohl (2012) Therapeutic antibody engineering: *Current and future advances driving the strongest growth area in the pharmaceutical industry*, Woodhead Publishing. Methods for producing and purifying antibodies and antigen-binding fragments are well known in the art and can be found, in Harlow and Lane (1988) Antibodies: A Laboratory Manual, *Cold Spring Harbor Laboratory Press*, Cold Spring Harbor, NY, chapters 5-8 and 15.

[00409] A "diseased cell" refers to the state of a cell, tissue or organism that diverges from the normal or healthy state and may result from the influence of a pathogen, a toxic substance, irradiation, or cell internal deregulation. A "diseased cell" may also refer to a cell that has been infected with a pathogenic virus. Further the term "diseased cell" may refer to a malignant cell or neoplastic cell that may constitute or give rise to cancer in an individual.

[00410] The term "cancer" is known medically as a malignant neoplasm. Cancer is a broad group of diseases involving upregulated cell growth. In cancer, cells (cancerous cells) divide and grow uncontrollably, forming malignant tumors, and invading nearby parts of the body. The cancer may also spread to more distant parts of the body through the lymphatic system or bloodstream. There are over 200 different known cancers that affect humans.

[00411] The term "malignant" or "malignancy" describes cells, groups of cells or tissues that constitute a neoplasm, are derived from a neoplasm or can be the origin of new neoplastic cells. The term is used to describe neoplastic cells in contrast to normal or healthy cells of a tissue. A malignant tumor contrasts with a non-cancerous benign tumor in that a malignancy is not self-limited in its growth, is capable of invading into adjacent tissues, and may be capable of spreading to distant tissues. A benign tumor has none of those properties. Malignancy is characterized by anaplasia, invasiveness, and metastasis as well as genome instability. The term "premalignant cells" refer to cells or tissue that is not yet malignant but is poised to become malignant.

[00412] The term "chemotherapy" refers to the treatment of cancer (cancerous cells) with one or more cytotoxic anti-neoplastic drugs ("chemotherapeutic agents" or

"chemotherapeutic drugs") as part of a standardized regimen. Chemotherapy may be given with a curative intent or it may aim to prolong life or to palliate symptoms. It is often used in conjunction with other cancer treatments, such as radiation therapy, surgery, and/or hyperthermia therapy. Traditional chemotherapeutic agents act by killing cells that divide rapidly, one of the main properties of most cancer cells. This means that chemotherapy also harms cells that divide rapidly under normal circumstances, such as cells in the bone marrow, digestive tract, and hair follicles. This results in the most common side-effects of chemotherapy, such as myelosuppression (decreased production of blood cells, hence also immunosuppression), mucositis (inflammation of the lining of the digestive tract), and alopecia (hair loss).

[00413] The term "immune cell" or "immune effector cell" refers to a cell that may be part of the immune system and executes a particular effector function such as alpha-beta T cells, NK cells (including ML-NKs and CIML-NKs), NKT cells (including iNKT cells),, B cells, innate lymphoid cells (ILC), cytokine induced killer (CIK) cells, lymphokine activated killer (LAK) cells, gamma-delta T cells, mesenchymal stem cells or mesenchymal stromal cells (MSC), monocytes and macrophages. Preferred immune cells are cells with cytotoxic effector function such as alpha-beta T cells, NK cells (including ML-NKs and CIML-NKs), NKT cells (including iNKT cells), ILC, CIK cells, LAK cells or gamma-delta T cells. "Effector function" means a specialized function of a cell, e.g. in a T cell an effector function may be cytolytic activity or helper activity including the secretion of cytokines.

[00414] The term "side-effects" refers to any complication, unwanted or pathological outcome of an immunotherapy with an antigen recognizing receptor that occurs in addition to the desired treatment outcome. The term "side effect" preferentially refers to on-target off-tumor toxicity, that might occur during immunotherapy in case of presence of the target antigen on a cell that is an antigen-expressing non-target cell but not a diseased cell as described herein. A side-effect of an immunotherapy may be the developing of graft versus host disease.

[00415] The term "reducing side-effects" refers to the decrease of severity of any complication, unwanted or pathological outcome of an immunotherapy with an antigen recognizing receptor such as toxicity towards an antigen-expressing non-target cell. "Reducing side-effects" also refers to measures that decrease or avoid pain, harm or the risk of death for the patient during the immunotherapy with an antigen recognizing receptor.

[00416] The term "combination immunotherapy" refers to the concerted application of two therapy approaches e.g. therapy approaches known in the art for the treatment of disease such as cancer. The term "combination immunotherapy" may also refer to the concerted application of an immunotherapy such as the treatment with an antigen recognizing receptor and another therapy such as the transplantation of hematopoietic cells e.g. hematopoietic cells resistant to recognition by the antigen recognizing receptor. Expression of an antigen on a cell means that the antigen is sufficient present on the cell surface of said cell, so that it can be detected, bound and/or recognized by an antigen-recognizing receptor.

[00417] The term "hematopoietic cells", refers to a population of cells of the hematopoietic lineage capable of hematopoiesis which include but is not limited to hematopoietic stem cells and/or hematopoietic progenitor cells (i.e., capable to proliferate and at least partially reconstitute different blood cell types, including erythroid cells, lymphocytes, and myelocytes). The term "hematopoietic cells" as used herein also includes the cells that are differentiated from the hematopoietic stem cells and/or hematopoietic progenitor cells to form blood cells (i.e. blood cell types, including erythroid cells, lymphocytes, and myelocytes).

[00418] A donor hematopoietic cell resistant to recognition of an antigen by an antigen-recognizing receptor means that said cell cannot as easily be detected, bound and/or recognized by an antigen-recognizing receptor specific for said antigen or that the detection, binding and/or recognizing is impaired, so the cell is not killed during immunotherapy.

[00419] The term "fratricide" refers to the observation that the antigen associated with disease may be, in addition to diseased cells, present on immune effector cells engineered, such as T cells expressing an antigen-recognizing receptor, such as a CAR. In that case the side-effects of the antigen recognizing receptor will affect the immune effector cells engineered to express the antigen recognizing receptor. Such side-effect is also known in the art as fratricide.

[00420] In general, the term "receptor" refers to a biomolecule that may be soluble or attached to the cell surface membrane and specifically binds a defined structure that may be attached to a cell surface membrane or soluble. Receptors include but are not restricted to antibodies and antibody like structures, adhesion molecules, transgenic or naturally occurring TCRs or CARs. In specific, the term "antigen-recognizing receptor" as used herein may be a membrane bound or soluble receptor such as a natural TCR, a

transgenic TCR, a CAR, a scFv or multimers thereof, a Fab-fragment or multimers thereof, an antibody or multimers thereof, a bi-specific T cell enhancer (BiTE), a diabody, or any other molecule that can execute specific binding with high affinity.

[00421] The term "target" or "target antigen" refers to any cell surface protein, glycoprotein, glycolipid or any other structure present on the surface of the target cell. The term also refers to any other structure present on target cells in particular but not restricted to structures that can be recognized by means of the adaptive immune system including but not restricted to antibodies or TCRs, or engineered molecules including but not restricted to transgenic TCRs, CARs, scFvs or multimers thereof, Fab-fragments or multimers thereof, antibodies or multimers thereof, single chain antibodies or multimers thereof, or any other molecule that can execute binding to a structure with high affinity.

[00422] The term "target cells" as used herein refers to cells which are recognized by the antigen-recognizing receptor which is or will be applied to the individual.

[00423] The term "system for use in immunotherapy" as used herein refers to the constellation that two kinds of compositions are needed to perform the combined immunotherapy as disclosed herein. Therefore, the system (or set or kit or the combination of compositions) comprises a) an antigen-recognizing receptor wherein said antigen-recognizing receptor specifically recognizes an antigen on target cells in said individual; b) hematopoietic cells resistant to recognition of said antigen by said antigen-recognizing receptor.

[00424] "Chimeric antigen receptor" or "CAR" refer to engineered receptors, which graft an antigen specificity onto cells, for example T cells. The CARs disclosed herein comprise an antigen binding domain also known as antigen targeting region, an extracellular spacer domain or hinge region, a transmembrane domain and at least one intracellular signaling domain or at least one co-stimulatory domain and at least one intracellular signaling domain.

[00425] In general, a CAR may comprise an extracellular domain (extracellular part) comprising the antigen binding domain, a transmembrane domain and an intracellular signaling domain. The extracellular domain may be linked to the transmembrane domain by a linker. The extracellular domain may also comprise a signal peptide.

[00426] A "signal peptide" refers to a peptide sequence that directs the transport and localization of the protein within a cell, e.g. to a certain cell organelle (such as the endoplasmic reticulum) and/or the cell surface.

[00427] An "antigen binding domain" refers to the region of the CAR that specifically binds to an antigen (and thereby is able to target a cell containing an antigen). CARs may comprise one or more antigen binding domains. Generally, the targeting regions on the CAR are extracellular. The antigen binding domain may comprise an antibody or an antigen-binding fragment thereof. The antigen binding domain may comprise, for example, full length heavy chain, Fab fragments, single chain Fv (scFv) fragments, divalent single chain antibodies or diabodies. Any molecule that binds specifically to a given antigen such as affibodies or ligand binding domains from naturally occurring receptors may be used as an antigen binding domain. Often the antigen binding domain is a scFv. Normally, in a scFv the variable portions of an immunoglobulin heavy chain and light chain are fused by a flexible linker to form a scFv. Such a linker may be for example the $(GGGG_4S)_3$. In some instances, it is beneficial for the antigen binding domain to be derived from the same species in which the CAR will be used in. For example, when it is planned to use it therapeutically in humans, it may be beneficial for the antigen binding domain of the CAR to comprise a human or humanized antibody or antigen-binding fragment thereof. Human or humanized antibodies or fragments thereof can be made by a variety of methods well known in the art.

[00428] "Spacer" or "hinge" as used herein refers to the hydrophilic region which is between the antigen binding domain and the transmembrane domain. The CARs disclosed herein may comprise an extracellular spacer domain but is it also possible to pass such a spacer. The spacer may include Fc fragments of antibodies or fragments thereof, hinge regions of antibodies or fragments thereof, CH2 or CH3 regions of antibodies, accessory proteins, artificial spacer sequences or combinations thereof. A prominent example of a spacer is the CD8alpha hinge.

[00429] The “transmembrane domain” of the CAR can be derived from any desired natural or synthetic source for such domain. When the source is natural the domain may be derived from any membrane-bound or transmembrane protein. The transmembrane domain may be derived for example from CD8alpha or CD28. When the key signaling and antigen recognition modules are on two (or even more) polypeptides then the CAR may have two (or more) transmembrane domains. Splitting key signaling and antigen recognition modules enables for a small molecule-dependent, titratable and reversible control over CAR cell expression (Wu et al, 2015, *Science* 350: 293-303) due to small molecule-dependent heterodimerizing domains in each polypeptide of the CAR.

[00430] The cytoplasmic domain or the intracellular signaling domain of the CAR is responsible for activation of at least one of the normal effector functions of the immune cell in which the CAR is expressed. "Effector function" means a specialized function of a cell, e.g. in a T cell an effector function may be cytolytic activity or helper activity including the secretion of cytokines. The intracellular signaling domain refers to the part of a protein which transduces the effector function signal and directs the cell expressing the CAR to perform a specialized function.

[00431] The intracellular signaling domain may include any complete or truncated part of the intracellular signaling domain of a given protein sufficient to transduce the effector function signal. Prominent examples of intracellular signaling domains for use in the CARs include the cytoplasmic sequences of the T cell receptor (TCR) and co-receptors that act in concert to initiate signal transduction following antigen receptor engagement.

[00432] Generally, T cell activation can be mediated by two distinct classes of cytoplasmic signaling sequences, firstly those that initiate antigen-dependent primary activation through the TCR (primary cytoplasmic signaling sequences) and secondly those that act in an antigen-independent manner to provide a secondary or co-stimulatory signal (secondary cytoplasmic signaling sequences, costimulatory signaling domain). Therefore, an intracellular signaling domain of a CAR may comprise a primary cytoplasmic signaling domain and/or a secondary cytoplasmic signaling domain.

[00433] Primary cytoplasmic signaling sequences that act in a stimulatory manner may contain ITAMs (immunoreceptor tyrosine-based activation motifs signaling motifs). Examples of ITAM containing primary cytoplasmic signaling sequences often used in CARs are that are those derived from TCR zeta (CD3 zeta), FcR gamma, FcR beta, CD3 gamma, CD3 delta, CD3 epsilon, CD5, CD22, CD79a, CD79b, and CD66d. Most prominent is sequence derived from CD3 zeta.

[00434] The cytoplasmic domain of the CAR can be designed to comprise the CD3-zeta signaling domain by itself or combined with any other desired cytoplasmic domain(s). The cytoplasmic domain of the CAR can comprise a CD3 zeta chain portion and a costimulatory signaling region. The costimulatory signaling region refers to a part of the CAR comprising the intracellular domain of a costimulatory molecule. A costimulatory molecule is a cell surface molecule other than an antigen receptor or their ligands that is required for an efficient response of lymphocytes to an antigen. Examples for a costimulatory molecule are CD27, CD28, 4-1BB (CD137), OX40, CD30, CD40,

PD-1, ICOS, lymphocyte function-associated antigen-1 (LFA-1), CD2, CD7, LIGHT, NKG2C, B7-H3. The cytoplasmic signaling sequences within the cytoplasmic signaling part of the CAR may be linked to each other in a random or specified order. A short oligo- or polypeptide linker, which is preferably between 2 and 10 amino acids in length, may form the linkage. A prominent linker is the glycine-serine doublet.

[00435] As an example, the cytoplasmic domain may comprise the signaling domain of CD3-zeta and the signaling domain of CD28. In another example the cytoplasmic domain may comprise the signaling domain of CD3-zeta and the signaling domain of CD27. In an further example, the cytoplasmic domain may comprise the signaling domain of CD3-zeta, the signaling domain of CD28, and the signaling domain of CD27.

[00436] As aforementioned either the extracellular part or the transmembrane domain or the cytoplasmic domain of a CAR may also comprise a heterodimerizing domain for the aim of splitting key signaling and antigen recognition modules of the CAR.

[00437] A CAR may be designed to comprise any portion or part of the above-mentioned domains as described herein in any combination resulting in a functional CAR.

[00438] A "chimeric antigen receptor" has at least an antigen-specific variable region (typically a single chain variable region comprised of antibody heavy and light chain variable regions) linked to an effector cell signaling domain: typically an intracellular domain of a T-cell receptor, exemplified by (but not limited to) the zeta domain of CD3. Upon binding of the antigen-specific region to the corresponding antigen, the signaling domain mediates an effector cell function in the host cell (such as cytotoxicity). The CAR may optionally but does not necessarily comprise additional domains, such as a linker, a transmembrane domain, and other intracellular signaling elements as described above.

[00439] The term "genetic modification" or genetically modified" refers to the alteration of the nucleic acid content including but not restricted to the genomic DNA of a cell. This includes but is not restricted to the alteration of a cells genomic DNA sequence by introduction exchange or deletion of single nucleotides or fragments of nucleic acid sequence. The term also refers to any introduction of nucleic acid into a cell independent of whether that leads to a direct or indirect alteration of the cells genomic DNA sequence or not.

[00440] The terms "engineered cell" and "genetically modified cell" as used herein can be used interchangeably. The terms mean containing and/or expressing a foreign gene or nucleic acid sequence, which in turn modifies the genotype or phenotype of the cell or its progeny. Especially, the terms refer to the fact that cells can be manipulated by recombinant methods well known in the art to express stably or transiently peptides or proteins, which are not expressed in these cells in the natural state. Genetic modification of cells may include but is not restricted to transfection, electroporation, nucleofection, transduction using retroviral vectors, lentiviral vectors, non-integrating retro- or lentiviral vectors, transposons, designer nucleases including zinc finger nucleases, TALENs or CRISPR/Cas.

[00441] The term "therapeutic effective amount" means an amount, which provides a therapeutic benefit.

[00442] Immunotherapy is a medical term defined as the "treatment of disease by inducing, enhancing, or suppressing an immune response" Immunotherapies designed to elicit or amplify an immune response are classified as activation immunotherapies, while immunotherapies that reduce or suppress are classified as suppression immunotherapies. Cancer immunotherapy as an activating immunotherapy attempts to stimulate the immune system to reject and destroy tumors. Adoptive cell transfer uses cell-based cytotoxic responses to attack cancer cells Immune cells such as T cells that have a natural or genetically engineered reactivity to a patient's cancer are generated in vitro and then transferred back into the cancer patient.

[00443] As used herein, the term "transplant" means administering to a subject a population of donor cells, e.g. hematopoietic cells or CAR-bearing immune effector cells.

[00444] The term "treatment" as used herein means to reduce the frequency or severity of at least one sign or symptom of a disease.

[00445] As used herein, the term "individual" refers to an animal. Preferentially, the individual is a mammal such as mouse, rat, cow, pig, goat, chicken dog, monkey or human. More preferentially, the individual is a human. The individual may be an individual suffering from a disease such as cancer (a patient), but the subject may be also a healthy subject.

[00446] As used herein, the term " fold selective," means having an affinity for one target (e.g., a first polymorphic variant of an antigen) that is at least x-fold greater than its affinity for another target (e.g., a second polymorphic variant of an antigen), wherein x is at

least 2, and may be higher, e.g., 10, 20, 50, 100, or 1000. In preferred embodiments, the fold selectivity is therapeutically meaningful, i.e., sufficient to permit cells expressing one target to be killed and cells bearing the other target to be killed.

Examples

Example 1: Identification of Targets for Polymorphically Selective Polypeptides

[00447] Polymorphically selective polypeptides may be identified for antigen targets which, optimally, 1) have a targetable portion in in extracellular domain 2) that is solvent-exposed and accessible to binding by a polymorphically selective polypeptide such as an scFv, 3) has a high population frequency so that donor patient mismatch is possible, and 4) has a high antigen density on target cells.

[00448] For example, CD33 ARG69GLY has a high population frequency, with a minor allele frequency (MAF) of 0.42. Similarly, CLL-1 LYS244GLN has a MAF of 0.35, and FLT3 THR227MET has a MAF of 0.40.

Example 2: Identification of Anti-Human CD33 scFv Clones

[00449] Selective anti-human-CD33 scFv clones were discovered by standard screening methodologies of a human antibody library using two recombinant polymorphic forms of human CD33 extracellular domain antigens ($CD33^{R69}$ and $CD33^{G69}$). Various panning tactics were employed to encourage enrichment of thermostable clones of a desired affinity range. The scFvs were screened for selective binding between two single nucleotide polymorphism (SNP) variants of human CD33 (Arginine 69 and Glycine 69) by flow cytometry and bio-layer interferometry (BLI), for example as described below in Examples 5 and 6. Selected sequences are disclosed below in Polypeptides 1-42.

[00450] Additional anti-human-CD33 polypeptides may be identified using these methods.

Table 4a. Sequences of Anti-CD33 R69-Selective Polypeptides (CDR Sequences)

Polypeptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
1	YSFTGYYIH	1	GWINPNSGGTNYA	26	CARDQWDGYNSGYFDYW	51	RASQTINDWLA	76	SASTLHS	101	CQQAYSTPWTF	126
2	FTFSDYYMS	2	SGISGSGYSTYYA	27	CARTFGRGPDWYFDLW	52	RASQSISRYLN	77	TASTLQS	102	CQQYDDLPLTF	127
3	FTFSNSDMN	3	SAISGSGGSTYYA	28	CARGREDDYGDYVFDYW	53	RASQSISSYLN	78	GASTLHS	103	CQQSYRIPYTF	128
4	GTFSSYAIS	4	GWINPNSGNTGYA	29	CAREHGDMDVW	54	RASQNINSDLA	79	GASTRAT	104	CQQYDSLPFTF	129
5	NTFTSYGIS	5	GWINPNSGGTKYA	30	CARESWFGELYYGMDVW	55	RSSQSLLHSNGYNYLD	80	LGSDRAS	105	CMQGLQTPITF	130
6	YTFTAYYTH	6	GWMNPNSGHTSYA	31	CAREAYDSFDYW	56	RASQSISSYLN	81	EASTLET	106	CQQANSFPFTF	131
7	YTFTDYYMH	7	GWINPNSGGTNYA	32	CARDSRIAVAASSFDYW	57	RASRGINNWLT	82	GASSLQS	107	CQQSYRIPYTF	132
8	FTFSSYAMS	8	SDISGSGSGTYYA	33	CARPGSDGEFDYW	58	RASQSVSSFLN	83	AASSLQS	108	CQQSYTTPLTF	133
9	GTFSSDAIN	9	GGFDPEDGETIYA	34	CARGPSGYDFEFDYW	59	RSSRNISHWLA	84	KASSLES	109	CQQAISFPLTF	134

10	DTFTTYAIS	10	GWINPNSGVATYA	35	CAREGIVGATDAFDIW	60	KSSQSVLHSSKNKNYLA	85	WASTRES	110	CQQYFTTPPTF	135
11	DTFTNHYMH	11	GWINPNSGGTNYA	36	CARDLVPAAVGGYFDYW	61	RASQSLGSWLA	86	AASSLQS	111	CQQANSFPLTF	136
12	FTFSSHWMS	12	SAISGSGGSTYYA	37	CARDDNSGSQADW	62	QASQDIDNYLN	87	DASNLET	112	CQQSYSTPLTF	137
13	YSFTGYYMH	13	GWINPNSGGTYFA	38	CVKDRGDRVVTSYLDYW	63	RASQGIRNWLA	88	AASSLQS	113	CQQSYRTPYTF	138
14	YTFTGYYMH	14	GIINPSGGSTSYA	39	CARAAPYYYDSSGYYSGGYYFDYW	64	KSSQSVLYSSNNKNYLA	89	WASTRES	114	CQQYYTTPLTF	139
15	FTFSIYEIH	15	SAISGSGGSTYYA	40	CARSYCGGDCWDYYYYYGMDVW	65	RSSQSLLHSNGYNYLD	90	LASNRAS	115	CKQTSHIPLTF	140
16	FTFSDNSMN	16	SYISSSGSTIYYA	41	CARGRASSWPNWFDPW	66	RSSQSLLHSNGYNYLD	91	SASNLQS	116	CMQALQTPPTF	141
17	FTFSSYAMS	17	SGISYDSDKIGYA	42	CAREWEGFDYW	67	RASQGISNNLN	92	ESSTLET	117	CQQSYSAPLTF	142
18	YTFTDHYMH	18	GWINPNSGGTNYA	43	CAKDKFGDEGSGWYGDFQHW	68	RSSQSLLHSNGYNYLD	93	LGSNRAS	118	CMQTLRTPLTF	143

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19	FTFSSYWMH	19	SGFSGSARTYYA	44	CAREWSGFDYW	69	RASQNIGPWLA	94	DAKDLHP	119	CQQANTFPMTF	144
20	YMFTGYYIH	20	GWINPNSGGTNYA	45	CAKDRFGSGNYGYMDVW	70	RASQSIDRWLA	95	GASSLQS	120	CQQSYSTPWTF	145
21	FTFSSYAMS	21	SAISGSGGSTYYA	46	CARELSHDYGGNSDFDYW	71	QASQDISNNLN	96	AASGLQS	121	CQQANSFPLTF	146
22	YTFTDYYIH	22	GWINPNSGGTNYA	47	CARDHRIAVAGSYFDYW	72	RASRSIRTWLA	97	AASSLQT	122	CQQSYSTPYTF	147
23	YPFTAHYIH	23	GWINPNSGGTNYA	48	CARDVEMATIGAYWYFDLW	73	RASQGINNWLA	98	DASNLET	123	CQQANSFPPTF	148
24	YSFTSYGIS	24	GWISAYNGNTNYG	49	CARARGAGTFFDYW	74	RSSQSLLHSNGYNYLD	99	DATNLPT	124	CMQALQTPFTF	149
25	YTFTGYYMH	25	GRINPNGGSTTYA	50	CARDDFYYYYLDFW	75	RASQSINDWLA	100	AASNLQS	125	CQQGYSTPPTF	150

Table 4b. Sequences of Anti-CD33 R69-Selective Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
1	QVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSS	151	DIQMTQSPSSLSASVGDRVTITCRASQTINDWLAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQAYSTPWTFGQGTKVEIKR	176

2	EVQLLESGGGLVQPGGSLRLSC AASGFTFSDYYMSWVRQAPGK GLEWVSGISGSGYSTYYADSV KGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARTFGRGPDW YFDLWGRGTLVTVSS	152	DIQMTQSPSSLSASVGDRVTITC RASQSISRYLNWYQQKPGKAPK LLIYTASTLQSGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQYD DLPLTFGGGTKVEIKR	177
3	EVQLLESGGGLVQPGGSLRLSC AASGFTFSNSDMNWVRQAPGK GLEWVSAISGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARGREDDYGD YVFDYWGQGTLVTVSS	153	DIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPK LLIYGASTLHSGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSY RIPYTFGQGTKLEIKR	178
4	QVQLVQSGAEVKKPGASVKVS CKASGGTFSSYAISWVRQAPG QGLEWMGWINPNSGNTGYAQ KFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAREHGDMD VWGQGTTVTVSS	154	EIVMTQSPATLSVSPGERATLSC RASQNINSDLAWYQQKPGQAPR LLIYGASTRATGIPARFSGSGSGT EFTLTISSLQSEDFAVYYCQQYD SLPFTFGPGTKVDIKR	179
5	QVQLVQSGAEVKKPGASVKVS CKASGNTFTSYGISWVRQAPG QGLEWMGWINPNSGGTKYAQ KFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARESWFGE LYYGMDVWGKGTTVTVSS	155	DIVMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYLGSDRASGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQGLQTPITFGQGTRLEIKR	180
6	QVQLVQSGAEVKKPGASVKVS CKASGYTFTAYYTHWVRQAP GQGLEWMGWMNPNSGHTSYA QKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAREAYDSF DYWGQGTLVTVSS	156	DIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPK LLIYEASTLETGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQAN SFPFTFGPGTKVDIKR	181

7	QVQLVQSGAEVKKPGASVKVS CKASGYTFTDYYMHWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARDSRIAV AASSFDYWGQGTLVTVSS	157	DIQMTQSPSSLSASVGDRVTITC RASRGINNWLTWYQQKPGKAP KLLIYGASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQS YRIPYTFGQGTKLEIKR	182
8	EVQLLESGGGLVQPGGSLRLSC AASGFTFSSYAMSWVRQAPGK GLEWVSDISGSGSGTYYADAV KGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARPGSDGEFDY WGQGTLVTVSS	158	DIQMTQSPSSLSASVGDRVTITC RASQSVSSFLNWYQQKPGKAPK LLIYAASSLQSGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSY TTPLTFGQGTKVEIKR	183
9	QVQLVQSGAEVKKPGSSVKVS CKASGGTFSSDAINWVRQAPG QGLEWMGGFDPEDGETIYAQK FQGRVTITADESTSTAYMELSS LRSEDTAVYYCARGPSGYDFE FDYWGQGTLVTVSS	159	DIQMTQSPSSLSASVGDRVTITC RSSRNISHWLAWYQQKPGKAPK LLIYKASSLESGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQAIS FPLTFGGGTKVEIKR	184
10	QVQLVQSGAEVKKPGASVKVS CKASGDTFTTYAISWVRQAPG QGLEWMGWINPNSGVATYAN KFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAREGIVGAT DAFDIWGQGTMVTVSS	160	DIVMTQSPDSLAVSLGERATINC KSSQSVLHSSKNKNYLAWYQQK PGQPPKLLIYWASTRESGVPDRF SGSGSGTDFTLTISSLQAEDVAV YYCQQYFTTPPTFGPGTKVDIKR	185
11	QVQLVQSGAEVKKPGASVKVS CKASGDTFTNHYMHWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARDLVPA AVGGYFDYWGQGTLVTVSS	161	DIQMTQSPSSLSASVGDRVTITC RASQSLGSWLAWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQA NSFPLTFGQGTKVEIKR	186

12	EVQLLESGGGLVQPGGSLRLSC AASGFTFSSHWMSWVRQAPG KGLEWVSAISGSGGSTYYADS VKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARDDNSGSQ ADWGQGTLVTVSS	162	DIQMTQSPSSLSASVGDRVTITC QASQDIDNYLNWYQQKPGKAP KLLIYDASNLETGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQ SYSTPLTFGGGTKLEIKR	187
13	QVQLVQSGAEVKKPGASVKVS CKASGYSFTGYYMHWVRQAP GQGLEWMGWINPNSGGTYFA QNFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCVKDRGDR VVTSYLDYWGQGTLVTVSS	163	DIQMTQSPSSLSASVGDRVTITC RASQGIRNWLAWYQQKPGKAP KLLIYAASSLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQS YRTPYTFGQGTKLEIKR	188
14	QVQLVQSGAEVKKPGASVKVS CKASGYTFTGYYMHWVRQAP GQGLEWMGIINPSGGSTSYAQ KFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARAAPYYY DSSGYYSGGYYFDYWGQGTL VTVSS	164	DIVMTQSPDSLAVSLGERATINC KSSQSVLYSSNNKNYLAWYQQK PGQPPKLLIYWASTRESGVPDRF SGSGSGTDFTLTISSLQAEDVAV YYCQQYYTTPLTFGQGTKLEIKR	189
15	EVQLLESGGGLVQPGGSLRLSC AASGFTFSIYEIHWVRQAPGKG LEWVSAISGSGGSTYYADSVK GRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARSYCGGDCWD YYYYYGMDVWGQGTTVTVSS	165	DIVMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYLASNRASGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CKQTSHIPLTFGQGTKVEIKR	190
16	EVQLVESGGGLVKPGGSLRLS CAASGFTFSDNSMNWVRQAPG KGLEWVSYISSSGSTIYYADSV KGRFTISRDDSKNTLYLQMNSL KTEDTAVYYCARGRASSWPN WFDPWGQGTLVTVSS	166	DIVMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYSASNLQSGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYC MQALQTPPTFGQGTKLEIKR	191

17	EVQLLESGGGLVQPGGSLRLSC AASGFTFSSYAMSWVRQAPGK GLEWVSGISYDSDKIGYADAV KGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCAREWEGFDYW GQGTLVTVSS	167	DIQMTQSPSSLSASVGDRVTITC RASQGISNNLNWYQQKPGKAPK LLIYESSTLETGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSYS APLTFGGGTKVEIKR	192
18	QVQLVQSGAEVKKPGASVKVS CKASGYTFTDHYMHWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDKFGD EGSGWYGDFQHWGQGTLVTV SS	168	DIVMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYLGSNRASGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQTLRTPLTFGGGTKVEIKR	193
19	EVQLLESGGGLVQPGGSLRLSC AASGFTFSSYWMHWVRQAPG KGLEWVSGFSGSARTYYADSV KGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCAREWSGFDYW GQGTLVTVSS	169	DIQMTQSPSSLSASVGDRVTITC RASQNIGPWLAWYQQKPGKAP KLLIYDAKDLHPGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQ ANTFPMTFGQGTRLEIKR	194
20	QVQLVQSGAEVKKPGASVKVS CKASGYMFTGYYIHWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDRFGS GNYGYMDVWGKGTTVTVSS	170	DIQMTQSPSSLSASVGDRVTITC RASQSIDRWLAWYQQKPGKAPK LLIYGASSLQSGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSYS TPWTFGQGTRLEIKR	195
21	EVQLLESGGGLVQPGGSLRLSC AASGFTFSSYAMSWVRQAPGK GLEWVSAISGSGGSTYYADSV KGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARELSHDYGGN SDFDYWGQGTLVTVSS	171	DIQMTQSPSSLSASVGDRVTITC QASQDISNNLNWYQQKPGKAPK LLIYAASGLQSGVPSRFSGSGSG TDFTLTISSLQPEDFATYYCQQA NSFPLTFGGGTKVEIKR	196

22	QVQLVQSGAEVKKPGASVKVS CKASGYTFTDYYIHWVRQAPG QGLEWMGWINPNSGGTNYAQ EFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDHRIAV AGSYFDYWGQGTLVTVSS	172	DIQMTQSPSSLSASVGDRVTITC RASRSIRTWLAWYQQKPGKAPK LLIYAASSLQTGVPSRFSGSGSGT DFTLTISSLQPEDFATYYCQQSYS TPYTFGQGTKLEIKR	197
23	QVQLVQSGAEVKKPGASVKVS CKASGYPFTAHYIHWVRQAPG QGLEWMGWINPNSGGTNYAQ KFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDVEMAT IGAYWYFDLWGRGTLVTVSS	173	DIQMTQSPSSLSASVGDRVTITC RASQGINNWLAWYQQKPGKAP KLLIYDASNLETGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQ ANSFPPTFGQGTKLEIKR	198
24	QVQLVQSGAEVKKPGSSVKVS CKASGYSFTSYGISWVRQAPG QGLEWLGWISAYNGNTNYGQ SLQGRVTITADESTSTAYMELS SLRSEDTAVYYCARARGAGTF FDYWGQGTLVTVSS	174	DIVMTQSPLSLPVTPGEPASISCR SSQSLLHSNGYNYLDWYLQKPG QSPQLLIYDATNLPTGVPDRFSG SGSGTDFTLKISRVEAEDVGVYY CMQALQTPFTFGQGTKLEIKR	199
25	QVQLVQSGAEVKKPGASVKVS CKASGYTFTGYYMHWVRQAP GQGLEWMGRINPNGGSTTYAQ KFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDDFYYY YLDFWGKGTTVTVSS	175	DIQMTQSPSSLSASVGDRVTITC RASQSINDWLAWYQQKPGKAP KLLIYAASNLQSGVPSRFSGSGS GTDFTLTISSLQPEDFATYYCQQ GYSTPPTFGQGTKVEIKR	200

Table 5a. Sequences of Anti-CD33 R69G-Selective Polypeptides (CDR Sequences)

Polypeptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
26	YTFTEN EMH	201	GWMN PNSGN TGYA	218	CAREG GDWPY YYMDV W	235	QASQDI RNYLN	252	AASSLQ S	269	CQQTSS TPLTF	286

27	YTLTG YYMH	202	GWMN PSSGNT GYA	219	CARASS DRYYY DGVWY FDLW	236	RASQDI RNNLG	253	GASSLQ S	270	CQQTYS SPPTF	287
28	FTFSTY AMH	203	SAISGS GGSTY YA	220	CARDG YGDYPF DYW	237	RASQGI DNYLA	254	QASTLE S	271	CQQSYS IPWTF	288
29	YTFTG YYLH	204	GVINV RRGST RYA	221	CARVS GSYYQP W	238	RASQSI SRWLA	255	DASNLE T	272	CQQGN SFPPIF	289
30	YTFSN YYMH	205	GWMN PDSGT TGYA	222	CVRDG TMVQGI FDYW	239	RASQSI SSWLA	256	GASSLQ S	273	CQQTY RTPLTF	290
31	GTFSTY AIT	206	GGIIPIV GRANY A	223	CARSG GHDLD YW	240	RASQGI GNDLG	257	GASSVQ S	274	CQQSYS TPITF	291
32	FTFSSY GMH	207	SSISGS GDTTY YA	224	CARDN PYGDY GGSFDY W	241	RASQSV SSSYLA	258	ATSTRA T	275	CQQYG SLPLTF	292
33	YTFTSY YMH	208	GIIDPS GGSTN YA	225	CARDY YGSGSY YGLDY W	242	RASQGI SNNLN	259	DASNLE T	276	CQQAN SFPLTF	293
34	YTFTD YYMH	209	GIINPS GGSTR YA	226	CARVD GRRWL QSDYW	243	RASQGI RNDLA	260	AASTLQ N	277	CQQSYS TPWTF	294
35	YTFTD YYMH	210	GIINPS GGSTR YA	227	CARVD GRRWL RSDYW	244	RASQGI RNDLA	261	AASTLQ N	278	CQQSYS TPWTF	295
36	GTFSSY AIS	211	GIISPS GRSAG YG	228	CARTD YGGHK WYFDL W	245	QASQGI NNYLN	262	AASTLQ R	279	CQQSY QTPLTF	296

37	YTFTG YYLH	212	GVISPS GGGTS YA	229	CARAG FGEGVF RHW	246	RASQSI SSYLN	263	AASSLQ S	280	CQQSYS TPLTF	297
38	YSFTSH AIS	213	GWIKP NSGDT KYA	230	CARGS DDYYG SYYFDY W	247	RASQGI SNYLA	264	TASTLQ S	281	CQQSYS TPLTF	298
39	FTFRNY GMG	214	SAISGS GGSTY YA	231	CARVK FYGMD VW	248	RASQGI SNDLA	265	GASNLE T	282	CQQAN SFPFTF	299
40	YTFTD YHMH	215	GWMSP NSGNT GYA	232	CARAD YYGSD YVKFD YW	249	RVSQGI SSYLN	266	EASTLE S	283	CQQGY STPPTF	300
41	YTFPN YGIS	216	GWINP NSGGT KYA	233	CARDR DILTGY YHFDY W	250	RSSQSL LQSNG YNYLD	267	LGSNRA S	284	CMQST HWPLTF	301
42	YTFTD YFMH	217	GWINP NSGNT GYA	234	CARLN DYGDY GGPATL DYW	251	RASQGI SNNLN	268	AASSLQ S	285	CQQSYS TPPTF	302

Table 5b. Sequences of Anti-CD33 R69G-Selective Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
26	QVQLVQSGAEVKKPGASVKV SCKASGYTFTENEMHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAREG GDWPYYYMDVWGKGTTVTV SS	303	DIQMTQSPSSLSASVGDRVTI TCQASQDIRNYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTSSTPLTFGPGTKVD IKR	320

27	QVQLVQSGAEVKKPGASVKV SCKASGYTLTGYYMHWVRQ APGQGLEWMGWMNPSSGNT GYAQQFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCAR ASSDRYYYDGVWYFDLWGR GTLVTVSS	304	DIQMTQSPSSLSASVGDRVTI TCRASQDIRNNLGWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYSSPPTFGQGTKLE IKR	321
28	EVQLLESGGGLVQPGGSLRLS CAASGFTFSTYAMHWVRQAP GKGLEWVSAISGSGGSTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDGYGD YPFDYWGQGTLVTVSS	305	DIQMTQSPSSLSASVGDRVTI TCRASQGIDNYLAWYQQKPG KAPKLLIYQASTLESGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPWTFGQGTKV EIKR	322
29	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYLHWVRQA PGQGLEWMGVINVRRGSTRY AQNFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARVSG SYYQPWGQGTLVTVSS	306	DIQMTQSPSSLSASVGDRVTI TCRASQSISRWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQGNSFPPIFGGGTKVE IKR	323
30	QVQLVQSGAEVKKPGASVKV SCKASGYTFSNYYMHWVRQA PGQGLEWMGWMNPDSGTTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCVRD GTMVQGIFDYWGQGTLVTVS S	307	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYRTPLTFGPGTKV DIKR	324
31	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSTYAITWVRQAP GQGLEWMGGIIPIVGRANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARSGGHDL DYWGQGTLVTVSS	308	DIQMTQSPSSLSASVGDRVTI TCRASQGIGNDLGWYQQKPG KAPKLLIYGASSVQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPITFGQGTRLEI KR	325

32	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYGMHWVRQAP GKGLEWVSSISGSGDTTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDNPYG DYGGSFDYWGQGTLVTVSS	309	EIVMTQSPATLSVSPGERATL SCRASQSVSSSYLAWYQQKP GQAPRLLIYATSTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYGSLPLTFGQGTK VEIKR	326
33	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIIDPSGGSTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDYYG SGSYYGLDYWGRGTLVTVSS	310	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPLTFGPGTKV DIKR	327
34	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWMGIINPSGGSTRYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARVDGR RWLQSDYWGQGTLVTVSS	311	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLAWYQQKPG KAPKLLIYAASTLQNGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKV EIKR	328
35	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWMGIINPSGGSTRYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARVDGR RWLRSDYWGQGTLVTVSS	312	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLAWYQQKPG KAPKLLIYAASTLQNGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKV EIKR	329
36	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWLGIISPSGRSAGYGR KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARTDYGG HKWYFDLWGRGTLVTVSS	313	DIQMTQSPSSLSASVGDRVTI TCQASQGINNYLNWYQQKPG KAPKLLIYAASTLQRGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYQTPLTFGGGTKV EIKR	330

37	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYLHWVRQA PGQGLEWMGVISPSGGGTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARAGFG EGVFRHWGQGTLVTVSS	314	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	331
38	QVQLVQSGAEVKKPGASVKV SCKASGYSFTSHAISWVRQAP GQGLEWMGWIKPNSGDTKYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGSDD YYGSYYFDYWGQGTLVTVSS	315	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYTASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	332
39	EVQLLESGGGLVQPGGSLRLS CAASGFTFRNYGMGWVRQAP GKGLEWVSAISGSGGSTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARVKFYG MDVWGQGTTVTVSS	316	DIQMTQSPSSLSASVGDRVTI TCRASQGISNDLAWYQQKPG KAPKLLIYGASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPFTFGPGTKV DIKR	333
40	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYHMHWVRQA PGQGLEWMGWMSPNSGNTG YAQNFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARA DYYGSDYVKFDYWGQGTLVT VSS	317	DIQMTQSPSSLSASVGDRVTI TCRVSQGISSYLNWYQQKPG KAPKLLIYEASTLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPPTFGQGTKVEI KR	334
41	QVQLVQSGAEVKKPGASVKV SCKASGYTFPNYGISWVRQAP GQGLEWMGWINPNSGGTKYA QRFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDRDI LTGYYHFDYWGQGTLVTVSS	318	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLQSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQSTHWPLTF GQGTRLEIKR	335

42	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYFMHWVRQA PGQGLEWMGWINPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARLND YGDYGGPATLDYWGQGTLVT VSS	319	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGQGTKLE IKR	336

Example 3: Identification of Anti-Human CLL-1 scFv Clones

[00451] Methods analogous to those above in Example 1 have been used to discover selective anti-human CLL-1 scFv clones. Selective anti-human CLL-1 scFv clones were discovered by standard screening methodologies of a human antibody library using two recombinant polymorphic forms of human CLL-1 extracellular domain antigens (CLL-1-K244 and CLL-1-Q244). Using these antigens various panning tactics were employed to encourage enrichment of thermostable clones of desired affinity range. The scFvs were screened for selective binding between two single nucleotide polymorphism (SNP) variants of human CLL-1 (Lysine 244 and Glutamine 244) by bio-layer interferometry (BLI).

Table 6a. Sequences of Anti-CLL-1 K244 Selective Polypeptides (CDR Sequences)

Polypeptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
43	YTFTNYYMH	337	GWISPYSGDTKYA	361	CARESMDRLDYW	385	RASQSISTYLN	409	DASNLET	433	CQQSYSTPVLTF	457
44	FTFSSYAMH	338	ADISGSGGLTYYA	362	CAREGDQYSSSSFFDYW	386	RSSQSLLHSNGYNYLD	410	LGSNRAS	434	CMQALQPPPTF	458
45	FTFDEFGMN	339	SYISGDSGYTNCA	363	CAAGYGGYYFDYW	387	QASQDIDIYLN	411	AASTLES	435	CQQSYSTPPTF	459
46	YTFTSYYMH	340	GMINPSAGSTSYA	364	CASVDSSGWYAPFDYW	388	RASQSISTYLN	412	DASNLET	436	CQQANSFPPTF	460
47	FTFDEYAMH	341	SAIGAGGSTYYA	365	CASSLGPELRGVDYYYYGMDVW	389	RSSQSLLHSNGYNYLD	413	AASSLQS	437	CMQGIQWPWTF	461
48	FNFDDYAMH	342	SVIYSGGSTYYA	366	CTRHDFDYW	390	RASQSISTYVN	414	AASSLQS	438	CQQDYSYPYTF	462
49	FTFSDYALH	343	SLISGDGGSTYYA	367	CARDLGGERSYW	391	RASQSISTWLA	415	AASTLQS	439	CLQDYSYPPTF	463
50	YTFTDYYMH	344	GIINPSDGSTTYA	368	CARDELPDSSGWYGYFQHW	392	RASQSISSWLA	416	AASSLQS	440	CQQSYDIPLTF	464
51	GTFSSYAIS	345	GEIIPFFGTANYA	369	CARAEYGGDLDYW	393	QASQDISNLLN	417	AASTLQS	441	CQQSYNTPWTF	465

52	DTFTRHYVH	346	GIINPRGGTHYA	370	CARRDCSGGSCYSDLDYW	394	QASQDIHNYLN	418	QASSLES	442	CQQANSFPLTF	466
53	GTFSSYAIS	347	GWINPDSGDASYA	371	CATFGEEAFDIW	395	RASQNIGSWLA	419	GASILQS	443	CQQANSFPLTF	467
54	GTFSSYAIS	348	GWIDPKNGDTNYA	372	CATEGSHHPYYYYGMDVW	396	RASQGIGNWLA	420	EASTLQS	444	CHQYNAYPWTF	468
55	YTFTGYHMH	349	GWINPNTGGTNYA	373	CARPNTAMVPPYYYYYGMDVW	397	QASQDISNYLN	421	AASSLQS	445	CQQYNSYPLTF	469
56	YTFTSYDIN	350	GWMNPNSGNTGYA	374	CARVSATGTYGLDYW	398	RASHSISSWLA	422	DASNLET	446	CQQADSFPLTF	470
57	YTFNNYGIT	351	GIINPITGVTTYA	375	CASGEQQLVLFDYW	399	QASQDINDYLN	423	GASNLQS	447	CLQHNSYPLTF	471
58	YTFTDYYLH	352	GWMNPNSGNTGYA	376	CAADVITAYGMDVW	400	RASQGISNYLA	424	DASNLET	448	CQQSYNVPPTF	472
59	FTFSNAWMS	353	ADISYDGTNDYYA	377	CTTEELRFGGFDYW	401	RASQSISSYLN	425	DASNLET	449	CQQANSFPLTF	473
60	GTFSSYAIS	354	GGIIPMFGTANYA	378	CARDLGYSNAGGTLHYW	402	RASQSIGTYLA	426	DASSRAT	450	CQQYKSYPLTF	474
61	YTFTNYYMH	355	GIINPSGGSTSYA	379	CARAEWDILTGYYIDYW	403	QASQDISNYLN	427	GASSLQS	451	CQQHNSYPWTF	475

62	YTFTDHFVH	356	GWISAYNGNTNYA	380	CARAEYSYGFDYW	404	RASQGIHNYLA	428	DASNLET	452	CQQTSSFPYTF	476
63	YTFTGYYVH	357	GVINPSGGGSPSYA	381	CARDRSDVDYGMDVW	405	QASQDISNYLN	429	DASNLQS	453	CLQHNSYPLTF	477
64	YTFTDYYMH	358	GLIDPSGGSTNSL	382	CARDVGFGELSFDIW	406	RSSQSLLHSNGYNYLD	430	AASTLQS	454	CMQGTHWPPTF	478
65	YTFTGYYMH	359	GWINPNSGGTNYA	383	CAREIGGYDNYYYYGMDVW	407	RASQSIGTYLN	431	AASSLQS	455	CQQSYTDPWTF	479
66	YTFNTYYMH	360	GWMHPNTGNTGYA	384	CARGTTSDAFDIW	408	RASQSIFSYLN	432	SASNLQS	456	CQQSYSTPITF	480

Table 6b. Sequences of Anti-CLL-1 K244 Selective Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
43	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWLGWISPYSGDTKYAQTLQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARESMDRLDYWGQGTLVTVSS	481	DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPVLTFGGGTKVEIKR	505
44	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVADISGSGGLTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREGDQYSSSSFFDYWGQGTLVTVSS	482	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQPPPTFGQGTRLEIKR	506

45	EVQLVESGGGLVKPGGSLRLS CAASGFTFDEFGMNWVRQAP GKGLEWISYISGDSGYTNCAD SVKGRFTISRDDSKNTLYLQM NSLKTEDTAVYYCAAGYGGY YFDYWGQGTLVTVSS	483	DIQMTQSPSSLSASVGDRVTI TCQASQDIDIYLNWYQQKPG KAPKLLIYAASTLESGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGGGTKV EIKR	507
46	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGMINPSAGSTSY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCASVDS SGWYAPFDYWGQGTLVTVSS	484	DIQMTQSPSSLSASVGDRVTI TCRASQSISTYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPPTFGGGTKV EIKR	508
47	EVQLLESGGGLVQPGGSLRLS CAASGFTFDEYAMHWVRQAP GKGLEWVSAIGAGGSTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCASSLGPEL RGVDYYYYGMDVWGQGTTV TVSS	485	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASSLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGIQWPWTF GQGTKVEIKR	509
48	EVQLLESGGGLVQPGGSLRLS CAASGFNFDDYAMHWVRQA PGKGLEWVSVIYSGGSTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCTRHDFDY WGQGTLVTVSS	486	DIQMTQSPSSLSASVGDRVTI TCRASQSISTYVNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQDYSYPYTFGQGTKV EIKR	510
49	EVQLVESGGGLVKPGGSLRLS CAASGFTFSDYALHWVRQAP GKGLEWVSLISGDGGSTYYA DSVKGRFTISRDDSKNTLYLQ MNSLKTEDTAVYYCARDLGG ERSYWGQGTLVTVSS	487	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCLQDYSYPPTFGQGTKV EIKR	511

50	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWMGIINPSDGSTTYA QSFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDELP DSSGWYGYFQHWGQGTLVT VSS	488	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYDIPLTFGGGTKVE IKR	512
51	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGEIIPFFGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARAEYGG DLDYWGQGTLVTVSS	489	DIQMTQSPSSLSASVGDRVTI TCQASQDISNLLNWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYNTPWTFGPGTKV DIKR	513
52	QVQLVQSGAEVKKPGASVKV SCKASGDTFTRHYVHWVRQA PGQGLEWMGIINPRGGTHYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARRDCS GGSCYSDLDYWGQGTLVTVS S	490	DIQMTQSPSSLSASVGDRVTI TCQASQDIHNYLNWYQQKPG KAPKLLIYQASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQANSFPLTFGGGTKLEI KR	514
53	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGWINPDSGDASYA RKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCATFGEE AFDIWGQGTMVTVSS	491	DIQMTQSPSSLSASVGDRVTI TCRASQNIGSWLAWYQQKPG KAPKLLIYGASILQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQANSFPLTFGGGTKLEI KR	515
54	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGWIDPKNGDTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCATEGS HHPYYYYGMDVWGQGTTVT VSS	492	DIQMTQSPSSLSASVGDRVTI TCRASQGIGNWLAWYQQKP GKAPKLLIYEASTLQSGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCHQYNAYPWTFGQGT KVEIKR	516

55	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYHMHWVRQA PGQGLEWMGWINPNTGGTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARPNT AMVPPYYYYYGMDVWGQGT LVTVSS	493	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYNSYPLTFGQGTKL EIKR	517
56	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDINWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARVSA TGTYGLDYWGQGTLVTVSS	494	DIQMTQSPSSLSASVGDRVTI TCRASHSISSWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQADSFPLTFGGGTKV EIKR	518
57	QVQLVQSGAEVKKPGASVKV SCKASGYTFNNYGITWVRQAP GQGLEWMGIINPITGVTTYAQ NFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCASGEQQL VLFDYWGQGTLVTVSS	495	DIQMTQSPSSLSASVGDRVTI TCQASQDINDYLNWYQQKPG KAPKLLIYGASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCLQHNSYPLTFGQGTKL EIKR	519
58	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYLHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAAD VITAYGMDVWGQGTMVTVSS	496	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYNVPPTFGQGTKV EIKR	520
59	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNAWMSWVRQAP GKGLEWVADISYDGTNDYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCTTEELRF GGFDYWGQGTLVTVSS	497	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPLTFGQGTKV EIKR	521

60	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGGIIPMFGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARDLGYS NAGGTLHYWGQGTLVTVSS	498	EIVMTQSPATLSVSPGERATL SCRASQSIGTYLAWYQQKPG QAPRLLIYDASSRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYKSYPLTFGGGTKVE IKR	522
61	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARAEW DILTGYYIDYWGQGTLVTVSS	499	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQHNSYPWTFGQGTK VEIKR	523
62	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDHFVHWVRQA PGQGLEWMGWISAYNGNTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARAEY SYGFDYWGQGTLVTVSS	500	DIQMTQSPSSLSASVGDRVTI TCRASQGIHNYLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTSSFPYTFGQGTKLE IKR	524
63	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYVHWVRQA PGQGLEWMGVINPSGGGSPSY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDRS DVDYGMDVWGQGTTVTVSS	501	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYDASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCLQHNSYPLTFGGGTKV EIKR	525
64	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWMGLIDPSGGSTNSL QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDVGF GELSFDIWGQGTTVTVSS	502	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASTLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGTHWPPTF GPGTKVDIKR	526

65	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAREIG GYDNYYYYGMDVWGQGTTV TVSS	503	DIQMTQSPSSLSASVGDRVTI TCRASQSIGTYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYTDPWTFGQGTKV EIKR	527
66	QVQLVQSGAEVKKPGASVKV SCKASGYTFNTYYMHWVRQA PGQGLEWMGWMHPNTGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARGT TSDAFDIWGQGTMVTVSS	504	DIQMTQSPSSLSASVGDRVTI TCRASQSIFSYLNWYQQKPG KAPKLLIYSASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPITFGQGTKVE IKR	528

Table 7a. Sequences of Anti-CLL-1 K244Q Selective Polypeptides (CDR Sequences)

Polypeptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
67	DTFTR HYVH	529	GRVNP RDGRT NSA	551	CAKD MFPTV TGTYY YYGM DVW	573	RASQG ISSYLA	595	DASNL ET	617	CQQAS GFPYT F	639
68	YTFSS YDIN	530	GWINP RNGGT DYA	552	CARHR WELDS FDYW	574	RASQSI SNYLN	596	ATSSL QS	618	CQQGY NIPFTF	640
69	YTFTS YYIH	531	GWMN PNDGK TAYA	553	CARDD DYGGY VAYW	575	RASESI SGWLA	597	DASNL ET	619	CQQYD TWPFT F	641
70	MSVTS NHMS	532	SSIYPD GKTYY A	554	CARDE EDWFD PW	576	QASQSI SNWLA	598	AASTL QS	620	CQQSY STPWT F	642

71	FTFSN HYMS	533	AVIWP DGSKE YYA	555	CARED YYGSG MDYW	577	QASQD ISNYL N	599	GASTL QS	621	CQQYD SYPPTF	643
72	GTFSN YAIS	534	GWISA YNGNS DYA	556	CAIGD YFDY W	578	QASED INKYL N	600	DASNL ET	622	CQQAN SFPLTF	644
73	FTVSS NYMS	535	AVIYS DGKTY YA	557	CARED SSGSH FDYW	579	RASQSI STYLN	601	DASNL ET	623	CQQAH SFPPTF	645
74	YTFTK YEIN	536	GGIIPIF GTANY A	558	CARGS GWYTP LFDYW	580	RASQG ISNNL N	602	DASYL ET	624	CQQSY SAPLTF	646
75	YTFTD YYIH	537	GLIDPS GGSTSI A	559	CARDY DILTGS GFDPW	581	RASQS VSSYL A	603	DASAR AT	625	CQQYR SSVTF	647
76	YTFTT YYMH	538	GIINVS AGTTS YA	560	CAKEP YPHQS GWFFD YW	582	QASQD INNYL N	604	DASNL ET	626	CQQAN SFPLTF	648
77	YTFTG HYMH	539	GWIST DNGNA NYA	561	CARDT ADYYF DYW	583	SASQS VGSSY FA	605	DVSTR AT	627	CQQYY STPLTF	649
78	GTFSR YPFS	540	GWMN PNNGD TGYA	562	CARGD YPYMD VW	584	QASQD ISNYL N	606	DASNL ET	628	CQQSY SIPYTF	650
79	YTFTS DYMH	541	GWMN PNSGG TNYA	563	CARDY ITGPSD W	585	RASQG IRNDL G	607	AASSL QP	629	CLQTN SFPWT F	651
80	FTFTSY YMH	542	GWMN PNSGN TGYA	564	CARGH SRTDY	586	RASQSI SSWLA	608	DTSSL QS	630	CQQGY STPLTF	652

					GMDV W							
81	FTFSD HYMS	543	SIIYPD GKTYY A	565	CAREG SYGDY DGMD VW	587	QASQD ISNYL N	609	GASTL QS	631	CQQSY STPWT F	653
82	GTFSN YDIS	544	GGIIPIF GTANY A	566	CAREA EEGGW FDPW	588	RASQS VSSYL A	610	GASTR AT	632	CQQYA FSPITF	654
83	YTFTD YYMH	545	GWMN PNSGY TAYA	567	CAKDT PGSGW SSGMD VW	589	RVSQG ISSYLN	611	DASNL ET	633	CQQSY STPLTF	655
84	GTFSN YAIS	546	GWINP NSGGT NYA	568	CARVG YYDSS GGGM DVW	590	RASQSI SSWLA	612	DASNL ET	634	CLQTH SFPLTF	656
85	YTFTG YYMH	547	GIINPI GGLTT YA	569	CASGA YGDYV DWYF DLW	591	RASQS VSNWL A	613	DASNL QT	635	CQQAN SFPLTF	657
86	YTFTT YGIS	548	GWINP NSGDT NYA	570	CARLT TATDS FDLW	592	RSSRSL LHSNG YNYLD	614	LGSYR AS	636	CMQGT HWPPT F	658
87	YSFTN YYIH	549	GWMN PYTGQ TGYA	571	CTTDE ETMDF HLW	593	RASQSI SRYLN	615	DASNL ET	637	CQQAN TFPITF	659
88	YTFTG YHIH	550	GRINP NSGGT DYA	572	CARET YSGSY EESFD YW	594	RSSRSL LHSNG YNYLD	616	LGSDR AS	638	CMQGT HWPPT F	660

Table 7b. Sequences of Anti-CLL-1 K244Q Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
67	QVQLVQSGAEVKKPGASVKV SCKASGDTFTRHYVHWVRQA PGQGLEWMGRVNPRDGRTNS AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDM FPTVTGTYYYYGMDVWGQG TTVTVSS	661	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQASGFPYTFGQGTRL EIKR	683
68	QVQLVQSGAEVKKPGASVKV SCKASGYTFSSYDINWVRQAP GQGLEWVGWINPRNGGTDYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARHRWE LDSFDYWGQGTLVTVSS	662	DIQMTQSPSSLSASVGDRVTI TCRASQSISNYLNWYQQKPG KAPKLLIYATSSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQGYNIPFTFGQGTKLEI KR	684
69	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYIHWVRQAP GQGLEWMGWMNPNDGKTAY AQRFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDD DYGGYVAYWGQGTLVTVSS	663	DIQMTQSPSSLSASVGDRVTI TCRASESISGWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYDTWPFTFGPGTKV DIKR	685
70	EVQLLESGGGLVQPGGSLRLS CAASGMSVTSNHMSWVRQAP GKGLEWVSSIYPDGKTYYADS VKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARDEEDWF DPWGQGTLVTVSS	664	DIQMTQSPSSLSASVGDRVTI TCQASQSISNWLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKV EIKR	686

71	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNHYMSWVRQAP GKGLEWVAVIWPDGSKEYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAREDYY GSGMDYWGQGTLVTVSS	665	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYGASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYDSYPPTFGGGTKV EIKR	687
72	QVQLVQSGAEVKKPGASVKV SCKASGGTFSNYAISWVRQAP GQGLEWMGWISAYNGNSDY AQNLQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAIGDY FDYWGQGTLVTVSS	666	DIQMTQSPSSLSASVGDRVTI TCQASEDINKYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPLTFGQGTKV EIKR	688
73	EVQLLESGGGLVQPGGSLRLS CAASGFTVSSNYMSWVRQAP GKGLEWVAVIYSDGKTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAREDSSGS HFDYWGQGTLVTVSS	667	DIQMTQSPSSLSASVGDRVTI TCRASQSISTYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAHSFPPTFGQGTRLE IKR	689
74	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTKYEINWVRQAP GQGLEWMGGIIPIFGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARGSGWY TPLFDYWGQGTLVTVSS	668	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLNWYQQKPG KAPKLLIYDASYLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSAPLTFGQGTKV EIKR	690
75	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYIHWVRQAP GQGLEWMGLIDPSGGSTSIAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARDYDIL TGSGFDPWGQGTLVTVSS	669	EIVMTQSPATLSVSPGERATL SCRASQSVSSYLAWYQQKPG QAPRLLIYDASARATGIPARF SGSGSGTEFTLTISSLQSEDFA VYYCQQYRSSVTFGQGTRLEI KR	691

76	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYYMHWVRQA PGQGLEWMGIINVSAGTTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAKEPYP HQSGWFFDYWGQGTLVTVSS	670	DIQMTQSPSSLSASVGDRVTI TCQASQDINNYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPLTFGGGTKV EIKR	692
77	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGHYMHWVRQA PGQGLEWMGWISTDNGNANY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDTA DYYFDYWGQGTLVTVSS	671	EIVMTQSPATLSVSPGERATL SCSASQSVGSSYFAWYQQKP GQAPRLLIYDVSTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYYSTPLTFGPGTK VDIKR	693
78	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSRYPFSWVRQAP GQGLEWMGWMNPNNGDTGY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARGDYP YMDVWGKGTTVTVSS	672	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPYTFGQGTKLE IKR	694
79	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSDYMHWVRQA PGQGLEWMGWMNPNSGGTN YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARD YITGPSDWGQGTLVTVSS	673	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPG KAPKLLIYAASSLQPGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCLQTNSFPWTFGQGTKL EIKR	695
80	QVQLVQSGAEVKKPGASVKV SCKASGFTFTSYYMHWVRQA PGQGLEWMGWMNPNSGNTG YAQRFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARG HSRTDYGMDVWGQGTTVTVS S	674	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDTSSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPLTFGQGTKVEI KR	696

81	EVQLLESGGGLVQPGGSLRLS CAASGFTFSDHYMSWVRQAP GKGLEWVSIIYPDGKTYYADS VKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAREGSYGD YDGMDVWGQGTTVTVSS	675	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYGASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKL EIKR	697
82	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSNYDISWVRQAP GQGLEWMGGIIPIFGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAREAEEGG WFDPWGQGTLVTVSS	676	EIVMTQSPATLSVSPGERATL SCRASQSVSSYLAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYAFSPITFGQGTKLEI KR	698
83	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWMGWMNPNSGYTA YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAKD TPGSGWSSGMDVWGQGTTVT VSS	677	DIQMTQSPSSLSASVGDRVTI TCRVSQGISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	699
84	QVQLVQSGAEVKKPGASVKV SCKASGGTFSNYAISWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARVGYY DSSGGGMDVWGQGTTVTVSS	678	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCLQTHSFPLTFGPGTKVD IKR	700
85	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGIINPIGGLTTYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCASGAYG DYVDWYFDLWGRGTLVTVSS	679	DIQMTQSPSSLSASVGDRVTI TCRASQSVSNWLAWYQQKP GKAPKLLIYDASNLQTGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQANSFPLTFGGGTK LEIKR	701

86	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYGISWVRQAP GQGLEWMGWINPNSGDTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARLTTA TDSFDLWGRGTLVTVSS	680	DIVMTQSPLSLPVTPGEPASIS CRSSRSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSYRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGTHWPPTF GQGTKLEIKR	702
87	QVQLVQSGAEVKKPGASVKV SCKASGYSFTNYYIHWVRQAP GQGLEWMGWMNPYTGQTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCTTDEE TMDFHLWGRGTLVTVSS	681	DIQMTQSPSSLSASVGDRVTI TCZASQSISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANTFPITFGQGTRLE IKR	703
88	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYHIHWVRQAP GQGLEWMGRINPNSGGTDYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARETYS GSYEESFDYWGQGTLVTVSS	682	DIVMTQSPLSLPVTPGEPASIS CRSSRSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSDRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGTHWPPTF GQGTKVEIKR	704

Example 4: Flow Cytometry (FACS)

[00452] For CD33. Jurkat cells were engineered to stably express either the huCD33-R69 or huCD33-G69 variant at > 200,000 receptors per cell. Parental, huCD33-R69, and huCD33-G69 Jurkat cell lines were stained with differing levels of CellTrace Violet Cell Proliferation Kit (ThermoFisher, cat. # C34557) to barcode each cell line. Barcoded Jurkat cell lines were fixed with paraformaldehyde and incubated with myc-labeled scFv periplasmic extracts and a secondary anti-myc PE-conjugated monoclonal antibody. Appropriate positive and negative controls were used. Stained cells were analyzed by flow cytometry (CytoFLEX, Beckman Coulter, Inc.) and binding was assessed by change in PE mean fluorescence intensity (MFI) of the barcoded cell populations.

[00453] For FLT3, Ramos cells were engineered to stably express either the huFLT3-T227 or huFLT3-M227 variant at > 200,000 receptors per cell. Parental, huFLT3-T227, and huFLT3-M227 Ramos cell lines were stained with differing levels of CellTrace Violet Cell Proliferation Kit (ThermoFisher, cat. # C34557) to barcode each cell line. Barcoded Ramos cell lines were fixed with paraformaldehyde and incubated with myc-labeled scFv periplasmic extracts and a secondary anti-myc PE-conjugated monoclonal antibody. Appropriate positive and negative controls were used. Stained cells were analyzed by flow cytometry (CytoFLEX, Beckman Coulter, Inc.) and binding was assessed by change in PE mean fluorescence intensity (MFI) of the barcoded cell populations.

[00454] Results from this assay for CD33 are shown in Table 8a, reporting fold change over parental as (-), indicating < 2 fold; (+), indicating 2-10 fold; (++), indicating 10-30 fold; and (+++), indicating > 30 fold. Data are also visualized in **Fig.s 2 and 3.**

Table 8a. Polypeptide Selectivity – CD33

Polypeptide No.	CD33 G69 Geometric Mean Fold Change over Jurkat Parental	CD33 R69 Geometric Mean Fold Change over Jurkat Parental
1	-	+++
2	-	++
3	-	+++
4	-	+++
5	-	+++

6	-	+++
7	-	++
8	-	++
9	-	+
10	-	+
11	-	+
12	-	+
13	-	++
14	-	+++
15	-	+
16	-	+
17	-	+
18	-	+
19	-	+++
20	-	++
21	-	+
22	-	+
23	-	+
24	-	+++
25	-	+++

26	+	-
27	+	-
28	++	-
29	+	-
30	++	-
31	++	-
32	++	-
33	+++	-
34	+	-
35	+	-
36	+	-
37	+	-
38	+++	-
39	++	-
40	++	-
41	+	-
42	++	-

[00455] The foregoing methods may be adapted to demonstrate the binding and polymorphic selectivity of other scFvs against antigens such as cancer antigens. For example, the methods are expected to demonstrate anti-FLT3 scFvs that selectively bind either the T227 or T227M polymorphism.

Example 5: Bio-Layer Interferometry (BLI)

[00456] Discovered scFvs were analyzed for binding to huCD33-R69-His or huCD33-G69-Fc recombinant proteins (for anti-CD33 scFvs; for CLL-1 scFvs, huCLL1-K244-Avi-Tev-His or huCLL1-Q244-Avi-Tev-His were used; for FLT3, huFLT3-T227-His or huFLT3-M227-Fc were used) using BLI on a ForteBio Octet HTX instrument. Streptavidin-coated biosensors were loaded with biotinylated anti-V5 tag monoclonal antibody for 5 min and were then quenched and blocked with 20 μM amine-PEG2-Biotin for 5 min. scFvs were captured on biosensors from scFv clone periplasmic extracts. huCD33 (or huCLL-1, or huFLT3) proteins were then associated with the captured scFvs for 2 minutes, followed by dissociation with buffer (1X HBST [10 mM HEPES pH 7.4, 150 mM NaCl, 0.05% Tween-20], 1 g/L BSA) for 5 minutes. Data was buffer referenced subtracted against a negative control scFv and report points were collected at a time point (115-sec or 119-sec) just before the end of the association step to assess yes/no binding. Data was fitted with 1:1 Langmuir equation and off-rate values were reported.

[00457] Results from this assay for CD33 are shown in Table 9a, reporting binding, no binding, or ambiguous.

Table 9a. Polypeptide Selectivity – CD33

Polypeptide No.	CD33 R69 BLI/Octet Binding	CD33 G69 BLI/Octet Binding
1	Yes	No
2	Yes	No
3	Yes	No
4	Yes	No
5	Yes	No
6	Yes	No
7	Yes	No
8	Yes	No
9	Yes	No
10	Yes	No

11	Yes	No
12	Yes	No
13	Yes	No
14	Yes	No
15	Yes	No
16	Yes	No
17	Yes	No
18	Yes	No
19	Yes	No
20	Yes	No
21	Yes	No
22	Yes	No
23	Yes	No
24	Yes	No
25	Yes	No
26	No	Yes
27	No	Yes
28	No	Yes
29	No	Yes
30	No	Yes
31	No	Yes
32	No	Yes
33	No	Yes
34	No	Yes
35	No	Yes
36	No	Yes
37	No	Yes
38	No	Yes
39	No	Yes
40	No	Yes
41	No	Yes
42	No	Yes

[00458] Analogous methods were used to assess selectivity of binding of polypeptides to CLL-1 K244 or CLL-1 Q244. Results from this assay are shown in Table 9b, reporting binding, no binding, or ambiguous.

Table 9b. Polypeptide Selectivity – CLL-1

Polypeptide No.	CLL-1 K244 BLI/Octet Binding	CLL-1 Q244 BLI/Octet Binding
43	Yes	No
44	Yes	No
45	Yes	No
46	Yes	No
47	Yes	No
48	Yes	No
49	Yes	No
50	Yes	No
51	Yes	No
52	Yes	No
53	Yes	No
54	Yes	No
55	Yes	No
56	Yes	No
57	Yes	No
58	Yes	No
59	Yes	No
60	Yes	No
61	Yes	No
62	Yes	No
63	Yes	No
64	Yes	No
65	Yes	No
66	Yes	No
67	No	Yes
68	No	Yes
69	No	Yes
70	No	Yes
71	No	Yes
72	No	Yes
73	No	Yes
74	No	Yes
75	No	Yes
76	No	Yes
77	No	Yes

78	No	Yes
79	No	Yes
80	No	Yes
81	No	Yes
82	No	Yes
83	No	Yes
84	No	Yes
85	No	Yes
86	No	Yes
87	No	Yes
88	No	Yes

Example 6: Chimeric Antigen Receptors Comprising ScFvs

[00459] Below in Tables 10 and Table 11 are provided examples of chimeric antigen receptors comprising scFvs as disclosed herein that may be constructed and expressed in immune effector cells according to methods known in the art and disclosed herein (CAR Examples 1-60). Tables 10 and 11 are intended to provide examples of how CARs comprising the V_H and V_L chains of the scFvs disclosed herein may be constructed. Further CARs may be constructed from other scFv V_H and V_L chains disclosed herein.

[00460] The CARs in Table 10 below are of the form:

|—[(signal)(scFv V_H)(linker)(scFv V_L)(hinge)(TMD)(costim)(effector)]—| + (tag)

or

|—[(signal)(scFv V_L)(linker)(scFv V_H)(hinge)(TMD)(costim)(effector)]—| + (tag),

wherein:

- the CD8a signal sequence MALPVTALLLPLALLLHAARP has SEQ ID NO: 1521, or alternatively, one of SEQ ID NO.s 1522-1525 may be used;
- the $(GGGGS)_4$ linker has SEQ ID NO: 1536, or alternatively, one of SEQ ID NO.s 1532-1535 may be used;
- the CD8 hinge sequence TTTPAPRPPTPAPTIASQPLSLRPEACRPAAGGAVHTR GLDFACD has SEQ ID NO: 1526;
- the CD28 transmembrane domain sequence FWVLVVVGGVLACYSLLVTVAFIIFWV has SEQ ID NO: 1527;

- the CD28 costim domain sequence RSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAP PRDFAAYRS has SEQ ID NO: 1530;
- the 4-1BB costim domain sequence KRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCEL has SEQ ID NO: 1529;
- the CD3z effector domain sequence RVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR has SEQ ID NO: 1531;
- P2A sequence GSGATNFSLLKQAGDVEENPGP has SEQ ID NO: 1532;
- the CD34 tag sequence MPRGWTALCLLSLLPSGFMSLDNNGTATPELPTQGTFSNV STNVSYQETTTPSTLGSTSLHPVSQHGNEATTNITETTVKFTSTSVITSVYGNTNSS VQSQTSVISTVFTTPANVSTPETTLKPSLSPGNVSDLSTTSTSLATSPTKPYTSSSPI LSDIKAEIKCSGIREVKLTQGICLEQNKTSSCAEFKKDRGEGLARVLCGEEQADA DAGAQVCSLLLAQSEVRPQCLLLVLANRTEISSKLQLMKKHQSDLKKLGILDFTE QDVASHQSYSQKTLIALVTSGALLAVLGITGYFLMNRRSWSPI has SEQ ID NO: 1537, or alternatively, a variant or truncated CD34 sequence may be used;
- the V_H and V_L domains of Ex.s 1-3 and 31-33, are from Polypeptide 1, e.g., SEQ ID NO: 151 and SEQ ID NO: 176, respectively;
- the V_H and V_L domains of Ex.s 4-6 and 34-36, are from Polypeptide 5, e.g., SEQ ID NO: 155 and SEQ ID NO: 180, respectively;
- the V_H and V_L domains of Ex.s 7-9 and 37-39, are from Polypeptide 6, e.g., SEQ ID NO: 156 and SEQ ID NO: 181, respectively;
- the V_H and V_L domains of Ex.s 10-12 and 40-42, are from Polypeptide 7, e.g., SEQ ID NO: 157 and SEQ ID NO: 182, respectively;
- the V_H and V_L domains of Ex.s 13-15 and 43-45, are from Polypeptide 25, e.g., SEQ ID NO: 175 and SEQ ID NO: 200, respectively;
- the V_H and V_L domains of Ex.s 16-18 and 46-48, are from Polypeptide 30, e.g., SEQ ID NO: 307 and SEQ ID NO: 324, respectively;
- the V_H and V_L domains of Ex.s 19-21 and 49-51, are from Polypeptide 31, e.g., SEQ ID NO: 308 and SEQ ID NO: 325, respectively;
- the V_H and V_L domains of Ex.s 22-24 and 52-54, are from Polypeptide 32, e.g., SEQ ID NO: 309 and SEQ ID NO: 326, respectively;

- the V_H and V_L domains of Ex.s 25-27 and 55-57, are from Polypeptide 33, e.g., SEQ ID NO: 310 and SEQ ID NO: 337, respectively; and
- the V_H and V_L domains of Ex.s 28-30 and 58-60, are from Polypeptide 38, e.g., SEQ ID NO: 315 and SEQ ID NO: 332, respectively.

Table 10. CAR Constructs

CAR Ex.	CD8a Signal SEQ ID NO	VH or VL SEQ ID NO	$(GGGGS)_4$ Linker SEQ ID NO	VH or VL SEQ ID NO	CD8 Hinge SEQ ID NO	CD28 TMD SEQ ID NO	CD28 CoStim SEQ ID NO	4-1BB CoStim SEQ ID NO	CD3z Effector SEQ ID NO
1	1521	151	1536	176	1526	1527	1530	-	1531
2	1521	151	1536	176	1526	1527	-	1529	1531
3	1521	151	1536	176	1526	1527	1530	1529	1531
4	1521	155	1536	180	1526	1527	1530	-	1531
5	1521	155	1536	180	1526	1527	-	1529	1531
6	1521	155	1536	180	1526	1527	1530	1529	1531
7	1521	156	1536	181	1526	1527	1530	-	1531
8	1521	156	1536	181	1526	1527	-	1529	1531
9	1521	156	1536	181	1526	1527	1530	1529	1531
10	1521	157	1536	182	1526	1527	1530	-	1531
11	1521	157	1536	182	1526	1527	-	1529	1531
12	1521	157	1536	182	1526	1527	1530	1529	1531
13	1521	175	1536	200	1526	1527	1530	-	1531
14	1521	175	1536	200	1526	1527	-	1529	1531
15	1521	175	1536	200	1526	1527	1530	1529	1531
16	1521	307	1536	324	1526	1527	1530	-	1531
17	1521	307	1536	324	1526	1527	-	1529	1531
18	1521	307	1536	324	1526	1527	1530	1529	1531
19	1521	308	1536	325	1526	1527	-	1529	1531
20	1521	308	1536	325	1526	1527	1530	1529	1531
21	1521	308	1536	325	1526	1527	1530	-	1531
22	1521	309	1536	326	1526	1527	-	1529	1531
23	1521	309	1536	326	1526	1527	1530	1529	1531
24	1521	309	1536	326	1526	1527	1530	-	1531
25	1521	310	1536	327	1526	1527	-	1529	1531
26	1521	310	1536	327	1526	1527	1530	1529	1531
27	1521	310	1536	327	1526	1527	1530	-	1531
28	1521	315	1536	332	1526	1527	-	1529	1531
29	1521	315	1536	332	1526	1527	1530	1529	1531
30	1521	315	1536	332	1526	1527	1530	-	1531
31	1521	176	1536	151	1526	1527	1530		1531

32	1521	176	1536	151	1526	1527		1529	1531
33	1521	176	1536	151	1526	1527	1530	1529	1531
34	1521	180	1536	155	1526	1527	1530		1531
35	1521	180	1536	155	1526	1527		1529	1531
36	1521	180	1536	155	1526	1527	1530	1529	1531
37	1521	181	1536	156	1526	1527	1530		1531
38	1521	181	1536	156	1526	1527		1529	1531
39	1521	181	1536	156	1526	1527	1530	1529	1531
40	1521	182	1536	157	1526	1527	1530		1531
41	1521	182	1536	157	1526	1527		1529	1531
42	1521	182	1536	157	1526	1527	1530	1529	1531
43	1521	200	1536	175	1526	1527	1530		1531
44	1521	200	1536	175	1526	1527		1529	1531
45	1521	200	1536	175	1526	1527	1530	1529	1531
46	1521	324	1536	307	1526	1527	1530		1531
47	1521	324	1536	307	1526	1527		1529	1531
48	1521	324	1536	307	1526	1527	1530	1529	1531
49	1521	325	1536	308	1526	1527		1529	1531
50	1521	325	1536	308	1526	1527	1530	1529	1531
51	1521	325	1536	308	1526	1527	1530		1531
52	1521	326	1536	309	1526	1527		1529	1531
53	1521	326	1536	309	1526	1527	1530	1529	1531
54	1521	326	1536	309	1526	1527	1530		1531
55	1521	327	1536	310	1526	1527		1529	1531
56	1521	327	1536	310	1526	1527	1530	1529	1531
57	1521	327	1536	310	1526	1527	1530		1531
58	1521	332	1536	315	1526	1527		1529	1531
59	1521	332	1536	315	1526	1527	1530	1529	1531
60	1521	332	1536	315	1526	1527	1530		1531

[00461] Accordingly, provided herein are chimeric antigen receptors comprising the sequences disclosed in the following illustrative examples.

Table 11. CAR Sequences

CAR Ex. No.	SEQ ID NO.	CAR Sequence

1	1539	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQTINDW LAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQAYSTPWTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYIHW VRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSSGGGGSGGGGSGGG GSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMK GERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
2	1540	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQTINDW LAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQAYSTPWTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYIHW VRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSSGGGGSGGGGSGGG GSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRP VQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLG RREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMK GERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
3	1541	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQTINDW LAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQAYSTPWTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYSFTGYYIHW VRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSSGGGGSGGGGSGGG GSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTP RRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGC SCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDK RRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHD GLYQGLSTATKDTYDALHMQALPPR
4	1542	MALPVTALLLPLALLLHAARPDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLDWYLQKPGQSPQLLIYLGSDRASGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCMQGLQTPITFGQGTRLEIKRTTTPAPRPPTPAPTIASQPLSLRPEA CRPAAGGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGNTFTSY GISWVRQAPGQGLEWMGWINPNSGGTKYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARESWFGELYYGMDVWGKGTTVTVSSGGGGSGGGGS GGGGSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
5	1543	MALPVTALLLPLALLLHAARPDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLDWYLQKPGQSPQLLIYLGSDRASGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCMQGLQTPITFGQGTRLEIKRTTTPAPRPPTPAPTIASQPLSLRPEA CRPAAGGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGNTFTSY GISWVRQAPGQGLEWMGWINPNSGGTKYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARESWFGELYYGMDVWGKGTTVTVSSGGGGSGGGGS GGGGSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPF MRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

6	1544	MALPVTALLLPLALLLHAARPDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSN GYNYLDWYLQKPGQSPQLLIYLGSDRASGVPDRFSGSGSGTDFTLKISRVEA EDVGVYYCMQGLQTPITFGQGTRLEIKRTTTPAPRPPTPAPTIASQPLSLRPEA CRPAAGGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGNTFTSY GISWVRQAPGQGLEWMGWINPNSGGTKYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARESWFGELYYGMDVWGKGTTVTVSSGGGGSGGGGS GGGGSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMN MTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
7	1545	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYEASTLETGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQANSFPFTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTAYYTHWV RQAPGQGLEWMGWMNPNSGHTSYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCAREAYDSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGS FWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTR KHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
8	1546	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYEASTLETGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQANSFPFTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTAYYTHWV RQAPGQGLEWMGWMNPNSGHTSYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCAREAYDSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGS FWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEE DGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDV LDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGK GHDGLYQGLSTATKDTYDALHMQALPPR
9	1547	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSISSYL NWYQQKPGKAPKLLIYEASTLETGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQANSFPFTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTAYYTHWV RQAPGQGLEWMGWMNPNSGHTSYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCAREAYDSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGS FWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTR KHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEE EEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
10	1548	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASRGINNW LTWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRIPYTFGQGTKLEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYYMHW VRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDSRIAVAASSFDYWGQGTLVTVSSGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

11	1549	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASRGINNW LTWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRIPYTFGQGTKLEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYYMHW VRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDSRIAVAASSFDYWGQGTLVTVSSGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
12	1550	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASRGINNW LTWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY YCQQSYRIPYTFGQGTKLEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTDYYMHW VRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARDSRIAVAASSFDYWGQGTLVTVSSGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
13	1551	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSINDW LAWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPPTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMH WVRQAPGQGLEWMGRINPNGGSTTYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDDFYYYYLDFWGKGTTVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
14	1552	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSINDW LAWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPPTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMH WVRQAPGQGLEWMGRINPNGGSTTYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDDFYYYYLDFWGKGTTVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
15	1553	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSINDW LAWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPPTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMH WVRQAPGQGLEWMGRINPNGGSTTYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDDFYYYYLDFWGKGTTVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR

16	1554	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSISSW LAWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQTYRTPLTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMH WVRQAPGQGLEWMGWMNPDSGTTGYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCVRDGTMVQGIFDYWGQGTLVTVSSGGGGSGGGGSGGGG SGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPR RPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
17	1555	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSISSW LAWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQTYRTPLTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMH WVRQAPGQGLEWMGWMNPDSGTTGYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCVRDGTMVQGIFDYWGQGTLVTVSSGGGGSGGGGSGGGG SGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
18	1556	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQSISSW LAWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQTYRTPLTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFSNYYMH WVRQAPGQGLEWMGWMNPDSGTTGYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCVRDGTMVQGIFDYWGQGTLVTVSSGGGGSGGGGSGGGG SGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPR RPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
19	1557	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGIGND LGWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPITFGQGTRLEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAITWVR QAPGQGLEWMGGIIPIVGRANYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCARSGGHDLDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSFW VLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDG CSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
20	1558	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGIGND LGWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPITFGQGTRLEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAITWVR QAPGQGLEWMGGIIPIVGRANYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCARSGGHDLDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSFW VLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEE GGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEM GGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLST ATKDTYDALHMQALPPR

21	1559	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGIGND LGWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPITFGQGTRLEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAAG GAVHTRGLDFACDQVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAITWVR QAPGQGLEWMGGIIPIVGRANYAQKFQGRVTITADESTSTAYMELSSLRSED TAVYYCARSGGHDLDYWGQGTLVTVSSGGGGSGGGGSGGGGSGGGGSFW VLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKH YQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLD KRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGH DGLYQGLSTATKDTYDALHMQALPPR
22	1560	MALPVTALLLPLALLLHAARPEIVMTQSPATLSVSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYATSTRATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYGSLPLTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWV RQAPGKGLEWVSSISGSGDTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARDNPYGDYGGSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
23	1561	MALPVTALLLPLALLLHAARPEIVMTQSPATLSVSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYATSTRATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYGSLPLTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWV RQAPGKGLEWVSSISGSGDTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARDNPYGDYGGSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
24	1562	MALPVTALLLPLALLLHAARPEIVMTQSPATLSVSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYATSTRATGIPARFSGSGSGTEFTLTISSLQSEDFAV YYCQQYGSLPLTFGQGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYGMHWV RQAPGKGLEWVSSISGSGDTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARDNPYGDYGGSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
25	1563	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNN LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQANSFPLTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHW VRQAPGQGLEWMGIIDPSGGSTNYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARDYYGSGSYYGLDYWGRGTLVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR

26	1564	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNN LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQANSFPLTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHW VRQAPGQGLEWMGIIDPSGGSTNYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARDYYGSGSYYGLDYWGRGTLVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
27	1565	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNN LNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQANSFPLTFGPGTKVDIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHW VRQAPGQGLEWMGIIDPSGGSTNYAQKFQGRVTMTRDTSTSTVYMELSSLRS EDTAVYYCARDYYGSGSYYGLDYWGRGTLVTVSSGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
28	1566	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNY LAWYQQKPGKAPKLLIYTASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYSFTSHAISWV RQAPGQGLEWMGWIKPNSGDTKYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARGSDDYYGSYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
29	1567	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNY LAWYQQKPGKAPKLLIYTASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYSFTSHAISWV RQAPGQGLEWMGWIKPNSGDTKYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARGSDDYYGSYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
30	1568	MALPVTALLLPLALLLHAARPDIQMTQSPSSLSASVGDRVTITCRASQGISNY LAWYQQKPGKAPKLLIYTASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPLTFGGGTKVEIKRTTTPAPRPPTPAPTIASQPLSLRPEACRPAA GGAVHTRGLDFACDQVQLVQSGAEVKKPGASVKVSCKASGYSFTSHAISWV RQAPGQGLEWMGWIKPNSGDTKYAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARGSDDYYGSYYFDYWGQGTLVTVSSGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

31	1569	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYSFT GYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGD RVTITCRASQTINDWLAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQAYSTPWTFGQGTKVEIKRGGGGSGGGGSGGGG SGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPR RPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGR REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKG ERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
32	1570	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYSFT GYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGD RVTITCRASQTINDWLAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQAYSTPWTFGQGTKVEIKRGGGGSGGGGSGGGG SGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
33	1571	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYSFT GYYIHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDQWDGYNSGYFDYWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGD RVTITCRASQTINDWLAWYQQKPGKAPKLLIYSASTLHSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQAYSTPWTFGQGTKVEIKRGGGGSGGGGSGGGG SGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPR RPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
34	1572	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGNTFT SYGISWVRQAPGQGLEWMGWINPNSGGTKYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARESWFGELYYGMDVWGKGTTVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIVMTQSPLSLPVTPGE PASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSDRASGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCMQGLQTPITFGQGTRLEIKRGGGGSGGGG SGGGGSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNE LNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
35	1573	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGNTFT SYGISWVRQAPGQGLEWMGWINPNSGGTKYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARESWFGELYYGMDVWGKGTTVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIVMTQSPLSLPVTPGE PASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSDRASGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCMQGLQTPITFGQGTRLEIKRGGGGSGGGG SGGGGSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQP FMRPVQTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNEL NLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEI GMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

36	1574	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGNTFT SYGISWVRQAPGQGLEWMGWINPNSGGTKYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARESWFGELYYGMDVWGKGTTVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIVMTQSPLSLPVTPGE PASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSDRASGVPDRFSGS GSGTDFTLKISRVEAEDVGVYYCMQGLQTPITFGQGTRLEIKRGGGGSGGGG SGGGGSGGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYM NMTPRRPGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQE EDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYD VLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRG KGHDGLYQGLSTATKDTYDALHMQALPPR
37	1575	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT AYYTHWVRQAPGQGLEWMGWMNPNSGHTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAREAYDSFDYWGQGTLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPKLLIYEASTLETGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQANSFPFTFGPGTKVDIKRGGGGSGGGGSGGGGSGGGGSF WVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRK HYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALHMQALPPR
38	1576	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT AYYTHWVRQAPGQGLEWMGWMNPNSGHTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAREAYDSFDYWGQGTLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPKLLIYEASTLETGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQANSFPFTFGPGTKVDIKRGGGGSGGGGSGGGGSGGGGSF WVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEED GCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVL DKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKG HDGLYQGLSTATKDTYDALHMQALPPR
39	1577	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT AYYTHWVRQAPGQGLEWMGWMNPNSGHTSYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAREAYDSFDYWGQGTLVTVSSTTTPAPRPPTPAPTI ASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVTITC RASQSISSYLNWYQQKPGKAPKLLIYEASTLETGVPSRFSGSGSGTDFTLTISS LQPEDFATYYCQQANSFPFTFGPGTKVDIKRGGGGSGGGGSGGGGSGGGGSF WVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRK HYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEE EGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPE MGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLS TATKDTYDALHMQALPPR
40	1578	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT DYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDSRIAVAASSFDYWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGD RVTITCRASRGINNWLTWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQSYRIPYTFGQGTKLEIKRGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

41	1579	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT DYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDSRIAVAASSFDYWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGD RVTITCRASRGINNWLTWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQSYRIPYTFGQGTKLEIKRGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
42	1580	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT DYYMHWVRQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDSRIAVAASSFDYWGQGTLVTVSSTTTPAPRPP TPAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGD RVTITCRASRGINNWLTWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQSYRIPYTFGQGTKLEIKRGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
43	1581	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYMHWVRQAPGQGLEWMGRINPNGGSTTYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDDFYYYYLDFWGKGTTVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVT ITCRASQSINDWLAWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQGYSTPPTFGQGTKVEIKRGGGGSGGGGSGGGGSGG GGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPG PTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
44	1582	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYMHWVRQAPGQGLEWMGRINPNGGSTTYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDDFYYYYLDFWGKGTTVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVT ITCRASQSINDWLAWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQGYSTPPTFGQGTKVEIKRGGGGSGGGGSGGGGSGG GGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTT QEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEY DVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRR GKGHDGLYQGLSTATKDTYDALHMQALPPR
45	1583	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT GYYMHWVRQAPGQGLEWMGRINPNGGSTTYAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDDFYYYYLDFWGKGTTVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVT ITCRASQSINDWLAWYQQKPGKAPKLLIYAASNLQSGVPSRFSGSGSGTDFTL TISSLQPEDFATYYCQQGYSTPPTFGQGTKVEIKRGGGGSGGGGSGGGGSGG GGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPG PTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRF PEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGR DPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQ GLSTATKDTYDALHMQALPPR

46	1584	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFS NYYMHWVRQAPGQGLEWMGWMNPDSGTTGYAQKFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCVRDGTMVQGIFDYWGQGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQSISSWLAWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQTYRTPLTFGPGTKVDIKRGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
47	1585	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFS NYYMHWVRQAPGQGLEWMGWMNPDSGTTGYAQKFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCVRDGTMVQGIFDYWGQGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQSISSWLAWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQTYRTPLTFGPGTKVDIKRGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPV QTTQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRR EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGE RRRGKGHDGLYQGLSTATKDTYDALHMQALPPR
48	1586	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFS NYYMHWVRQAPGQGLEWMGWMNPDSGTTGYAQKFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCVRDGTMVQGIFDYWGQGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQSISSWLAWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQTYRTPLTFGPGTKVDIKRGGGGSGGGGSGGGGS GGGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRR PGPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSC RFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
49	1587	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGSSVKVSCKASGGTFST YAITWVRQAPGQGLEWMGGIIPIVGRANYAQKFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARSGGHDLDYWGQGTLVTVSSTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVTITCRASQ GIGNDLGWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPITFGQGTRLEIKRGGGGSGGGGSGGGGSGGGGSFWVL VVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQTTQEEDGCS CRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKR RGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDG LYQGLSTATKDTYDALHMQALPPR
50	1588	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGSSVKVSCKASGGTFST YAITWVRQAPGQGLEWMGGIIPIVGRANYAQKFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARSGGHDLDYWGQGTLVTVSSTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVTITCRASQ GIGNDLGWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPITFGQGTRLEIKRGGGGSGGGGSGGGGSGGGGSFWVL VVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQP YAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCRFPEEEEGGC ELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGK PRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATK DTYDALHMQALPPR

51	1589	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGSSVKVSCKASGGTFST YAITWVRQAPGQGLEWMGGIIPIVGRANYAQKFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARSGGHDLDYWGQGTLVTVSSTTTPAPRPPTPAPTIASQP LSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDRVTITCRASQ GIGNDLGWYQQKPGKAPKLLIYGASSVQSGVPSRFSGSGSGTDFTLTISSLQP EDFATYYCQQSYSTPITFGQGTRLEIKRGGGGSGGGGSGGGGSGGGGSFWVL VVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQP YAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRR GRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGL YQGLSTATKDTYDALHMQALPPR
52	1590	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSISGSGDTTYYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDNPYGDYGGSFDYWGQGTLVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDEIVMTQSPATLSVSPGERAT LSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSTRATGIPARFSGSGSGTEFT LTISSLQSEDFAVYYCQQYGSLPLTFGQGTKVEIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
53	1591	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSISGSGDTTYYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDNPYGDYGGSFDYWGQGTLVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDEIVMTQSPATLSVSPGERAT LSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSTRATGIPARFSGSGSGTEFT LTISSLQSEDFAVYYCQQYGSLPLTFGQGTKVEIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
54	1592	MALPVTALLLPLALLLHAARPEVQLLESGGGLVQPGGSLRLSCAASGFTFSSY GMHWVRQAPGKGLEWVSSISGSGDTTYYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDNPYGDYGGSFDYWGQGTLVTVSSTTTPAPRPPTPA PTIASQPLSLRPEACRPAAGGAVHTRGLDFACDEIVMTQSPATLSVSPGERAT LSCRASQSVSSSYLAWYQQKPGQAPRLLIYATSTRATGIPARFSGSGSGTEFT LTISSLQSEDFAVYYCQQYGSLPLTFGQGTKVEIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
55	1593	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT SYYMHWVRQAPGQGLEWMGIIDPSGGSTNYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYYGSGSYYGLDYWGRGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQGISNNLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQANSFPLTFGPGTKVDIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR

56	1594	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT SYYMHWVRQAPGQGLEWMGIIDPSGGSTNYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYYGSGSYYGLDYWGRGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQGISNNLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQANSFPLTFGPGTKVDIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
57	1595	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYTFT SYYMHWVRQAPGQGLEWMGIIDPSGGSTNYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYYGSGSYYGLDYWGRGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQGISNNLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQANSFPLTFGPGTKVDIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR
58	1596	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYSFT SHAISWVRQAPGQGLEWMGWIKPNSGDTKYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGSDDYYGSYYFDYWGQGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQGISNYLAWYQQKPGKAPKLLIYTASTLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVKRGRKKLLYIFKQPFMRPVQT TQEEDGCSCRFPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREE YDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERR RGKGHDGLYQGLSTATKDTYDALHMQALPPR
59	1597	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYSFT SHAISWVRQAPGQGLEWMGWIKPNSGDTKYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGSDDYYGSYYFDYWGQGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQGISNYLAWYQQKPGKAPKLLIYTASTLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSKRGRKKLLYIFKQPFMRPVQTTQEEDGCSCR FPEEEEGGCELRVKFSRSADAPAYKQGQNQLYNELNLGRREEYDVLDKRRG RDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGERRRGKGHDGLY QGLSTATKDTYDALHMQALPPR
60	1598	MALPVTALLLPLALLLHAARPQVQLVQSGAEVKKPGASVKVSCKASGYSFT SHAISWVRQAPGQGLEWMGWIKPNSGDTKYAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGSDDYYGSYYFDYWGQGTLVTVSSTTTPAPRPPT PAPTIASQPLSLRPEACRPAAGGAVHTRGLDFACDDIQMTQSPSSLSASVGDR VTITCRASQGISNYLAWYQQKPGKAPKLLIYTASTLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQSYSTPLTFGGGTKVEIKRGGGGSGGGGSGGGGSG GGGSFWVLVVVGGVLACYSLLVTVAFIIFWVRSKRSRLLHSDYMNMTPRRP GPTRKHYQPYAPPRDFAAYRSRVKFSRSADAPAYKQGQNQLYNELNLGRRE EYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQKDKMAEAYSEIGMKGER RRGKGHDGLYQGLSTATKDTYDALHMQALPPR

[00462] Similar CARs comprising scFvs with variations are possible as well.

[00463] For example, the CD34 tag may be included in the expression vector along with a P2A sequence (so that it is co-expressed as a discrete protein), or the $(GGGGS)_4$ linker may be substituted for a $(GGGGS)_3$, $(GGGGS)_2$, or $(GGGGS)_1$ linker. For example, also provided are:

- CAR Examples 1a-60a which are identical to those above, except that they are accompanied by the CD34 tag;
- CAR Examples 1b-60b which are identical to those above, except that they have a $(GGGGS)_3$ linker;
- CAR Examples 1c-60c which are identical to those above, except that they have a $(GGGGS)_3$ linker and they are accompanied by the CD34 tag;
- CAR Examples 1d-60d which are identical to those above, except that they have a $(GGGGS)_2$ linker;
- CAR Examples 1e-60e which are identical to those above, except that they have a $(GGGGS)_2$ linker and they are accompanied by the CD34 tag;
- CAR Examples 1f-60f which are identical to those above, except that they have a (GGGGS) linker; and
- CAR Examples 1g-60g which are identical to those above, except that they have a (GGGGS) linker and they are accompanied by the CD34 tag.

Example 7: CAR-Bearing Immune Effector Cells

[00464] CAR-bearing immune effector cells may be constructed, optionally with a genome editing step to effect deletion or suppression of one or more surface proteins. Such surface proteins many include, for example, those that form part of the TCR complex, which may induce GvHD if the cells are administered to patients in the allogeneic setting, or those that are the target antigen of the CAR, which may induce fratricide if expression of the antigen on CAR-T is not suppressed.

[00465] For example, in one protocol, on Day 0, CD4+ CD8+ T cells are thawed in a cell culture media. The required number of cells are centrifuged at 200xg for 10 minutes at room temperature. Supernatant is removed completely, cells resuspended cell culture media (TexMacs) supplemented with IL-7 (10 ng/ml) and IL-15 (10 ng/ml) at concentration of $1x10^6$/ml. T cells are stimulated with Miltenyi research grade TransAct™ (10µl/ml).

[00466] On day 1, the required amount of viral vector comprising CAR is added to the activated cells at the required M.O.I (Multiplicity of Infection). Cells and virus are mixed and placed back in incubator at 37°C.

Table 12.

CAR-T Example	Name	Media	Stimulation	Cas9 p	gRNA	Virus
1	NTD	TexMacs	T Cell TransAct™ (10µl/ml)	-	-	-
2	CART-CD33	TexMacs	T Cell TransAct™ (50µl)			CAR-CD33
3	CART-$CD33^{G69}$	TexMacs	T Cell TransAct™ (50µl)			CAR-$CD33^{G69}$
4	CART-$CD33^{R69}$	TexMacs	T Cell TransAct™ (50µl)			CAR-$CD33^{R69}$
5	UCART-CD33	TexMacs	T Cell TransAct™ (50µl)	10 µg	20 µg TRAC	CAR-CD33
6	UCART-$CD33^{G69}$	TexMacs	T Cell TransAct™ (50µl)	10 µg	20 µg TRAC	CAR-$CD33^{G69}$
7	UCART-$CD33^{R69}$	TexMacs	T Cell TransAct™ (50µl)	10 µg	20 µg TRAC	CAR-$CD33^{R69}$
8	CART-CLL-1	TexMacs	T Cell TransAct™ (50µl)			CAR-CLL-1
9	CART-CLL-1^{K244}	TexMacs	T Cell TransA			CAR-CLL-1^{K244}

			ct™ (50µl)			
10	CART-CLL-1^{Q244}	TexMacs	T Cell TransAct™ (50µl)			CAR-CLL-1^{Q244}
11	UCART-CLL-1	TexMacs	T Cell TransAct™ (50µl)	10 µg	20 µg TRAC	CAR-CLL-1
12	UCART-CLL-1^{K244}	TexMacs	T Cell TransAct™ (50µl)	10 µg	20 µg TRAC	CAR-CLL-1^{K244}
13	UCART-CLL-1^{Q244}	TexMacs	T Cell TransAct™ (50µl)	10 µg	20 µg TRAC	CAR-CLL-1^{Q244}

[00467] On day 3, activated cells are washed to remove stimulation.

[00468] If genome editing is desired, cells are harvested and counted. The required number of cells are centrifuged at 100xg for 10 minutes at room temperature. Supernatant is removed completely, cells resuspended in Electroporation buffer (1ml) (e.g. Maxcyte EP buffer) and transferred to a microcentrifuge tube, and centrifuged at 100xg for 10 minutes at room temperature. Supernatant is removed completely, and cells then resuspended in electroporation buffer (e.g., MaxCyte EP buffer), at the desired concentration (e.g. 5 x 10^7 / ml).

[00469] Commercially available Cas9 Protein (10 µg) and commercially synthesized gRNA (20 µg) are complexed at room temperature for 10 minutes.

[00470] Cells (100 µl) are transferred to the tube containing complexed Cas9/gRNA, gently mixed, and everything transferred into a MaxCyte OC100 cuvette.. Electroporation is thereafter commenced using Maxcyte program Expanded T cell 2. After this procedure, the activated cells may be transferred to 10 ml of pre-warmed media and returned to the incubator to expand for an additional 7-12 days.

[00471] FACS analysis may be used to show the purity of CAR-transduced cells (CAR expression and target gene deletion).

Example 8: In Vitro Cell Killing Assay

[00472] Target AML cell lines may be obtained from commercially vendors (ATCC). Target expression was confirmed by FACS analysis and target cell genotype obtained through DNA sequencing. Cells were modified to express CBR-GFP (Click beetle luciferase and Green Fluorescent Protein). Jurkat cells (target negative) were engineered to over express either the $CD33^{G69}$ variant or $CD33^{R69}$ variant in conjunction with a CD90.1 marker to enable discrimination by FACS in a target protein independent manor. Target cells were co-incubated with:

- $CART33^{ARG69}$ comprising an antigen-recognition domain comprising the V_H and V_L domains disclosed in polypeptide no. 6, or
- $CART33^{GLY69}$ comprising an antigen-recognition domain comprising the V_H and V_L domains disclosed in polypeptide no. 30; or
- positive control, variant nonspecific CART33,

at a range of effector to target cell ratio ranging from, e.g., E:T 2:1 to E:T 1:32 for 24 hours prior to FACS analysis. Absolute cell counts of viable target cells were quantified by flow cytometry (attune using absolute counts in a defined volume). Percent cytotoxicity is defined as viable targets relative to tumor only controls. Data was analyzed using FlowJo V10.

[00473] Results are shown in **Fig. 4** and **Fig. 5**. $CART33^{ARG69}$ effectively kill $CD33^{ARG69}$ targets but not $CD33^{GLY69}$ targets. $CART33^{GLY69}$ effectively kill $CD33^{GLY69}$ targets but not $CD33^{ARG69}$ targets. CART33 kill both $CD33^{ARG69}$ and $CD33^{GLY69}$ targets.

[00474] The above assay may be repeated with other CAR cells comprising alternate polypeptides and cells expressing the appropriate targets, and may be varied according to methods known in the art; for example, different ratios of effector to target may be used. It is expected that in further experiments of this type, cells expressing polymorphically selective CARS will kill cells expressing the selected target polymorph.

[00475] For example, CART33 will kill CD33+ targets independent of the CD33 genotype ($CD33^{R69}$ or $CD33^{G69}$). CART-$CD33^{G69}$ is expected to kill $CD33^{G69}$ targets (e.g., HL60, KG1a, or Jurkat $CD33^{G69}$), but not kill $CD33^{R69}$ targets (e.g., TF1, THP1, or Jurkat $CD33^{R69}$). CART-$CD33^{R69}$ is expected to kill $CD33^{R69}$ targets (e.g., TF1, THP1 or Jurkat $CD33^{R69}$), but not kill $CD33^{G69}$ targets (e.g., HL60, KG1a , Jurkat $CD33^{G69}$).

[00476] Similarly, cells expressing polymorphically selective CARS targeting polymorphisms of FLT3 and CLL1 will kill cells expressing the selected target polymorph, and will spare cells expressing the other polymorph. CART-FLT3 will kill FLT3+ targets independent of the FLT3 genotype ($FLT3^{T227}$ or $FLT3^{M227}$). CART-$FLT3^{M227}$ is expected to kill $FLT3^{M227}$ targets (e.g., Jurkat $FLT3^{M227}$), but not kill $FLT3^{T227}$ targets (e.g., Jurkat $FLT3^{T227}$). CART-$FLT3^{T227}$ is expected to kill $FLT3^{T227}$ targets (e.g., Jurkat $FLT3^{T227}$), but not kill $FLT3^{M227}$ targets (e.g., Jurkat $FLT3^{M227}$). CART-CLL1 will kill CLL1+ targets independent of the CLL1 genotype ($CLL1^{K244}$ or $CLL1^{Q244}$). CART- $CLL1^{Q244}$ is expected to kill $CLL1^{Q244}$ targets (e.g., Jurkat $CLL1^{Q244}$), but not kill $CLL1^{K244}$ targets (e.g., Jurkat $CLL1^{K244}$). CART-$CLL1^{K244}$ is expected to kill $CLL1^{K244}$ targets (e.g., Jurkat $CLL1^{K244}$), but not kill $CLL1^{Q244}$ targets (e.g., Jurkat $CLL1^{Q244}$).

Example 9: AML Cell Line Xenograft Model of CAR-T activity

[00477] Six to ten week old immunodeficient NOD.Cg-Prkdcscid Il2rgtm1Wjl Tg(CMV-IL3,CSF2,KITLG)1Eav/ MloySzJ (NSG-SGM3) mice may be used in murine patient-derived xenograft experiments. Both male and female mice may be used in experiments and randomly assigned to a treatment group.

[00478] Target AML cell lines may be obtained from commercially vendors (ATCC). Target expression is confirmed by FACS analysis and target cell genotype obtained through DNA sequencing. Cells were modified to express CBR-GFP (Click beetle luciferase and Green Fluorescent Protein).

[00479] Mice are engrafted with an appropriate amount, e.g., $1x10^6$ cells on day -7 followed by infusion of an appropriate amount, e.g., $2x10^6$ CAR-T cells and appropriate controls on day 0.

[00480] For example, a $CD33^{G69}$ AML Cell line, KG1a, may be engrafted into mice and treated with either $CD33^{G69}$ CAR-T cells or $CD33^{R69}$ CAR-T cells, a positive control (CD33 CAR-T cells) or a negative control (e.g., CAR negative T cells).

[00481] Tumor burden may be monitored by bioluminescent imaging (BLI) weekly. Mice will be monitored for survival. Bone marrow may be extracted from mice and tumor burden assessed using FACS.

[00482] It is expected that CART33 (positive control) will kill CD33+ targets independent of the CD33 genotype ($CD33^{R69}$ or $CD33^{G69}$), reduce tumor burden, and prolong survival. CART-$CD33^{G69}$ is expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a), reduce tumor burden, and prolong survival of mice. $CD33^{R69}$ targets (e.g., TF1, THP1, or Jurkat $CD33^{R69}$) would not be killed by CART-$CD33^{G69}$ and thus CART-$CD33^{G69}$ would not offer a survival advantage or reduce tumor burden. CART-$CD33^{R69}$ is expected to kill $CD33^{R69}$ targets (e.g., TF1 or THP1), reduce tumor burden, and prolong survival of mice. CART-$CD33^{R69}$ is not expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a) and thus CART-$CD33^{R69}$ would not offer a survival advantage or reduce tumor burden in mice bearing $CD33^{G69}$ target cell lines.

Example 10: AML Cell Line Humanized Xenograft Model of CAR-T activity

[00483] Human CD34+ hematopoietic stem cell-engrafted NOD.Cg-Prkdcscid Il2rgtm1Wjl Tg(CMV-IL3,CSF2,KITLG)1Eav/ MloySzJ (CD34+ hu-NSG-SGM3) mice may be used in patient-derived xenograft experiments. Both male and female mice may be used in experiments and randomly assigned to a treatment group.

[00484] Mice are bled and the engrafted human cells genotyped using PCR based sequencing to determine the phenotype of the polymorphic target.

[00485] Target AML cell lines may be obtained from commercially vendors (ATCC). Target expression is confirmed by FACS analysis and target cell genotype obtained through DNA sequencing. Cells were modified to express CBR-GFP (Click beetle luciferase and Green Fluorescent Protein).

[00486] Mice are engrafted with, an appropriate amount, e.g., $1x10^6$ AML cells 8-10 weeks following CD34 cord blood engraftment, followed by infusion of an appropriate amount, e.g., $2x10^6$ CAR-T cells and appropriate controls on day 0.

[00487] For example, a $CD33^{G69}$ AML Cell line, KG1a, may be engrafted into humanized CD34+ $CD33^{R69}$ mice and treated with either $CD33^{G69}$ CAR-T cells or $CD33^{R69}$ CAR-T cells, a positive control (CD33 CAR-T cells) or a negative control (e.g., CAR negative T cells).

[00488] Tumor burden may be monitored by bioluminescent imaging (BLI) weekly. Mice may be monitored for survival. Bone marrow may be extracted from mice and tumor burden assessed using FACS. CD33 expression on engrafted cord blood derived cells, obtained from the blood, spleen and bone marrow of mice will be analyzed by FACS. Red blood cells are lysed using Red Blood Cell Lysing Buffer (Sigma-Aldrich) and washed with ice cold PBS. Samples

were prepared for flow cytometry by re-suspending cells in staining buffer (PBS supplemented with 0.5% bovine serum albumin and 2 mM EOTA) and incubating for 30 min at 4°C with pre-titrated saturating dilutions of appropriate fluorochrome-labeled monoclonal antibodies. Data may be analyzed using FlowJo V10.

[00489] It is expected that CART33 (positive control) will kill CD33+ targets independent of the CD33 genotype ($CD33^{R69}$+ or $CD33^{G69}$) and reduce tumor burden, but also lose human engrafted hematopoietic cells. CART-$CD33^{G69}$ is expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a) and not kill $CD33^{R69}$ engrafted stem cells, prolonging survival by reducing tumor burden while maintaining human hematopoietic cells. CART-$CD33^{R69}$ is expected to kill $CD33^{R69}$ targets (e.g., TF1, THP) and not kill $CD33^{G69}$ engrafted stem cells, prolonging survival by reducing tumor burden while maintaining human hematopoietic cells. Mice which have the same CD33 variant on both AML and engrafted stem cells would be expected have a reduced tumor burden but fail to maintain human hematopoietic cells.

Example 11: Patient-Derived Xenograft Model of CAR-T Activity.

[00490] Six to ten week old immunodeficient NOD.Cg-Prkdcscid Il2rgtm1Wjl Tg(CMV-IL3,CSF2,KITLG)1Eav/ MloySzJ (NSG-SGM3) mice may be used in murine patient-derived xenograft experiments. Both male and female mice may be used in experiments and randomly assigned to a treatment group.

[00491] Xenografts of human hematologic cancers, e.g. AML, may be obtained from a variety of sources known in the art including, for example, the Public Repository of Xenografts (PRoXe, www.PRoXe.org). Mice are engrafted with an appropriate amount, e.g., $1x10^6$ cells on day -7 followed by infusion of an appropriate amount, e.g., $2x10^6$ CAR-T cells and appropriate controls on day 0.

[00492] For example, a $CD33^{R69}$ AML xenograft may be engrafted into mice and treated with either $CD33^{G69}$ CAR-T cells or $CD33^{R69}$ CAR-T cells, or a negative control (e.g., CAR negative T cells).

[00493] Peripheral blood and spleens are analyzed by flow cytometry after two weeks, four weeks and six weeks post CAR-T infusion. Red blood cells are lysed using Red Blood Cell Lysing Buffer (Sigma-Aldrich) and washed with ice cold PBS. Samples were prepared for flow cytometry by re-suspending cells in staining buffer (PBS supplemented with 0.5% bovine serum albumin and 2 mM EDTA) and incubating for 30 min at 4°C with pre-titrated saturating dilutions

of appropriate fluorochrome-labeled monoclonal antibodies. Data may be analyzed using FlowJo V10.

[00494] It is expected that $CD33^{R69}$ CAR-T would kill engrafted $CD33^{R69}$ AML cells, reducing tumor burden and prolonging survival. It is expected that $CD33^{G69}$ CAR-T would be unable to kill engrafted $CD33^{R69}$ AML cells and would offer no survival advantage or reduction in tumor burden. If the engrafted AML was heterozygous, expressing both $CD33^{R69}$ and $CD33^{G69}$, both $CD33^{G69}$ CAR-T and $CD33^{R69}$ CAR-T would be effective at killing the engrafted primary AML, prolonging survival of mice.

Example 12: AML Cell Line In Vitro CAR-NK Activity

[00495] Target AML cell lines may be obtained from commercial vendors (ATCC). Target expression was confirmed by FACS analysis and target cell genotype obtained through DNA sequencing.

[00496] For example, a $CD33^{G69}$ AML Cell line (such as KG1a or HL60), and $CD33^{R69}$ AML cell lines (such as TF1 or THP1) may be cultured in vitro.

[00497] NK cells engineered to express scFv-CARs to $CD33^{R69}$ would then be added to the $CD33^{R69}$ or $CD33^{G69}$ cells in culture for 4-24 hours. After culture, death of the $CD33^{R69}$ cells would be expected to be enhanced, while death of $CD33^{G69}$ cells would be no higher than background killing by unmodified NK cells. scFv-CAR NKs to $CD33^{G69}$ would be expected to kill $CD33^{G69}$ cells but would not be enhanced in killing $CD33^{R69}$ cells. As a positive control, an anti-CD33 CAR could be used, and as a negative control, NK cells alone could be used.

[00498] Alternatively, NK cells could be cultured in the presence of $CD33^{R69}$ or $CD33^{G69}$ AML cell lines and in the presence of an antibody with a human IgG1 or IgG3 isotype targeting $CD33^{R69}$. After co-culture, the death of the AML cell lines would be assessed, and would be expected to be higher for $CD33^{R69}$ AML cells. As a positive control, an anti-CD33 antibody could be used, and as a negative control, NK cells alone could be used.

[00499] It is expected that CARNK33 (positive control) will kill CD33+ targets independent of the CD33 genotype of the AML ($CD33^{R69}$ or $CD33^{G69}$). CARNK-$CD33^{G69}$ is expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a). $CD33^{R69}$ targets (e.g., TF1 or THP1) would not be killed by CARNK-$CD33^{G69}$ and thus CARNK-$CD33^{G69}$ would not be enhanced in this in vitro assay. CARNK-$CD33^{R69}$ is expected to kill $CD33^{R69}$ targets (e.g., TF1 or THP1).

CARNK-CD33^{R69} is not expected to kill CD33^{G69} targets (e.g., HL60 or KG1a) and thus CARNK-CD33^{R69} would not be enhanced in this in vitro assay.

[00500] It is expected that treatment comprising administration of NK cells together with an anti-CD33 antibody (positive control) will kill CD33+ targets independent of the CD33 genotype of the AML (CD33^{R69} or CD33^{G69}). NK cells cultured with an anti-CD33^{G69} antibody are expected to kill CD33^{G69} targets (e.g., HL60 or KG1a). CD33^{R69} targets (e.g., TF1 or THP1) would not be killed by NK cells cultured with an anti-CD33^{G69} antibody and thus NK cells administered with an anti-CD33^{G69} antibody would not increase AML cell death in this assay against CD33^{R69} target cell lines. NK cells administered with an anti-CD33^{R69} antibody are expected to kill CD33^{R69} targets (e.g., TF1 or THP1). NK cells cultured with an anti-CD33^{R69} antibody are not expected to kill CD33^{G69} targets (e.g., HL60 or KG1a) and thus NK cells administered with an anti-CD33^{R69} antibody would not increase AML cell death in this assay against CD33^{G69} target cell lines.

Example 13: AML Cell Line Xenograft Model of CAR-NK Activity

[00501] Six to ten week old immunodeficient NOD.Cg-Prkdcscid Il2rgtm1Wjl Tg(CMV-IL3,CSF2,KITLG)1Eav/ MloySzJ (NSG-SGM3) mice may be used in murine patient-derived xenograft experiments. Both male and female mice may be used in experiments and randomly assigned to a treatment group.

[00502] Target AML cell lines may be obtained from commercially vendors (ATCC). Target expression was confirmed by FACS analysis and target cell genotype obtained through DNA sequencing. Cells were modified to express CBR-GFP (Click beetle luciferase and Green Fluorescent Protein).

[00503] Mice are engrafted with an appropriate amount, e.g., 1x10^6 cells on day -7 followed by infusion of an appropriate amount, e.g., 5x10^6 CAR-NK or NK cells and appropriate controls on day 0.

[00504] For example, a CD33^{G69} AML Cell line, KG1a, may be engrafted into mice and treated with either CD33^{G69} CAR-NK cells or CD33^{R69} CAR-NK cells, a positive control (CD33 CAR-NK cells) or a negative control (e.g., CAR negative NK cells).

[00505] Alternatively, a CD33^{R69} AML Cell line, TF1 may be engrafted into mice and treated with either NK cells co-administered with CD33^{G69} or CD33^{R69}-directed antibodies of the

human IgG1 or human IgG3 isotype, a positive control (NK cells with a general anti-CD33 antibody) or a negative control (e.g., NK cells only).

[0001] Tumor burden may be monitored by bioluminescent imaging (BLI) weekly and bone. Mice will be monitored for survival. Bone marrow may be extracted from mice and tumor burden assessed using FACS.

[00506] It is expected that CARNK33 (positive control) will kill CD33+ targets independent of the CD33 genotype of the AML ($CD33^{R69}$ or $CD33^{G69}$), reduce tumor burden and prolong survival. CARNK-$CD33^{G69}$ is expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a), reduce tumor burden, and prolong survival of mice. $CD33^{R69}$ targets (e.g., TF1 or THP1) would not be killed by CARNK-$CD33^{G69}$ and thus CARNK-$CD33^{G69}$ would not offer a survival advantage or reduce tumor burden. CARNK-$CD33^{R69}$ is expected to kill $CD33^{R69}$ targets (e.g., TF1 or THP1), reduce tumor burden, and prolong survival of mice. CARNK-$CD33^{R69}$ is not expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a) and thus CARNK-$CD33^{R69}$ would not offer a survival advantage or reduce tumor burden in mice bearing $CD33^{G69}$ target cell lines.

[00507] It is expected that treatment comprising administration of NK cells together with an anti-CD33 antibody (positive control) will kill CD33+ targets independent of the CD33 genotype of the AML ($CD33^{R69}$ or $CD33^{G69}$), reduce tumor burden, and prolong survival. NK cells administered with an anti-$CD33^{G69}$ antibody is expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a), reduce tumor burden, and prolong survival of mice. $CD33^{R69}$ targets (e.g., TF1 or THP1,) would not be killed by NK cells administered with an anti-$CD33^{G69}$ antibody and thus NK cells administered with an anti-$CD33^{G69}$ antibody would not offer a survival advantage or reduce tumor burden. NK cells administered with an anti-$CD33^{R69}$ antibody are expected to kill $CD33^{R69}$ targets (e.g., TF1 or THP1), reduce tumor burden, and prolong survival of mice. NK cells administered with an anti-$CD33^{R69}$ antibody are not expected to kill $CD33^{G69}$ targets (e.g., HL60 or KG1a) and thus NK cells administered with an anti-$CD33^{R69}$ antibody would not offer a survival advantage or reduce tumor burden in mice bearing $CD33^{G69}$ target cell lines.

Example 14: Antibodies Comprising scFvs

[00508] Antibodies may be constructed from the scFvs disclosed herein using methods known in the art. For example, antibodies disclosed herein may be generated from expression cassettes of the form:

|—[(leader)(scFv V_H)(hCγ1)(hCγ2)(hCγ3)(Cγs)]—|

in a pFuse IgG1 Fc-fusion protein expression plasmid (e.g., Invivogen) and

$$\text{I—[(leader)(scFv } V_L)(hC_{\kappa/\lambda})]\text{—I}$$

in a pFuse IgK Fc-fusion protein expression plasmid (e.g., Invivogen).

[00509] Alternatively, an anti-CD33-R69 or anti-CD33-G69 antibody may be generated from an expression cassette of the form:

$$\text{I—[(leader)(scFv } V_H)(hC\gamma1)(hC\gamma2)(hC\gamma3)(C\gamma s)]\text{-[P2A]-[(leader)(scFv } V_L)(C_{\kappa/\lambda})]\text{–I}.$$

In either of the foregoing, Cγs may optionally be part of the hCγ3 domain.

[00510] The antibodies may be of various isotypes, the constant domains for which are known in the art. For example, for an IgG1 or IgG4, the sequence components may be as shown in Table 13:

Table 13. Human Antibody Fc Components

	hIgG1 AA	**hIgG1 Nucleotide**	**hIgG4 AA**	**hIgG4 Nucleotide**
IL2 Leader	MYRMQLLSCI ALSLALVTNS SEQ ID NO:1599	atgtacaggatgcaactcctgtcttgcat tgcactaagtcttgcacttgtcacgaatt cg SEQ ID NO:1600	MYRMQLLSCI ALSLALVTNS SEQ ID NO:1601	atgtacaggatgcaactcctgtctt gcattgcactaagtcttgcacttgtc acgaattcg SEQ ID NO:1602
Cy1	STKGPSVFPLA PSSKSTSGGTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY SLSSVVTVPSS SLGTQTYICNV NHKPSNTKVD KKV SEQ ID NO:1603	tccaccaagggcccatcggtcttcccc ctggcaccctcctccaagagcacctct gggggcacagcggccctgggctgcct ggtcaaggactacttccccgaaccggt gacggtgtcgtggaactcaggcgccct gaccagcggcgtgcacaccttcccgg ctgtcctacagtcctcaggactctactcc ctcagcagcgtggtgaccgtgccctcc agcagcttgggcacccagacctacatc tgcaacgtgaatcacaagcccagcaac accaaggtggacaagaaagtt SEQ ID NO:1604	STKGPSVFPL APCSRSTSEST AALGCLVKD YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTKTYT CNVDHKPSNT KVDKRV SEQ ID NO:1605	tccaccaagggcccctcgtgttc ccctggccccctgctcccgctcc acctccgagtccaccgccgccct gggctgcctggtgaaggactactt ccccgagcccgtgaccgtgtcct ggaactccggcgccctgacctcc ggcgtgcacaccttccccgccgt gctgcagtcctccggcctgtactc cctgtcctccgtggtgaccgtgcc ctcctcctccctgggcaccaagac ctacacctgcaacgtggaccaca agccctccaacaccaaggtggac aagcgcgtg SEQ ID NO:1606
Hinge (CH)	EPKSCDKTHT CPPCP SEQ ID NO:1607	GAGCCCAAATCTTGTGA CAAAACTCACACATGCC CACCGTGCCCA SEQ ID NO:1608	SKYGPPCPSCP SEQ ID NO:1609	tccaaatatggtccccatgcccat catgccca SEQ ID NO:1610

Cy2	PELLGGPSVFL FPPKPKDTLMI SRTPEVTCVV VDVSHEDPEV KFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD WLNGKEYKC KVSNKALPAPI EKTISKAK SEQ ID NO:1611	cctgaactcctgggggaccgtcagtc ttcctcttcccccaaaacccaaggaca ccctcatgatctcccggaccccctgaggt cacatgcgtggtggtggacgtgagcca cgaagaccctgaggtcaagttcaactg gtacgtggacggcgtggaggtgcataa tgccaagacaaagccgcgggaggag cagtacaacagcacgtaccgtgtggtc agcgtcctcaccgtcctgcaccaggac tggctgaatggcaaggagtacaagtgc aaggtctccaacaaagccctcccagcc cccatcgagaaaaccatctccaaagcc aaa SEQ ID NO:1612	PEFLGGPSVFL FPPKPKDTLMI SRTPEVTCVV VDVSQEDPEV QFNWYVDGV EVHNAKTKPR EEQFNSTYRV VSVLTVLHQD WLNGKEYKC KVSNKGLPSSI EKTISKAK SEQ ID NO:1613	cctgagttcctgggggaccatca gtcttcctgttcccccaaaaccca aggacactctcatgatctcccgga cccctgaggtcacgtgcgtggtg gtggacgtgagccaggaagacc ccgaggtccagttcaactggtacg tggatggcgtggaggtgcataatg ccaagacaaagccgcgggagga gcagttcaacagcacgtaccgtgt ggtcagcgtcctcaccgtcctgca ccaggactggctgaacggcaag gagtacaagtgcaaggtctccaac aaaggcctcccgtcctccatcgag aaaaccatctccaaagccaaa SEQ ID NO:1614
Cy3	QPREPQVYTL PPSREEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSKLTV DKSRWQQGN VFSCSVMHEA LHNHYTQKSL SLSP SEQ ID NO:1615	cagccccgagaaccacaggtgtacac cctgccccatcccgggaggagatga ccaagaaccaggtcagcctgacctgcc tggtcaaaggcttctatcccagcgacat cgccgtggagtgggagagcaatgggc agccggagaacaactacaagaccacg cctcccgtgctggactccgacggctcct tcttcctctacagcaagctcaccgtgga caagagcaggtggcagcaggggaac gtcttctcatgctccgtgatgcacgagg ctctgcacaaccactacacgcagaaga gcctctccctgtctccg SEQ ID NO:1616	QPREPQVYTL PPSQEEMTKN QVSLTCLVKG FYPSDIAVEW ESNGQPENNY KTTPPVLDSD GSFFLYSRLT VDKSRWQEG NVFSCSVMHE ALHNHYTQKS LSLSL SEQ ID NO:1617	cagccccgagagccacaggtgta cacctgccccatcccaggagg agatgaccaagaaccaggtcagc ctgacctgcctggtcaaaggcttct accccagcgacatcgccgtggag tgggagagcaatgggcagccgg agaacaactacaagaccacgcct cccgtgctggactccgacggctc cttcttcctctacagcaggctaacc gtggacaagagcaggtggcagg aggggaatgtcttctcatgctccgt gatgcatgaggctctgcacaacca ctacacacagaagagcctctccct gtctctg SEQ ID NO:1618
Secre-tion (Cs)	GK SEQ ID NO:1619	ggtaaatga SEQ ID NO:1620	GK SEQ ID NO:1621	ggtaaatga SEQ ID NO:1622
IgK-Ck1	TVAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSSTL TLSKADYEKH KVYACEVTHQ GLSSPVTKSFN RGEC SEQ ID NO:1623	acggtggctgcaccatctgtcttcatctt cccgccatctgatgagcagttgaaatct ggaactgcctctgttgtgtgcctgctga ataacttctatcccagagaggccaaagt acagtggaaggtggataacgccctcca atcgggtaactcccaggagagtgtcac agagcaggacagcaaggacagcacct acagcctcagcagcaccctgacgctga gcaaagcagactacgagaaacacaaa gtctacgcctgcgaagtcacccatcag ggcctgagctcgcccgtcacaaagag cttcaacaggggagagtgttag SEQ ID NO:1624	TVAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPREAKVQW KVDNALQSG NSQESVTEQD SKDSTYSLSST LTLSKADYEK HKVYACEVT HQGLSSPVTK SFNRGEC SEQ ID NO:1625	acggtggctgcaccatctgtcttca tcttcccgccatctgatgagcagtt gaaatctggaactgcctctgttgtg tgcctgctgaataacttctatccca gagaggccaaagtacagtggaa ggtggataacgccctccaatcgg gtaactcccaggagagtgtcaca gagcaggacagcaaggacagca cctacagcctcagcagcaccctg acgctgagcaaagcagactacga gaaacacaaagtctacgcctgcg aagtcacccatcagggcctgagct cgcccgtcacaaagagcttcaac aggggagagtgttag SEQ ID NO:1626

[00511] The foregoing may be combined with, for example: a V_H domain which has a polypeptide sequence of any of SEQ ID NOs 151-175, and/or a V_L domain which has a polypeptide sequence of any of SEQ ID NOs 176-200; a V_H domain which has a polypeptide sequence of any of SEQ ID NOs 303-319, and/or a V_L domain which has a polypeptide sequence of any of SEQ ID NOs 320-336; a V_H domain which has a polypeptide sequence of any of SEQ ID NOs 481-504, and/or a V_L domain which has a polypeptide sequence of any of SEQ ID NOs 505-528; or a V_H domain which has a polypeptide sequence of any of SEQ ID NOs 661-682, or a nucleotide sequence encoding any of SEQ ID NOs 661-682, and/or a V_L domain which has a polypeptide sequence of any of SEQ ID NOs 683-704; or a nucleotide sequence encoding any of the foregoing.

[00512] Additional antibodies may be constructed from V_H and V_L domains which are nonselective for a particular polymorphism. For example, the elements in Table 13 may be combined, for example, with a V_H domain which has a polypeptide sequence of any of SEQ ID NOs 1035-1089, and/or a V_L domain which has a polypeptide sequence of any of SEQ ID NOs 1090-1144; or a V_H domain which has a polypeptide sequence of any of SEQ ID NOs 1427-1473, and/or a V_L domain which has a polypeptide sequence of any of SEQ ID NOs 1474-1520; or a nucleotide sequence encoding any of the foregoing.

[00513] A cloning vector, for example a plasmid, comprising sequence of the foregoing form may be expressed in an appropriate cell line, for example 293F cells; transient transfection is typically sufficient. The 293F cells are grown in IgG free FBS with agitation (e.g., roller bottles), and the supernatant harvested over the course of several (e.g., 5) days. Supernatant is purified using Protein A or G columns and the antibody is recovered using methods known on the art.

[00514] The antibody so generated may comprise VH and VL domains as shown below in Table 14. Antibody (mAb) Examples 1-42 target CD33, and 43-88 target CLL-1.

Table 14 – IgG1 Antibodies

mAb Ex	IgG1 Heavy Chain	SEQ ID NO	IgG1 Light Chain	SEQ ID NO

1	QVQLVQSGAEVKKPGASVKVSCKASGYS FTGYYIHWVRQAPGQGLEWMGWINPNSG GTNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDQWDGYNSGYFDYW GQGTLVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1627	DIQMTQSPSSLSASV GDRVTITCRASQTIN DWLAWYQQKPGKA PKLLIYSASTLHSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQAYSTPWTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1715
2	EVQLLESGGGLVQPGGSLRLSCAASGFTFS DYYMSWVRQAPGKGLEWVSGISGSGYST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARTFGRGPDWYFDLWGRGT LVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1628	DIQMTQSPSSLSASV GDRVTITCRASQSIS RYLNWYQQKPGKA PKLLIYTASTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQYDDLPLTFGGGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1716
3	EVQLLESGGGLVQPGGSLRLSCAASGFTFS NSDMNWVRQAPGKGLEWVSAISGSGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARGREDDYGDYVFDYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1629	DIQMTQSPSSLSASV GDRVTITCRASQSISS YLNWYQQKPGKAP KLLIYGASTLHSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYRIPYTFGQGTKLEI KRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1717

4	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGWINPNSG NTGYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCAREHGDMDVWGQGTTVT VSSSTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVDKTHTCPPCPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	1630	EIVMTQSPATLSVSP GERATLSCRASQNIN SDLAWYQQKPGQAP RLLIYGASTRATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQ QYDSLPFTFGPGTKV DIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1718
5	QVQLVQSGAEVKKPGASVKVSCKASGNT FTSYGISWVRQAPGQGLEWMGWINPNSG GTKYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARESWFGELYYGMDVWG KGTTVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1631	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYLGSDRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQGLQTPITFG QGTRLEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1719
6	QVQLVQSGAEVKKPGASVKVSCKASGYT FTAYYTHWVRQAPGQGLEWMGWMNPNS GHTSYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCAREAYDSFDYWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1632	DIQMTQSPSSLSASV GDRVTITCRASQSISS YLNWYQQKPGKAP KLLIYEASTLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ ANSFPFTFGPGTKVD IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1720

7	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDSRIAVAASSFDYW GQGTLVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1633	DIQMTQSPSSLSASV GDRVTITCRASRGIN NWLTWYQQKPGKA PKLLIYGASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYRIPYTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1721
8	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSDISGSGSGT YYADAVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARPGSDGEFDYWGQGTLVT VSSSTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVDKTHTCPPCPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	1634	DIQMTQSPSSLSASV GDRVTITCRASQSVS SFLNWYQQKPGKAP KLLIYAASSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYTTPLTFGQGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1722
9	QVQLVQSGAEVKKPGSSVKVSCKASGGTF SSDAINWVRQAPGQGLEWMGGFDPEDGE TIYAQKFQGRVTITADESTSTAYMELSSLR SEDTAVYYCARGPSGYDFEFDYWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1635	DIQMTQSPSSLSASV GDRVTITCRSSRNIS HWLAWYQQKPGKA PKLLIYKASSLESGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQAISFPLTFGGGTK VEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1723

10	QVQLVQSGAEVKKPGASVKVSCKASGDT FTTYAISWVRQAPGQGLEWMGWINPNSG VATYANKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCAREGIVGATDAFDIWGQG TMVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1636	DIVMTQSPDSLAVSL GERATINCKSSQSVL HSSKNKNYLAWYQ QKPGQPPKLLIYWAS TRESGVPDRFSGSGS GTDFTLTISSLQAED VAVYYCQQYFTTPP TFGPGTKVDIKRTVA APSVFIFPPSDEQLKS GTASVVCLLNNFYP REAKVQWKVDNAL QSGNSQESVTEQDS KDSTYSLSSTLTLSK ADYEKHKVYACEVT HQGLSSPVTKSFNRG EC	1724
11	QVQLVQSGAEVKKPGASVKVSCKASGDT FTNHYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDLVPAAVGGYFDY WGQGTLVTVSSSTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVDKTHTCPPCP PELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1637	DIQMTQSPSSLSASV GDRVTITCRASQSLG SWLAWYQQKPGKA PKLLIYAASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1725
12	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SHWMSWVRQAPGKGLEWVSAISGSGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARDDNSGSQADWGQGTLVT VSSSTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVDKTHTCPPCPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	1638	DIQMTQSPSSLSASV GDRVTITCQASQDID NYLNWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPLTFGGGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1726

13	QVQLVQSGAEVKKPGASVKVSCKASGYS FTGYYMHWVRQAPGQGLEWMGWINPNS GGTYFAQNFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCVKDRGDRVVTSYLDYW GQGTLVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1639	DIQMTQSPSSLSASV GDRVTITCRASQGIR NWLAWYQQKPGKA PKLLIYAASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYRTPYTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1727
14	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGIINPSGG STSYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARAAPYYYDSSGYYSGG YYFDYWGQGTLVTVSSSTKGPSVFPLAPS SKSTSGGTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVPS SSLGTQTYICNVNHKPSNTKVDKKVDKTH TCPPCPPELLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVKFNWYVDGVEV HNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKALPAPIEKTISKAKQ PREPQVYTLPPSREEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVM HEALHNHYTQKSLSLSPGK	1640	DIVMTQSPDSLAVSL GERATINCKSSQSVL YSSNNKNYLAWYQ QKPGQPPKLLIYWAS TRESGVPDRFSGSGS GTDFTLTISSLQAED VAVYYCQQYYTTPL TFGQGTKLEIKRTVA APSVFIFPPSDEQLKS GTASVVCLLNNFYP REAKVQWKVDNAL QSGNSQESVTEQDS KDSTYSLSSTLTLSK ADYEKHKVYACEVT HQGLSSPVTKSFNRG EC	1728
15	EVQLLESGGGLVQPGGSLRLSCAASGFTFS IYEIHWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCARSYCGGDCWDYYYYYGMD VWGQGTTVTVSSSTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVDKTHTCPPC PPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	1641	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYLASNRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCKQTSHIPLTFGQ GTKVEIKRTVAAPSV FIFPPSDEQLKSGTAS VVCLLNNFYPREAK VQWKVDNALQSGN SQESVTEQDSKDSTY SLSSTLTLSKADYEK HKVYACEVTHQGLS SPVTKSFNRGEC	1729

16	EVQLVESGGGLVKPGGSLRLSCAASGFTFS DNSMNWVRQAPGKGLEWVSYISSSGSTIY YADSVKGRFTISRDDSKNTLYLQMNSLKT EDTAVYYCARGRASSWPNWFDPWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1642	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYSASNLQ SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQALQTPPTFG QGTKLEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1730
17	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSGISYDSDKI GYADAVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCAREWEGFDYWGQGTLVTVS SSTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVDKTHTCPPCPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	1643	DIQMTQSPSSLSASV GDRVTITCRASQGIS NNLNWYQQKPGKA PKLLIYESSTLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSAPLTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1731
18	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDHYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAKDKFGDEGSGWYGD FQHWGQGTLVTVSSSTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVDKTHTCP PCPPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	1644	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYLGSNRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQTLRTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1732

19	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYWMHWVRQAPGKGLEWVSGFSGSART YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCAREWSGFDYWGQGTLVTVS SSTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVDKTHTCPPCPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	1645	DIQMTQSPSSLSASV GDRVTITCRASQNIG PWLAWYQQKPGKA PKLLIYDAKDLHPGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANTFPMTFGQGT RLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1733
20	QVQLVQSGAEVKKPGASVKVSCKASGYM FTGYYIHWVRQAPGQGLEWMGWINPNSG GTNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCAKDRFGSGNYGYMDVW GKGTTVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1646	DIQMTQSPSSLSASV GDRVTITCRASQSID RWLAWYQQKPGKA PKLLIYGASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPWTFGQGT RLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1734
21	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMSWVRQAPGKGLEWVSAISGSGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARELSHDYGGNSDFDYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1647	DIQMTQSPSSLSASV GDRVTITCQASQDIS NNLNWYQQKPGKA PKLLIYAASGLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGGGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1735

22	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYIHWVRQAPGQGLEWMGWINPNSG GTNYAQEFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDHRIAVAGSYFDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1648	DIQMTQSPSSLSASV GDRVTITCRASRSIR TWLAWYQQKPGKA PKLLIYAASSLQTGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPYTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1736
23	QVQLVQSGAEVKKPGASVKVSCKASGYP FTAHYIHWVRQAPGQGLEWMGWINPNSG GTNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDVEMATIGAYWYFDL WGRGTLVTVSSSTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVDKTHTCPPCP PELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1649	DIQMTQSPSSLSASV GDRVTITCRASQGIN NWLAWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPPTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1737
24	QVQLVQSGAEVKKPGSSVKVSCKASGYSF TSYGISWVRQAPGQGLEWLGWISAYNGN TNYGQSLQGRVTITADESTSTAYMELSSLR SEDTAVYYCARARGAGTFFDYWGQGTLV TVSSSTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVDKTHTCPPCPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK	1650	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYDATNLP TGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQALQTPFTFG QGTKLEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1738

25	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGRINPNG GSTTYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARDDFYYYYLDFWGKG TTVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1651	DIQMTQSPSSLSASV GDRVTITCRASQSIN DWLAWYQQKPGKA PKLLIYAASNLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQGYSTPPTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1739
26	QVQLVQSGAEVKKPGASVKVSCKASGYT FTENEMHWVRQAPGQGLEWMGWMNPNS GNTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAREGGDWPYYYYMDV WGKGTTVTVSSSTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVDKTHTCPPCP PELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1652	DIQMTQSPSSLSASV GDRVTITCQASQDIR NYLNWYQQKPGKA PKLLIYAASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQTSSTPLTFGPGTK VDIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1740
27	QVQLVQSGAEVKKPGASVKVSCKASGYT LTGYYMHWVRQAPGQGLEWMGWMNPSS GNTGYAQQFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARASSDRYYYDGVWY FDLWGRGTLVTVSSSTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVDKTHTCP PCPPELLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	1653	DIQMTQSPSSLSASV GDRVTITCRASQDIR NNLGWYQQKPGKA PKLLIYGASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQTYSSPPTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1741

28	EVQLLESGGGLVQPGGSLRLSCAASGFTFS TYAMHWVRQAPGKGLEWVSAISGSGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARDGYGDYPFDYWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1654	DIQMTQSPSSLSASV GDRVTITCRASQGID NYLAWYQQKPGKA PKLLIYQASTLESGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSIPWTFGQGTK VEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1742
29	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYLHWVRQAPGQGLEWMGVINVRRG STRYAQNFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARVSGSYYQPWGQGTLV TVSSSTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVDKTHTCPPCPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK	1655	DIQMTQSPSSLSASV GDRVTITCRASQSIS RWLAWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQGNSFPPIFGGGTK VEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1743
30	QVQLVQSGAEVKKPGASVKVSCKASGYT FSNYYMHWVRQAPGQGLEWMGWMNPD SGTTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCVRDGTMVQGIFDYW GQGTLVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1656	DIQMTQSPSSLSASV GDRVTITCRASQSISS WLAWYQQKPGKAP KLLIYGASSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ TYRTPLTFGPGTKVD IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1744

31	QVQLVQSGAEVKKPGSSVKVSCKASGGTF STYAITWVRQAPGQGLEWMGGIIPIVGRA NYAQKFQGRVTITADESTSTAYMELSSLRS EDTAVYYCARSGGHDLDYWGQGTLVTVS SSTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVDKTHTCPPCPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	1657	DIQMTQSPSSLSASV GDRVTITCRASQGIG NDLGWYQQKPGKA PKLLIYGASSVQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPITFGQGTR LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1745
32	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYGMHWVRQAPGKGLEWVSSISGSGDTT YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARDNPYGDYGGSFDYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1658	EIVMTQSPATLSVSP GERATLSCRASQSVS SSYLAWYQQKPGQA PRLLIYATSTRATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQ QYGSLPLTFGQGTK VEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1746
33	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYYMHWVRQAPGQGLEWMGIIDPSGG STNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDYYGSGSYYGLDYWG RGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1659	DIQMTQSPSSLSASV GDRVTITCRASQGIS NNLNWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGPGTK VDIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1747

34	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGIINPSGG STRYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARVDGRRWLQSDYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1660	DIQMTQSPSSLSASV GDRVTITCRASQGIR NDLAWYQQKPGKA PKLLIYAASTLQNGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPWTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1748
35	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGIINPSGG STRYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARVDGRRWLRSDYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1661	DIQMTQSPSSLSASV GDRVTITCRASQGIR NDLAWYQQKPGKA PKLLIYAASTLQNGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPWTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1749
36	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWLGIISPSGRSA GYGRKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARTDYGGHKWYFDLWGRG TLVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1662	DIQMTQSPSSLSASV GDRVTITCQASQGIN NYLNWYQQKPGKA PKLLIYAASTLQRGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYQTPLTFGGGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1750

37	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYLHWVRQAPGQGLEWMGVISPSGG GTSYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARAGFGEGVFRHWGQGT LVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1663	DIQMTQSPSSLSASV GDRVTITCRASQSISS YLNWYQQKPGKAP KLLIYAASSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPLTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1751
38	QVQLVQSGAEVKKPGASVKVSCKASGYS FTSHAISWVRQAPGQGLEWMGWIKPNSG DTKYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARGSDDYYGSYYFDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1664	DIQMTQSPSSLSASV GDRVTITCRASQGIS NYLAWYQQKPGKA PKLLIYTASTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPLTFGGGTK VEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1752
39	EVQLLESGGGLVQPGGSLRLSCAASGFTFR NYGMGWVRQAPGKGLEWVSAISGSGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARVKFYGMDVWGQGTTVT VSSSTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVDKTHTCPPCPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	1665	DIQMTQSPSSLSASV GDRVTITCRASQGIS NDLAWYQQKPGKA PKLLIYGASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPFTFGPGTK VDIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1753

40	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYHMHWVRQAPGQGLEWMGWMSPNS GNTGYAQNFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARADYYGSDYVKFDY WGQGTLVTVSSSTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVDKTHTCPPCP PELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1666	DIQMTQSPSSLSASV GDRVTITCRVSQGIS SYLNWYQQKPGKAP KLLIYEASTLESGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ GYSTPPTFGQGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1754
41	QVQLVQSGAEVKKPGASVKVSCKASGYT FPNYGISWVRQAPGQGLEWMGWINPNSG GTKYAQRFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDRDILTGYYHFDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1667	DIVMTQSPLSLPVTP GEPASISCRSSQSLLQ SNGYNYLDWYLQKP GQSPQLLIYLGSNRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQSTHWPLTFG QGTRLEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1755
42	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYFMHWVRQAPGQGLEWMGWINPNS GNTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARLNDYGDYGGPATLD YWGQGTLVTVSSSTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVDKTHTCPPC PPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	1668	DIQMTQSPSSLSASV GDRVTITCRASQGIS NNLNWYQQKPGKA PKLLIYAASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPPTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1756

43	QVQLVQSGAEVKKPGASVKVSCKASGYT FTNYYMHWVRQAPGQGLEWLGWISPYSG DTKYAQTLQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARESMDRLDYWGQGTLV TVSSSTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVDKTHTCPPCPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK	1669	DIQMTQSPSSLSASV GDRVTITCRASQSIST YLNWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPVLTFGGGTKV EIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1757
44	EVQLLESGGGLVQPGGSLRLSCAASGFTFS SYAMHWVRQAPGKGLEWVADISGSGGLT YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCAREGDQYSSSSFFDYWGQG TLVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1670	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYLGSNRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQALQPPPTFG QGTRLEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1758
45	EVQLVESGGGLVKPGGSLRLSCAASGFTF DEFGMNWVRQAPGKGLEWISYISGDSGYT NCADSVKGRFTISRDDSKNTLYLQMNSLK TEDTAVYYCAAGYGGYYFDYWGQGTLV TVSSSTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVDKTHTCPPCPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK	1671	DIQMTQSPSSLSASV GDRVTITCQASQDID IYLNWYQQKPGKAP KLLIYAASTLESGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPPTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1759

46	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYYMHWVRQAPGQGLEWMGMINPSA GSTSYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCASVDSSGWYAPFDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1672	DIQMTQSPSSLSASV GDRVTITCRASQSIST YLNWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ ANSFPPTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1760
47	EVQLLESGGGLVQPGGSLRLSCAASGFTF DEYAMHWVRQAPGKGLEWVSAIGAGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCASSLGPELRGVDYYYYGMD VWGQGTTVTVSSSTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVDKTHTCPPC PPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	1673	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYAASSLQ SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQGIQWPWTF GQGTKVEIKRTVAA PSVFIFPPSDEQLKSG TASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1761
48	EVQLLESGGGLVQPGGSLRLSCAASGFNF DDYAMHWVRQAPGKGLEWVSVIYSGGST YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCTRHDFDYWGQGTLVTVSSS TKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVDKTHTCPPCPPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPREEQYNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKQPREPQVYTLPPSREEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGK	1674	DIQMTQSPSSLSASV GDRVTITCRASQSIST YVNWYQQKPGKAP KLLIYAASSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ DYSYPYTFGQGTKV EIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1762

49	EVQLVESGGGLVKPGGSLRLSCAASGFTFS DYALHWVRQAPGKGLEWVSLISGDGGST YYADSVKGRFTISRDDSKNTLYLQMNSLK TEDTAVYYCARDLGGERSYWGQGTLVTV SSSTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVDKTHTCPPCPPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG K	1675	DIQMTQSPSSLSASV GDRVTITCRASQSIST WLAWYQQKPGKAP KLLIYAASTLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCLQ DYSYPPTFGQGTKV EIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1763
50	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGIINPSDG STTYAQSFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDELPDSSGWYGYFQH WGQGTLVTVSSSTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ TYICNVNHKPSNTKVDKKVDKTHTCPPCP PELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1676	DIQMTQSPSSLSASV GDRVTITCRASQSISS WLAWYQQKPGKAP KLLIYAASSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYDIPLTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1764
51	QVQLVQSGAEVKKPGSSVKVSCKASGGTF SSYAISWVRQAPGQGLEWMGEIIPFFGTAN YAQKFQGRVTITADESTSTAYMELSSLRSE DTAVYYCARAEYGGDLDYWGQGTLVTVS SSTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVDKTHTCPPCPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	1677	DIQMTQSPSSLSASV GDRVTITCQASQDIS NLLNWYQQKPGKAP KLLIYAASTLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYNTPWTFGPGTKV DIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1765

52	QVQLVQSGAEVKKPGASVKVSCKASGDT FTRHYVHWVRQAPGQGLEWMGIINPRGG THYAQKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARRDCSGGSCYSDLDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1678	DIQMTQSPSSLSASV GDRVTITCQASQDIH NYLNWYQQKPGKA PKLLIYQASSLESGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGGGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1766
53	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGWINPDSG DASYARKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCATFGEEAFDIWGQGTMVT VSSSTKGPSVFPLAPSSKSTSGGTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTQTYICNVNH KPSNTKVDKKVDKTHTCPPCPPELLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLS PGK	1679	DIQMTQSPSSLSASV GDRVTITCRASQNIG SWLAWYQQKPGKA PKLLIYGASILQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ ANSFPLTFGGGTKLE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1767
54	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGWIDPKNG DTNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCATEGSHHPYYYYGMDVW GQGTTVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1680	DIQMTQSPSSLSASV GDRVTITCRASQGIG NWLAWYQQKPGKA PKLLIYEASTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC HQYNAYPWTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1768

55	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYHMHWVRQAPGQGLEWMGWINPNT GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARPNTAMVPPYYYYY GMDVWGQGTLVTVSSSTKGPSVFPLAPSS KSTSGGTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTQTYICNVNHKPSNTKVDKKVDKTHT CPPCPPELLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	1681	DIQMTQSPSSLSASV GDRVTITCQASQDIS NYLNWYQQKPGKA PKLLIYAASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQYNSYPLTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1769
56	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYDINWVRQAPGQGLEWMGWMNPNS GNTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARVSATGTYGLDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1682	DIQMTQSPSSLSASV GDRVTITCRASHSISS WLAWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ ADSFPLTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1770
57	QVQLVQSGAEVKKPGASVKVSCKASGYT FNNYGITWVRQAPGQGLEWMGIINPITGV TTYAQNFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCASGEQQLVLFDYWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1683	DIQMTQSPSSLSASV GDRVTITCQASQDIN DYLNWYQQKPGKA PKLLIYGASNLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC LQHNSYPLTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1771

58	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYLHWVRQAPGQGLEWMGWMNPNS GNTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAADVITAYGMDVWGQ GTMVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1684	DIQMTQSPSSLSASV GDRVTITCRASQGIS NYLAWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYNVPPTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1772
59	EVQLLESGGGLVQPGGSLRLSCAASGFTFS NAWMSWVRQAPGKGLEWVADISYDGTN DYYADSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCTTEELRFGGFDYWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1685	DIQMTQSPSSLSASV GDRVTITCRASQSISS YLNWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ ANSFPLTFGQGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1773
60	QVQLVQSGAEVKKPGSSVKVSCKASGGTF SSYAISWVRQAPGQGLEWMGGIIPMFGTA NYAQKFQGRVTITADESTSTAYMELSSLRS EDTAVYYCARDLGYSNAGGTLHYWGQGT LVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1686	EIVMTQSPATLSVSP GERATLSCRASQSIG TYLAWYQQKPGQAP RLLIYDASSRATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQ QYKSYPLTFGGGTK VEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1774

61	QVQLVQSGAEVKKPGASVKVSCKASGYT FTNYYMHWVRQAPGQGLEWMGIINPSGG STSYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARAEWDILTGYYIDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1687	DIQMTQSPSSLSASV GDRVTITCQASQDIS NYLNWYQQKPGKA PKLLIYGASSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQHNSYPWTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1775
62	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDHFVHWVRQAPGQGLEWMGWISAYN GNTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARAEYSYGFDYWGQG TLVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1688	DIQMTQSPSSLSASV GDRVTITCRASQGIH NYLAWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQTSSFPYTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1776
63	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYVHWVRQAPGQGLEWMGVINPSGG GSPSYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARDRSDVDYGMDVWG QGTTVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1689	DIQMTQSPSSLSASV GDRVTITCQASQDIS NYLNWYQQKPGKA PKLLIYDASNLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC LQHNSYPLTFGGGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1777

64	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGLIDPSGG STNSLQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDVGFGELSFDIWGQGT TVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1690	DIVMTQSPLSLPVTP GEPASISCRSSQSLLH SNGYNYLDWYLQKP GQSPQLLIYAASTLQ SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQGTHWPPTFG PGTKVDIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1778
65	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAREIGGYDNYYYYGM DVWGQGTTVTVSSSTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVDKTHTCPP CPPELLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEAL HNHYTQKSLSLSPGK	1691	DIQMTQSPSSLSASV GDRVTITCRASQSIG TYLNWYQQKPGKAP KLLIYAASSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYTDPWTFGQGTKV EIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1779
66	QVQLVQSGAEVKKPGASVKVSCKASGYT FNTYYMHWVRQAPGQGLEWMGWMHPN TGNTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARGTTSDAFDIWGQG TMVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1692	DIQMTQSPSSLSASV GDRVTITCRASQSIFS YLNWYQQKPGKAP KLLIYSASNLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPITFGQGTKVEI KRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1780

67	QVQLVQSGAEVKKPGASVKVSCKASGDT FTRHYVHWVRQAPGQGLEWMGRVNPRD GRTNSAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCAKDMFPTVTGTYYYYG MDVWGQGTTVTVSSSTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTQTYICNVNHKPSNTKVDKKVDKTHTC PPCPPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKQPRE PQVYTLPPSREEMTKNQVSLTCLVKGFYP SDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVFSCSVMHEA LHNHYTQKSLSLSPGK	1693	DIQMTQSPSSLSASV GDRVTITCRASQGIS SYLAWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ ASGFPYTFGQGTRLE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1781
68	QVQLVQSGAEVKKPGASVKVSCKASGYT FSSYDINWVRQAPGQGLEWVGWINPRNG GTDYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARHRWELDSFDYWGQGT LVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1694	DIQMTQSPSSLSASV GDRVTITCRASQSIS NYLNWYQQKPGKA PKLLIYATSSLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQGYNIPFTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1782
69	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYYIHWVRQAPGQGLEWMGWMNPND GKTAYAQRFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDDDYGGYVAYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1695	DIQMTQSPSSLSASV GDRVTITCRASESISG WLAWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ YDTWPFTFGPGTKV DIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1783

70	EVQLLESGGGLVQPGGSLRLSCAASGMSV TSNHMSWVRQAPGKGLEWVSSIYPDGKT YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCARDEEDWFDPWGQGTLVTV SSSTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVDKTHTCPPCPPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG K	1696	DIQMTQSPSSLSASV GDRVTITCQASQSIS NWLAWYQQKPGKA PKLLIYAASTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPWTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1784
71	EVQLLESGGGLVQPGGSLRLSCAASGFTFS NHYMSWVRQAPGKGLEWVAVIWPDGSK EYYADSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCAREDYYGSGMDYWGQGT LVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1697	DIQMTQSPSSLSASV GDRVTITCQASQDIS NYLNWYQQKPGKA PKLLIYGASTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQYDSYPPTFGGGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1785
72	QVQLVQSGAEVKKPGASVKVSCKASGGT FSNYAISWVRQAPGQGLEWMGWISAYNG NSDYAQNLQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCAIGDYFDYWGQGTLVTVS SSTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVVTVPSSSLGTQTYICNVNHKP SNTKVDKKVDKTHTCPPCPPELLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQ QGNVFSCSVMHEALHNHYTQKSLSLSPGK	1698	DIQMTQSPSSLSASV GDRVTITCQASEDIN KYLNWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1786

73	EVQLLESGGGLVQPGGSLRLSCAASGFTV SSNYMSWVRQAPGKGLEWVAVIYSDGKT YYADSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCAREDSSGSHFDYWGQGTLV TVSSSTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVDKTHTCPPCPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK	1699	DIQMTQSPSSLSASV GDRVTITCRASQSIST YLNWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ AHSFPPTFGQGTRLE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1787
74	QVQLVQSGAEVKKPGSSVKVSCKASGYTF TKYEINWVRQAPGQGLEWMGGIIPIFGTA NYAQKFQGRVTITADESTSTAYMELSSLRS EDTAVYYCARGSGWYTPLFDYWGQGTLV TVSSSTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVDKTHTCPPCPPELLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQY NSTYRVVSVLTVLHQDWLNGKEYKCKVS NKALPAPIEKTISKAKQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK	1700	DIQMTQSPSSLSASV GDRVTITCRASQGIS NNLNWYQQKPGKA PKLLIYDASYLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSAPLTFGQGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1788
75	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYIHWVRQAPGQGLEWMGLIDPSGGS TSIAQKFQGRVTMTRDTSTSTVYMELSSLR SEDTAVYYCARDYDILTGSGFDPWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1701	EIVMTQSPATLSVSP GERATLSCRASQSVS SYLAWYQQKPGQAP RLLIYDASARATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQ QYRSSVTFGQGTRLE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1789

76	QVQLVQSGAEVKKPGASVKVSCKASGYT FTTYYMHWVRQAPGQGLEWMGIINVSAG TTSYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCAKEPYPHQSGWFFDYWG QGTLVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1702	DIQMTQSPSSLSASV GDRVTITCQASQDIN NYLNWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGGGT KVEIKRTVAAPSVFI FPPSDEQLKSGTASV VCLLNNFYPREAKV QWKVDNALQSGNS QESVTEQDSKDSTYS LSSTLTLSKADYEKH KVYACEVTHQGLSS PVTKSFNRGEC	1790
77	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGHYMHWVRQAPGQGLEWMGWISTDN GNANYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDTADYYFDYWGQG TLVTVSSSTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1703	EIVMTQSPATLSVSP GERATLSCSASQSVG SSYFAWYQQKPGQA PRLLIYDVSTRATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQ QYYSTPLTFGPGTKV DIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1791
78	QVQLVQSGAEVKKPGSSVKVSCKASGGTF SRYPFSWVRQAPGQGLEWMGWMNPNNG DTGYAQKFQGRVTITADESTSTAYMELSS LRSEDTAVYYCARGDYPYMDVWGKGTT VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1704	DIQMTQSPSSLSASV GDRVTITCQASQDIS NYLNWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSIPYTFGQGTK LEIKRTVAAPSVFIFP PSDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1792

79	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSDYMHWVRQAPGQGLEWMGWMNPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDYITGPSDWGQGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1705	DIQMTQSPSSLSASV GDRVTITCRASQGIR NDLGWYQQKPGKA PKLLIYAASSLQPGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC LQTNSFPWTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1793
80	QVQLVQSGAEVKKPGASVKVSCKASGFTF TSYYMHWVRQAPGQGLEWMGWMNPNS GNTGYAQRFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARGHSRTDYGMDVWG QGTTVTVSSSTKGPSVFPLAPSSKSTSGGT AALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVDKTHTCPPCPPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKALPAPIEKTISKAKQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSK LTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK	1706	DIQMTQSPSSLSASV GDRVTITCRASQSISS WLAWYQQKPGKAP KLLIYDTSSLQSGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ GYSTPLTFGQGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1794
81	EVQLLESGGGLVQPGGSLRLSCAASGFTFS DHYMSWVRQAPGKGLEWVSIIYPDGKTY YADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAREGSYGDYDGMDVWGQGT TVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1707	DIQMTQSPSSLSASV GDRVTITCQASQDIS NYLNWYQQKPGKA PKLLIYGASTLQSGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPWTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1795

82	QVQLVQSGAEVKKPGSSVKVSCKASGGTF SNYDISWVRQAPGQGLEWMGGIIPIFGTAN YAQKFQGRVTITADESTSTAYMELSSLRSE DTAVYYCAREAEEGGWFDPWGQGTLVTV SSSTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYICNVNHK PSNTKVDKKVDKTHTCPPCPPELLGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPREEQYNST YRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKQPREPQVYTLPPSREEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG K	1708	EIVMTQSPATLSVSP GERATLSCRASQSVS SYLAWYQQKPGQAP RLLIYGASTRATGIP ARFSGSGSGTEFTLTI SSLQSEDFAVYYCQ QYAFSPITFGQGTKL EIKRTVAAPSVFIFPP SDEQLKSGTASVVC LLNNFYPREAKVQW KVDNALQSGNSQES VTEQDSKDSTYSLSS TLTLSKADYEKHKV YACEVTHQGLSSPV TKSFNRGEC	1796
83	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGWMNPN SGYTAYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDTPGSGWSSGMD VWGQGTTVTVSSSTKGPSVFPLAPSSKSTS GGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVDKTHTCPPC PPELLGGPSVFLFPPKPKDTLMISRTPEVTC VVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIA VEWESNGQPENNYKTTPPVLDSDGSFFLY SKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	1709	DIQMTQSPSSLSASV GDRVTITCRVSQGIS SYLNWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPLTFGGGTKVE IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1797
84	QVQLVQSGAEVKKPGASVKVSCKASGGT FSNYAISWVRQAPGQGLEWMGWINPNSG GTNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARVGYYDSSGGGMDVW GQGTTVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1710	DIQMTQSPSSLSASV GDRVTITCRASQSISS WLAWYQQKPGKAP KLLIYDASNLETGVP SRFSGSGSGTDFTLTI SSLQPEDFATYYCLQ THSFPLTFGPGTKVD IKRTVAAPSVFIFPPS DEQLKSGTASVVCL LNNFYPREAKVQWK VDNALQSGNSQESV TEQDSKDSTYSLSST LTLSKADYEKHKVY ACEVTHQGLSSPVT KSFNRGEC	1798

85	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGIINPIGG LTTYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCASGAYGDYVDWYFDLW GRGTLVTVSSSTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVDKTHTCPPCPP ELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKQPREPQVY TLPPSREEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS KLTVDKSRWQQGNVFSCSVMHEALHNHY TQKSLSLSPGK	1711	DIQMTQSPSSLSASV GDRVTITCRASQSVS NWLAWYQQKPGKA PKLLIYDASNLQTGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQANSFPLTFGGGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1799
86	QVQLVQSGAEVKKPGASVKVSCKASGYT FTTYGISWVRQAPGQGLEWMGWINPNSG DTNYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARLTTATDSFDLWGRGTL VTVSSSTKGPSVFPLAPSSKSTSGGTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTQTYICNV NHKPSNTKVDKKVDKTHTCPPCPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQ YNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVD KSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGK	1712	DIVMTQSPLSLPVTP GEPASISCRSSRSLLH SNGYNYLDWYLQKP GQSPQLLIYLGSYRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQGTHWPPTFG QGTKLEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1800
87	QVQLVQSGAEVKKPGASVKVSCKASGYS FTNYYIHWVRQAPGQGLEWMGWMNPYT GQTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCTTDEETMDFHLWGRGT LVTVSSSTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVDKTHTCPPCPPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREE QYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKQPREPQVYTLPPS REEMTKNQVSLTCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNHYTQKS LSLSPGK	1713	DIQMTQSPSSLSASV GDRVTITCRASQSIS RYLNWYQQKPGKA PKLLIYDASNLETGV PSRFSGSGSGTDFTL TISSLQPEDFATYYC QQSYSTPWTFGQGT KLEIKRTVAAPSVFIF PPSDEQLKSGTASVV CLLNNFYPREAKVQ WKVDNALQSGNSQE SVTEQDSKDSTYSLS STLTLSKADYEKHK VYACEVTHQGLSSP VTKSFNRGEC	1801

88	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYHIHWVRQAPGQGLEWMGRINPNSG GTDYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARETYSGSYEESFDYWGQ GTLVTVSSSTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVDKTHTCPPCPPELL GGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPRE EQYNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTISKAKQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK	1714	DIVMTQSPLSLPVTP GEPASISCRSSRSLLH SNGYNYLDWYLQKP GQSPQLLIYLGSDRA SGVPDRFSGSGSGTD FTLKISRVEAEDVGV YYCMQGTHWPPTFG QGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPRE AKVQWKVDNALQS GNSQESVTEQDSKD STYSLSSTLTLSKAD YEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1802

Table 15. IgG4 Antibodies

[00515] Antibody (mAb) Examples 89-130 target CD33, and 131-176 target CLL-1.

mAb Ex.	Heavy Chain	SEQ ID NO	Light Chain	SEQ ID NO
89	QVQLVQSGAEVKKPGASVKVSCKASGYS FTGYYIHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDQWDGYNSGYFD YWGQGTLVTVSSSTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVSKYGPPC PSCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1803	DIQMTQSPSSLSASVG DRVTITCRASQTINDW LAWYQQKPGKAPKLL IYSASTLHSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQAYSTPW TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1891

90	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDYYMSWVRQAPGKGLEWVSGISGSGYS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARTFGRGPDWYFDLWG RGTLVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1804	DIQMTQSPSSLSASVG DRVTITCRASQSISRYL NWYQQKPGKAPKLLI YTASTLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQYDDLPL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1892
91	EVQLLESGGGLVQPGGSLRLSCAASGFTF SNSDMNWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARGREDDYGDYVFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1805	DIQMTQSPSSLSASVG DRVTITCRASQSISSYL NWYQQKPGKAPKLLI YGASTLHSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYRIPYT FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1893
92	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGWINPNSG NTGYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCAREHGDMDVWGQGTT VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1806	EIVMTQSPATLSVSPG ERATLSCRASQNINSD LAWYQQKPGQAPRLL IYGASTRATGIPARFSG SGSGTEFTLTISSLQSE DFAVYYCQQYDSLPF TFGPGTKVDIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1894

93	QVQLVQSGAEVKKPGASVKVSCKASGNT FTSYGISWVRQAPGQGLEWMGWINPNSG GTKYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARESWFGELYYGMDV WGKGTTVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1807	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYLGSDRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ GLQTPITFGQGTRLEIK RTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNF YPREAKVQWKVDNA LQSGNSQESVTEQDSK DSTYSLSSTLTLSKAD YEKHKVYACEVTHQG LSSPVTKSFNRGEC	1895
94	QVQLVQSGAEVKKPGASVKVSCKASGYT FTAYYTHWVRQAPGQGLEWMGWMNPN SGHTSYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAREAYDSFDYWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1808	DIQMTQSPSSLSASVG DRVTITCRASQSISSYL NWYQQKPGKAPKLLI YEASTLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQANSFPFT FGPGTKVDIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1896
95	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDSRIAVAASSFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1809	DIQMTQSPSSLSASVG DRVTITCRASRGINNW LTWYQQKPGKAPKLL IYGASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYRIPY TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1897

96	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYAMSWVRQAPGKGLEWVSDISGSGSG TYYADAVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARPGSDGEFDYWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1810	DIQMTQSPSSLSASVG DRVTITCRASQSVSSF LNWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYTTPL TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1898
97	QVQLVQSGAEVKKPGSSVKVSCKASGGT FSSDAINWVRQAPGQGLEWMGGFDPEDG ETIYAQKFQGRVTITADESTSTAYMELSSL RSEDTAVYYCARGPSGYDFEFDYWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1811	DIQMTQSPSSLSASVG DRVTITCRSSRNISHW LAWYQQKPGKAPKLL IYKASSLESGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQAISFPLT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1899
98	QVQLVQSGAEVKKPGASVKVSCKASGDT FTTYAISWVRQAPGQGLEWMGWINPNSG VATYANKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCAREGIVGATDAFDIWG QGTMVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1812	DIVMTQSPDSLAVSLG ERATINCKSSQSVLHS SKNKNYLAWYQQKP GQPPKLLIYWASTRES GVPDRFSGSGSGTDFT LTISSLQAEDVAVYYC QQYFTTPPTFGPGTKV DIKRTVAAPSVFIFPPS DEQLKSGTASVVCLL NNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSTYSLSSTLTL SKADYEKHKVYACEV THQGLSSPVTKSFNRG EC	1900

99	QVQLVQSGAEVKKPGASVKVSCKASGDT FTNHYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDLVPAAVGGYFDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1813	DIQMTQSPSSLSASVG DRVTITCRASQSLGSW LAWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPL TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1901
100	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSHWMSWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARDDNSGSQADWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1814	DIQMTQSPSSLSASVG DRVTITCQASQDIDNY LNWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTPL TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1902
101	QVQLVQSGAEVKKPGASVKVSCKASGYS FTGYYMHWVRQAPGQGLEWMGWINPNS GGTYFAQNFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCVKDRGDRVVTSYLDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1815	DIQMTQSPSSLSASVG DRVTITCRASQGIRNW LAWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYRTP YTFGQGTKLEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1903

102	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGIINPSG GSTSYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARAAPYYYDSSGYYS GGYYFDYWGQGTLVTVSSSTKGPSVFPL APCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVV TVPSSSLGTKTYTCNVDHKPSNTKVDKR VSKYGPPCPSCPPEFLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSQEDPEVQFNW YVDGVEVHNAKTKPREEQFNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKGLPSSIE KTISKAKQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLSLGK	1816	DIVMTQSPDSLAVSLG ERATINCKSSQSVLYS SNNKNYLAWYQQKP GQPPKLLIYWASTRES GVPDRFSGSGSGTDFT LTISSLQAEDVAVYYC QQYYTTPLTFGQGTK LEIKRTVAAPSVFIFPP SDEQLKSGTASVVCLL NNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSTYSLSSTLTL SKADYEKHKVYACEV THQGLSSPVTKSFNRG EC	1904
103	EVQLLESGGGLVQPGGSLRLSCAASGFTF SIYEIHWVRQAPGKGLEWVSAISGSGGST YYADSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARSYCGGDCWDYYYYYG MDVWGQGTTVTVSSSTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTKTYTCNVDHKPSNTKVDKRVSKYG PPCPSCPPEFLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAK QPREPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	1817	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYLASNRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCKQT SHIPLTFGQGTKVEIKR TVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYP REAKVQWKVDNALQ SGNSQESVTEQDSKDS TYSLSSTLTLSKADYE KHKVYACEVTHQGLS SPVTKSFNRGEC	1905
104	EVQLVESGGGLVKPGGSLRLSCAASGFTF SDNSMNWVRQAPGKGLEWVSYISSSGSTI YYADSVKGRFTISRDDSKNTLYLQMNSL KTEDTAVYYCARGRASSWPNWFDPWGQ GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1818	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYSASNLQSGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ ALQTPPTFGQGTKLEI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1906

105	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYAMSWVRQAPGKGLEWVSGISYDSDK IGYADAVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCAREWEGFDYWGQGTLVT VSSSTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTKTYTCNV DHKPSNTKVDKRVSKYGPPCPSCPPEFLG GPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPR EEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKQPREPQVYTL PPSQEEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSLGK	1819	DIQMTQSPSSLSASVG DRVTITCRASQGISNN LNWYQQKPGKAPKLL IYESSTLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSAPLT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1907
106	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDHYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAKDKFGDEGSGWYGD FQHWGQGTLVTVSSSTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGA LTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTKTYTCNVDHKPSNTKVDKRVSKYGP PCPSCPPEFLGGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAK QPREPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	1820	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYLGSNRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ TLRTPLTFGGGTKVEI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1908
107	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYWMHWVRQAPGKGLEWVSGFSGSAR TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCAREWSGFDYWGQGTLV TVSSSTKGPSVFPLAPCSRSTSESTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVSKYGPPCPSCPPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1821	DIQMTQSPSSLSASVG DRVTITCRASQNIGPW LAWYQQKPGKAPKLL IYDAKDLHPGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANTFP MTFGQGTRLEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1909

108	QVQLVQSGAEVKKPGASVKVSCKASGY MFTGYYIHWVRQAPGQGLEWMGWINPN SGGTNYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDRFGSGNYGYMD VWGKGTTVTVSSSTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVSKYGPPC PSCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1822	DIQMTQSPSSLSASVG DRVTITCRASQSIDRW LAWYQQKPGKAPKLL IYGASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTP WTFGQGTRLEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1910
109	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYAMSWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARELSHDYGGNSDFDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1823	DIQMTQSPSSLSASVG DRVTITCQASQDISNN LNWYQQKPGKAPKLL IYAASGLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1911
110	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYIHWVRQAPGQGLEWMGWINPNS GGTNYAQEFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDHRIAVAGSYFDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1824	DIQMTQSPSSLSASVG DRVTITCRASRSIRTW LAWYQQKPGKAPKLL IYAASSLQTGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTPY TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1912

111	QVQLVQSGAEVKKPGASVKVSCKASGYP FTAHYIHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDVEMATIGAYWYF DLWGRGTLVTVSSSTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVSKYGPP CPSCPPEFLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKGLPSSIEKTISKAKQ PREPQVYTLPPSQEEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSLGK	1825	DIQMTQSPSSLSASVG DRVTITCRASQGINNW LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPP TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1913
112	QVQLVQSGAEVKKPGSSVKVSCKASGYS FTSYGISWVRQAPGQGLEWLGWISAYNG NTNYGQSLQGRVTITADESTSTAYMELSS LRSEDTAVYYCARARGAGTFFDYWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1826	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYDATNLPTGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ ALQTPFTFGQGTKLEI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1914
113	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGRINPNG GSTTYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDDFYYYYLDFWGK GTTVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1827	DIQMTQSPSSLSASVG DRVTITCRASQSINDW LAWYQQKPGKAPKLL IYAASNLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQGYSTPP TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1915

114	QVQLVQSGAEVKKPGASVKVSCKASGYT FTENEMHWVRQAPGQGLEWMGWMNPN SGNTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAREGGDWPYYYMD VWGKGTTVTVSSSTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVSKYGPPC PSCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1828	DIQMTQSPSSLSASVG DRVTITCQASQDIRNY LNWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQTSSTPL TFGPGTKVDIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1916
115	QVQLVQSGAEVKKPGASVKVSCKASGYT LTGYYMHWVRQAPGQGLEWMGWMNPS SGNTGYAQQFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARASSDRYYYDGVW YFDLWGRGTLVTVSSSTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTKTYTCNVDHKPSNTKVDKRVSKYG PPCPSCPPEFLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAK QPREPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	1829	DIQMTQSPSSLSASVG DRVTITCRASQDIRNN LGWYQQKPGKAPKLL IYGASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQTYSSPP TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1917
116	EVQLLESGGGLVQPGGSLRLSCAASGFTF STYAMHWVRQAPGKGLEWVSAISGSGGS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARDGYGDYPFDYWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1830	DIQMTQSPSSLSASVG DRVTITCRASQGIDNY LAWYQQKPGKAPKLL IYQASTLESGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSIPWT FGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1918

117	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYLHWVRQAPGQGLEWMGVINVRR GSTRYAQNFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARVSGSYYQPWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1831	DIQMTQSPSSLSASVG DRVTITCRASQSISRW LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQGNSFPP IFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1919
118	QVQLVQSGAEVKKPGASVKVSCKASGYT FSNYYMHWVRQAPGQGLEWMGWMNPD SGTTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCVRDGTMVQGIFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1832	DIQMTQSPSSLSASVG DRVTITCRASQSISSW LAWYQQKPGKAPKLL IYGASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQTYRTP LTFGPGTKVDIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1920
119	QVQLVQSGAEVKKPGSSVKVSCKASGGT FSTYAITWVRQAPGQGLEWMGGIIPIVGR ANYAQKFQGRVTITADESTSTAYMELSSL RSEDTAVYYCARSGGHDLDYWGQGTLV TVSSSTKGPSVFPLAPCSRSTSESTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVSKYGPPCPSCPPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1833	DIQMTQSPSSLSASVG DRVTITCRASQGIGND LGWYQQKPGKAPKLL IYGASSVQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTPI TFGQGTRLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1921

120	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYGMHWVRQAPGKGLEWVSSISGSGDT TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARDNPYGDYGGSFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1834	EIVMTQSPATLSVSPG ERATLSCRASQSVSSS YLAWYQQKPGQAPRL LIYATSTRATGIPARFS GSGSGTEFTLTISSLQS EDFAVYYCQQYGSLP LTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1922
121	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYYMHWVRQAPGQGLEWMGIIDPSGG STNYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARDYYGSGSYYGLDY WGRGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1835	DIQMTQSPSSLSASVG DRVTITCRASQGISNN LNWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPL TFGPGTKVDIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1923
122	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGIINPSG GSTRYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARVDGRRWLQSDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1836	DIQMTQSPSSLSASVG DRVTITCRASQGIRND LAWYQQKPGKAPKLL IYAASTLQNGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTP WTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1924

123	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGIINPSG GSTRYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARVDGRRWLRSDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1837	DIQMTQSPSSLSASVG DRVTITCRASQGIRND LAWYQQKPGKAPKLL IYAASTLQNGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTP WTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1925
124	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWLGIISPSGRSA GYGRKFQGRVTMTRDTSTSTVYMELSSL RSEDTAVYYCARTDYGGHKWYFDLWGR GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1838	DIQMTQSPSSLSASVG DRVTITCQASQGINNY LNWYQQKPGKAPKLL IYAASTLQRGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYQTP LTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1926
125	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYLHWVRQAPGQGLEWMGVISPSG GGTSYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARAGFGEGVFRHWGQ GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1839	DIQMTQSPSSLSASVG DRVTITCRASQSISSYL NWYQQKPGKAPKLLI YAASSLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSTPLT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1927

126	QVQLVQSGAEVKKPGASVKVSCKASGYS FTSHAISWVRQAPGQGLEWMGWIKPNSG DTKYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARGSDDYYGSYYFDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1840	DIQMTQSPSSLSASVG DRVTITCRASQGISNY LAWYQQKPGKAPKLL IYTASTLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSTPLT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1928
127	EVQLLESGGGLVQPGGSLRLSCAASGFTF RNYGMGWVRQAPGKGLEWVSAISGSGG STYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARVKFYGMDVWGQGTT VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1841	DIQMTQSPSSLSASVG DRVTITCRASQGISND LAWYQQKPGKAPKLL IYGASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPF TFGPGTKVDIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1929
128	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYHMHWVRQAPGQGLEWMGWMSPN SGNTGYAQNFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARADYYGSDYVKFD YWGQGTLVTVSSSTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVSKYGPPC PSCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1842	DIQMTQSPSSLSASVG DRVTITCRVSQGISSYL NWYQQKPGKAPKLLI YEASTLESGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQGYSTPPT FGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1930

129	QVQLVQSGAEVKKPGASVKVSCKASGYT FPNYGISWVRQAPGQGLEWMGWINPNSG GTKYAQRFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARDRDILTGYYHFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1843	DIVMTQSPLSLPVTPG EPASISCRSSQSLLQSN GYNYLDWYLQKPGQS PQLLIYLGSNRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQS THWPLTFGQGTRLEIK RTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNF YPREAKVQWKVDNA LQSGNSQESVTEQDSK DSTYSLSSTLTLSKAD YEKHKVYACEVTHQG LSSPVTKSFNRGEC	1931
130	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYFMHWVRQAPGQGLEWMGWINPNS GNTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARLNDYGDYGGPATL DYWGQGTLVTVSSSTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVSKYGPP CPSCPPEFLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKGLPSSIEKTISKAKQ PREPQVYTLPPSQEEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSLGK	1844	DIQMTQSPSSLSASVG DRVTITCRASQGISNN LNWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTPP TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1932
131	QVQLVQSGAEVKKPGASVKVSCKASGYT FTNYYMHWVRQAPGQGLEWLGWISPYS GDTKYAQTLQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARESMDRLDYWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1845	DIQMTQSPSSLSASVG DRVTITCRASQSISTYL NWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSTPVL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1933

132	EVQLLESGGGLVQPGGSLRLSCAASGFTF SSYAMHWVRQAPGKGLEWVADISGSGG LTYYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAREGDQYSSSSFFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1846	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYLGSNRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ ALQPPPTFGQGTRLEI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1934
133	EVQLVESGGGLVKPGGSLRLSCAASGFTF DEFGMNWVRQAPGKGLEWISYISGDSGY TNCADSVKGRFTISRDDSKNTLYLQMNSL KTEDTAVYYCAAGYGGYYFDYWGQGTL VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1847	DIQMTQSPSSLSASVG DRVTITCQASQDIDIYL NWYQQKPGKAPKLLI YAASTLESGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSTPPT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1935
134	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYYMHWVRQAPGQGLEWMGMINPSA GSTSYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCASVDSSGWYAPFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1848	DIQMTQSPSSLSASVG DRVTITCRASQSISTYL NWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQANSFPPT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1936

135	EVQLLESGGGLVQPGGSLRLSCAASGFTF DEYAMHWVRQAPGKGLEWVSAIGAGGS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCASSLGPELRGVDYYYYG MDVWGQGTTVTVSSSTKGPSVFPLAPCS RSTSESTAALGCLVKDYFPEPVTVSWNSG ALTSGVHTFPAVLQSSGLYSLSSVVTVPSS SLGTKTYTCNVDHKPSNTKVDKRVSKYG PPCPSCPPEFLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAK QPREPQVYTLPPSQEEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGK	1849	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYAASSLQSGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ GIQWPWTFGQGTKVE IKRTVAAPSVFIFPPSD EQLKSGTASVVCLLN NFYPREAKVQWKVD NALQSGNSQESVTEQ DSKDSTYSLSSTLTLS KADYEKHKVYACEVT HQGLSSPVTKSFNRGE C	1937
136	EVQLLESGGGLVQPGGSLRLSCAASGFNF DDYAMHWVRQAPGKGLEWVSVIYSGGS TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCTRHDFDYWGQGTLVTV SSSTKGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVVTVPSSSLGTKTYTCNVD HKPSNTKVDKRVSKYGPPCPSCPPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVS QEDPEVQFNWYVDGVEVHNAKTKPREE QFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNKGLPSSIEKTISKAKQPREPQVYTLP PSQEEMTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSR LTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSLGK	1850	DIQMTQSPSSLSASVG DRVTITCRASQSISTYV NWYQQKPGKAPKLLI YAASSLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQDYSYPY TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1938
137	EVQLVESGGGLVKPGGSLRLSCAASGFTF SDYALHWVRQAPGKGLEWVSLISGDGGS TYYADSVKGRFTISRDDSKNTLYLQMNS LKTEDTAVYYCARDLGGERSYWGQGTL VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1851	DIQMTQSPSSLSASVG DRVTITCRASQSISTW LAWYQQKPGKAPKLL IYAASTLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCLQDYSYPP TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1939

138	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGIINPSD GSTTYAQSFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDELPDSSGWYGYF QHWGQGTLVTVSSSTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVSKYGPP CPSCPPEFLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKGLPSSIEKTISKAKQ PREPQVYTLPPSQEEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSLGK	1852	DIQMTQSPSSLSASVG DRVTITCRASQSISSW LAWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYDIPL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1940
139	QVQLVQSGAEVKKPGSSVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGEIIPFFGT ANYAQKFQGRVTITADESTSTAYMELSSL RSEDTAVYYCARAEYGGDLDYWGQGTL VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1853	DIQMTQSPSSLSASVG DRVTITCQASQDISNL LNWYQQKPGKAPKLL IYAASTLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYNTP WTFGPGTKVDIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1941
140	QVQLVQSGAEVKKPGASVKVSCKASGDT FTRHYVHWVRQAPGQGLEWMGIINPRGG THYAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARRDCSGGSCYSDLDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1854	DIQMTQSPSSLSASVG DRVTITCQASQDIHNY LNWYQQKPGKAPKLL IYQASSLESGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQANSFPLT FGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1942

141	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGWINPDSG DASYARKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCATFGEEAFDIWGQGTM VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1855	DIQMTQSPSSLSASVG DRVTITCRASQNIGSW LAWYQQKPGKAPKLL IYGASILQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQANSFPLT FGGGTKLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1943
142	QVQLVQSGAEVKKPGASVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGWIDPKNG DTNYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCATEGSHHPYYYYGMDV WGQGTTVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1856	DIQMTQSPSSLSASVG DRVTITCRASQGIGNW LAWYQQKPGKAPKLL IYEASTLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCHQYNAYP WTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1944
143	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYHMHWVRQAPGQGLEWMGWINPN TGGTNYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARPNTAMVPPYYYY YGMDVWGQGTLVTVSSSTKGPSVFPLAP CSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVS KYGPPCPSCPPEFLGGPSVFLFPPKPKDTL MISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	1857	DIQMTQSPSSLSASVG DRVTITCQASQDISNY LNWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQYNSYP LTFGQGTKLEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1945

144	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYDINWVRQAPGQGLEWMGWMNPNS GNTGYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARVSATGTYGLDYWG QGTLVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1858	DIQMTQSPSSLSASVG DRVTITCRASHSISSW LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQADSFPL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1946
145	QVQLVQSGAEVKKPGASVKVSCKASGYT FNNYGITWVRQAPGQGLEWMGIINPITGV TTYAQNFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCASGEQQLVLFDYWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1859	DIQMTQSPSSLSASVG DRVTITCQASQDINDY LNWYQQKPGKAPKLL IYGASNLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCLQHNSYP LTFGQGTKLEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1947
146	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYLHWVRQAPGQGLEWMGWMNPN SGNTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAADVITAYGMDVWG QGTMVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1860	DIQMTQSPSSLSASVG DRVTITCRASQGISNY LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYNVP PTFGQGTKVEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1948

147	EVQLLESGGGLVQPGGSLRLSCAASGFTF SNAWMSWVRQAPGKGLEWVADISYDGT NDYYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCTTEELRFGGFDYWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1861	DIQMTQSPSSLSASVG DRVTITCRASQSISSYL NWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQANSFPLT FGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1949
148	QVQLVQSGAEVKKPGSSVKVSCKASGGT FSSYAISWVRQAPGQGLEWMGGIIPMFGT ANYAQKFQGRVTITADESTSTAYMELSSL RSEDTAVYYCARDLGYSNAGGTLHYWG QGTLVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1862	EIVMTQSPATLSVSPG ERATLSCRASQSIGTY LAWYQQKPGQAPRLL IYDASSRATGIPARFSG SGSGTEFTLTISSLQSE DFAVYYCQQYKSYPL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1950
149	QVQLVQSGAEVKKPGASVKVSCKASGYT FTNYYMHWVRQAPGQGLEWMGIINPSG GSTSYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARAEWDILTGYYIDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1863	DIQMTQSPSSLSASVG DRVTITCQASQDISNY LNWYQQKPGKAPKLL IYGASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQHNSYP WTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1951

150	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDHFVHWVRQAPGQGLEWMGWISAYN GNTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARAEYSYGFDYWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1864	DIQMTQSPSSLSASVG DRVTITCRASQGIHNY LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQTSSFPY TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1952
151	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYVHWVRQAPGQGLEWMGVINPSG GGSPSYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARDRSDVDYGMDV WGQGTTVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1865	DIQMTQSPSSLSASVG DRVTITCQASQDISNY LNWYQQKPGKAPKLL IYDASNLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCLQHNSYP LTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1953
152	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGLIDPSG GSTNSLQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDVGFGELSFDIWGQ GTTVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1866	DIVMTQSPLSLPVTPG EPASISCRSSQSLLHSN GYNYLDWYLQKPGQS PQLLIYAASTLQSGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ GTHWPPTFGPGTKVDI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1954

153	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGWINPNS GGTNYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAREIGGYDNYYYYGM DVWGQGTTVTVSSSTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSL GTKTYTCNVDHKPSNTKVDKRVSKYGPP CPSCPPEFLGGPSVFLFPPKPKDTLMISRTP EVTCVVVDVSQEDPEVQFNWYVDGVEV HNAKTKPREEQFNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKGLPSSIEKTISKAKQ PREPQVYTLPPSQEEMTKNQVSLTCLVKG FYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVM HEALHNHYTQKSLSLSLGK	1867	DIQMTQSPSSLSASVG DRVTITCRASQSIGTY LNWYQQKPGKAPKLL IYAASSLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYTDP WTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1955
154	QVQLVQSGAEVKKPGASVKVSCKASGYT FNTYYMHWVRQAPGQGLEWMGWMHPN TGNTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARGTTSDAFDIWGQ GTMVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1868	DIQMTQSPSSLSASVG DRVTITCRASQSIFSYL NWYQQKPGKAPKLLI YSASNLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSTPIT FGQGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1956
155	QVQLVQSGAEVKKPGASVKVSCKASGDT FTRHYVHWVRQAPGQGLEWMGRVNPRD GRTNSAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAKDMFPTVTGTYYYY GMDVWGQGTTVTVSSSTKGPSVFPLAPC SRSTSESTAALGCLVKDYFPEPVTVSWNS GALTSGVHTFPAVLQSSGLYSLSSVVTVP SSSLGTKTYTCNVDHKPSNTKVDKRVSK YGPPCPSCPPEFLGGPSVFLFPPKPKDTLM ISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKGLPSSIEKTIS KAKQPREPQVYTLPPSQEEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLGK	1869	DIQMTQSPSSLSASVG DRVTITCRASQGISSYL AWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQASGFPY TFGQGTRLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1957

156	QVQLVQSGAEVKKPGASVKVSCKASGYT FSSYDINWVRQAPGQGLEWVGWINPRNG GTDYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARHRWELDSFDYWGQ GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1870	DIQMTQSPSSLSASVG DRVTITCRASQSISNYL NWYQQKPGKAPKLLI YATSSLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQGYNIPFT FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1958
157	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSYYIHWVRQAPGQGLEWMGWMNPND GKTAYAQRFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCARDDDYGGYVAYWG QGTLVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1871	DIQMTQSPSSLSASVG DRVTITCRASESISGW LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQYDTWP FTFGPGTKVDIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1959
158	EVQLLESGGGLVQPGGSLRLSCAASGMS VTSNHMSWVRQAPGKGLEWVSSIYPDGK TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCARDEEDWFDPWGQGTL VTVSSSTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1872	DIQMTQSPSSLSASVG DRVTITCQASQSISNW LAWYQQKPGKAPKLL IYAASTLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTP WTFGQGTKVEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1960

159	EVQLLESGGGLVQPGGSLRLSCAASGFTF SNHYMSWVRQAPGKGLEWVAVIWPDGS KEYYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAREDYYGSGMDYWGQ GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1873	DIQMTQSPSSLSASVG DRVTITCQASQDISNY LNWYQQKPGKAPKLL IYGASTLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQYDSYP PTFGGGTKVEIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1961
160	QVQLVQSGAEVKKPGASVKVSCKASGGT FSNYAISWVRQAPGQGLEWMGWISAYN GNSDYAQNLQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAIGDYFDYWGQGTLV TVSSSTKGPSVFPLAPCSRSTSESTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPA VLQSSGLYSLSSVVTVPSSSLGTKTYTCN VDHKPSNTKVDKRVSKYGPPCPSCPPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1874	DIQMTQSPSSLSASVG DRVTITCQASEDINKY LNWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPL TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1962
161	EVQLLESGGGLVQPGGSLRLSCAASGFTV SSNYMSWVRQAPGKGLEWVAVIYSDGK TYYADSVKGRFTISRDNSKNTLYLQMNS LRAEDTAVYYCAREDSSGSHFDYWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1875	DIQMTQSPSSLSASVG DRVTITCRASQSISTYL NWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQAHSFPPT FGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1963

162	QVQLVQSGAEVKKPGSSVKVSCKASGYT FTKYEINWVRQAPGQGLEWMGGIIPIFGT ANYAQKFQGRVTITADESTSTAYMELSSL RSEDTAVYYCARGSGWYTPLFDYWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1876	DIQMTQSPSSLSASVG DRVTITCRASQGISNN LNWYQQKPGKAPKLL IYDASYLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSAPL TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1964
163	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYIHWVRQAPGQGLEWMGLIDPSGG STSIAQKFQGRVTMTRDTSTSTVYMELSS LRSEDTAVYYCARDYDILTGSGFDPWGQ GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1877	EIVMTQSPATLSVSPG ERATLSCRASQSVSSY LAWYQQKPGQAPRLL IYDASARATGIPARFS GSGSGTEFTLTISSLQS EDFAVYYCQQYRSSV TFGQGTRLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1965
164	QVQLVQSGAEVKKPGASVKVSCKASGYT FTTYYMHWVRQAPGQGLEWMGIINVSA GTTSYAQKFQGRVTMTRDTSTSTVYMEL SSLRSEDTAVYYCAKEPYPHQSGWFFDY WGQGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1878	DIQMTQSPSSLSASVG DRVTITCQASQDINNY LNWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPL TFGGGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1966

165	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGHYMHWVRQAPGQGLEWMGWISTD NGNANYAQKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDTADYYFDYWG QGTLVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1879	EIVMTQSPATLSVSPG ERATLSCSASQSVGSS YFAWYQQKPGQAPRL LIYDVSTRATGIPARFS GSGSGTEFTLTISSLQS EDFAVYYCQQYYSTP LTFGPGTKVDIKRTVA APSVFIFPPSDEQLKSG TASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1967
166	QVQLVQSGAEVKKPGSSVKVSCKASGGT FSRYPFSWVRQAPGQGLEWMGWMNPNN GDTGYAQKFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARGDYPYMDVWGKG TTVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1880	DIQMTQSPSSLSASVG DRVTITCQASQDISNY LNWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSIPY TFGQGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1968
167	QVQLVQSGAEVKKPGASVKVSCKASGYT FTSDYMHWVRQAPGQGLEWMGWMNPN SGGTNYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARDYITGPSDWGQG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1881	DIQMTQSPSSLSASVG DRVTITCRASQGIRND LGWYQQKPGKAPKLL IYAASSLQPGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCLQTNSFP WTFGQGTKLEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1969

168	QVQLVQSGAEVKKPGASVKVSCKASGFT FTSYYMHWVRQAPGQGLEWMGWMNPN SGNTGYAQRFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARGHSRTDYGMDV WGQGTTVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1882	DIQMTQSPSSLSASVG DRVTITCRASQSISSW LAWYQQKPGKAPKLL IYDTSSLQSGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQGYSTPL TFGQGTKVEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1970
169	EVQLLESGGGLVQPGGSLRLSCAASGFTF SDHYMSWVRQAPGKGLEWVSIIYPDGKT YYADSVKGRFTISRDNSKNTLYLQMNSL RAEDTAVYYCAREGSYGDYDGMDVWG QGTTVTVSSSTKGPSVFPLAPCSRSTSEST AALGCLVKDYFPEPVTVSWNSGALTSGV HTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVSKYGPPCPSC PPEFLGGPSVFLFPPKPKDTLMISRTPEVT CVVVDVSQEDPEVQFNWYVDGVEVHNA KTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKQPREP QVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLGK	1883	DIQMTQSPSSLSASVG DRVTITCQASQDISNY LNWYQQKPGKAPKLL IYGASTLQSGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQSYSTP WTFGQGTKLEIKRTV AAPSVFIFPPSDEQLKS GTASVVCLLNNFYPRE AKVQWKVDNALQSG NSQESVTEQDSKDSTY SLSSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	1971
170	QVQLVQSGAEVKKPGSSVKVSCKASGGT FSNYDISWVRQAPGQGLEWMGGIIPIFGT ANYAQKFQGRVTITADESTSTAYMELSSL RSEDTAVYYCAREAEEGGWFDPWGQGT LVTVSSSTKGPSVFPLAPCSRSTSESTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTF PAVLQSSGLYSLSSVVTVPSSSLGTKTYTC NVDHKPSNTKVDKRVSKYGPPCPSCPPEF LGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSQEDPEVQFNWYVDGVEVHNAKTKP REEQFNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKGLPSSIEKTISKAKQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAV EWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNH YTQKSLSLSLGK	1884	EIVMTQSPATLSVSPG ERATLSCRASQSVSSY LAWYQQKPGQAPRLL IYGASTRATGIPARFSG SGSGTEFTLTISSLQSE DFAVYYCQQYAFSPIT FGQGTKLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1972

171	QVQLVQSGAEVKKPGASVKVSCKASGYT FTDYYMHWVRQAPGQGLEWMGWMNPN SGYTAYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDTPGSGWSSGMD VWGQGTTVTVSSSTKGPSVFPLAPCSRST SESTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLG TKTYTCNVDHKPSNTKVDKRVSKYGPPC PSCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1885	DIQMTQSPSSLSASVG DRVTITCRVSQGISSYL NWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQSYSTPLT FGGGTKVEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1973
172	QVQLVQSGAEVKKPGASVKVSCKASGGT FSNYAISWVRQAPGQGLEWMGWINPNSG GTNYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARVGYYDSSGGGMDV WGQGTTVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1886	DIQMTQSPSSLSASVG DRVTITCRASQSISSW LAWYQQKPGKAPKLL IYDASNLETGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCLQTHSFPL TFGPGTKVDIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1974
173	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYYMHWVRQAPGQGLEWMGIINPIGG LTTYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCASGAYGDYVDWYFDL WGRGTLVTVSSSTKGPSVFPLAPCSRSTS ESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVSKYGPPCP SCPPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVH NAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKQP REPQVYTLPPSQEEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLSLGK	1887	DIQMTQSPSSLSASVG DRVTITCRASQSVSNW LAWYQQKPGKAPKLL IYDASNLQTGVPSRFS GSGSGTDFTLTISSLQP EDFATYYCQQANSFPL TFGGGTKLEIKRTVAA PSVFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGN SQESVTEQDSKDSTYS LSSTLTLSKADYEKHK VYACEVTHQGLSSPV TKSFNRGEC	1975

174	QVQLVQSGAEVKKPGASVKVSCKASGYT FTTYGISWVRQAPGQGLEWMGWINPNSG DTNYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARLTTATDSFDLWGRG TLVTVSSSTKGPSVFPLAPCSRSTSESTAA LGCLVKDYFPEPVTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVSKYGPPCPSCPPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVV VDVSQEDPEVQFNWYVDGVEVHNAKTK PREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1888	DIVMTQSPLSLPVTPG EPASISCRSSRSLLHSN GYNYLDWYLQKPGQS PQLLIYLGSYRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ GTHWPPTFGQGTKLEI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1976
175	QVQLVQSGAEVKKPGASVKVSCKASGYS FTNYYIHWVRQAPGQGLEWMGWMNPY TGQTGYAQKFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCTTDEETMDFHLWGR GTLVTVSSSTKGPSVFPLAPCSRSTSESTA ALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSSLGTKTY TCNVDHKPSNTKVDKRVSKYGPPCPSCPP EFLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSQEDPEVQFNWYVDGVEVHNAKT KPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKQPREPQV YTLPPSQEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	1889	DIQMTQSPSSLSASVG DRVTITCRASQSISSYL NWYQQKPGKAPKLLI YDASNLETGVPSRFSG SGSGTDFTLTISSLQPE DFATYYCQQANTFPIT FGQGTRLEIKRTVAAP SVFIFPPSDEQLKSGTA SVVCLLNNFYPREAK VQWKVDNALQSGNS QESVTEQDSKDSTYSL SSTLTLSKADYEKHKV YACEVTHQGLSSPVT KSFNRGEC	1977
176	QVQLVQSGAEVKKPGASVKVSCKASGYT FTGYHIHWVRQAPGQGLEWMGRINPNSG GTDYAQKFQGRVTMTRDTSTSTVYMELS SLRSEDTAVYYCARETYSGSYEESFDYW GQGTLVTVSSSTKGPSVFPLAPCSRSTSES TAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTK TYTCNVDHKPSNTKVDKRVSKYGPPCPS CPPEFLGGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSQEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKQPR EPQVYTLPPSQEEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHE ALHNHYTQKSLSLSLGK	1890	DIVMTQSPLSLPVTPG EPASISCRSSRSLLHSN GYNYLDWYLQKPGQS PQLLIYLGSDRASGVP DRFSGSGSGTDFTLKIS RVEAEDVGVYYCMQ GTHWPPTFGQGTKVEI KRTVAAPSVFIFPPSDE QLKSGTASVVCLLNN FYPREAKVQWKVDN ALQSGNSQESVTEQDS KDSTYSLSSTLTLSKA DYEKHKVYACEVTHQ GLSSPVTKSFNRGEC	1978

Example 15: AML Cell Line Xenograft Model using Antibody Drug Conjugate

[00516] Antibody drug conjugates may be generated by conjugating a biologically active compound to a variant specific antibody. Examples may include the conjugation of molecules such as saporin (a ribosome inactivating protein), MMAE, MMAF, DM1, or DM4 to an anti-$CD33^{R69}$ antibody or anti-$CD33^{G69}$ antibody, leading to cell death upon antigen binding and antibody mediated internalization of the drug.

[00517] Six to ten week old immunodeficient NOD.Cg-Prkdcscid Il2rgtm1Wjl Tg(CMV-IL3,CSF2,KITLG)1Eav/ MloySzJ (NSG-SGM3) mice may be used in murine patient-derived xenograft experiments. Both male and female mice may be used in experiments and randomly assigned to a treatment group.

[00518] Target AML cell lines may be obtained from commercially vendors (ATCC). Target expression was confirmed by FACS analysis and target cell genotype obtained through DNA sequencing. Cells may be modified to express CBR-GFP (Click beetle luciferase and Green Fluorescent Protein).

[00519] Mice are engrafted with an appropriate amount, e.g., $1x10^6$ cells on day -7. On day 0 mice are treated with an appropriate amount of ADC (e.g., dosing ranging from 0.1 mg/kg to 5 mg/kg) on days 0, +7, and +14.

[00520] For example, a $CD33^{R69}$ AML Cell line, KG1a, may be engrafted into mice and treated with either anti-$CD33^{G69}$-saporin or anti-$CD33^{R69}$-saporin, a positive control (anti-CD33-saporin) or a negative control (anti-CD33 and free saporin).

[00521] Tumor burden may be monitored by bioluminescent imaging (BLI) weekly. Mice will be monitored for survival Bone marrow may be extracted from mice and tumor burden assessed using FACS.

[00522] It is expected that anti-CD33-saporin (positive control) will kill CD33+ targets independent of the CD33 genotype ($CD33^{R69}$ or $CD33^{G69}$), reduce tumor burden, and prolong survival. Anti-$CD33^{R69}$-saporin is expected to kill $CD33^{R69}$ targets (example KG1a), reduce tumor burden, and prolong survival of mice. Anti-$CD33^{G69}$-saporin would not be expected to kill $CD33^{R69}$ targets and would not offer a survival advantage or reduce tumor burden.

Example 16: Clinical Applications

[00523] Several clinical applications of polymorphically selective treatment of subjects are given below. In the examples below, the polymorphic antigen may be, e.g., CD33, FLT3, or CLL-1; for illustrative purposes, CD33 will be used.

[00524] *Scenario 1: No prior screening, screen patients upon relapse.* In this scenario, a subject with cancer, e.g. MDS or AML, is conditioned and transplanted with HSC from a related or unrelated histocompatible donor, whether from a human leukocyte antigen (HLA)-identical sibling, a HLA-matched donor, a cord blood unit, or a haploidentical donor, screened for a low probability of allorejection and graft-versus-host disease (GvHD). Most HSCT recipients eventually relapse. If relapse occurs, the subject becomes eligible for therapy with polymorphically selective treatment such as CAR-bearing immune effector cells (e.g., TCR-deleted CAR-T or CAR-NK or CAR-iNKT), or NK cells in combination with an antibody that induces ADCC) that target an antigen expressed on the surface of the subject's malignant cells.

[00525] If the subject relapses post-transplant, the subject is then genotyped using either a protein- (e.g. FACS) or DNA- (PCR) based approach to ensure the HSC donor and patient express different variants of the target antigen, e.g., CD33. If the subject and donor do express different variants of target antigen, e.g. one expresses $CD33^{R69}$ and the other expresses $CD33^{G69}$, the subject is eligible for polymorphic treatment. The subject is then conditioned (e.g., cyclophosphamide/fludarabine, 3 days) and treated with CAR-bearing immune effector cells (e.g., TCR-deleted CAR-T or CAR-NK or CAR-iNKT), or NK cells in combination with an antibody that induces ADCC targeting the patient specific target antigen. For example, the patient whose cells express $CD33^{R69}$ and whose HSCT graft expresses may be treated with $CD33^{G69}$ may be treated with TCR-deleted $CD33^{R69}$-CART, or $CD33^{R69}$-CAR-NK, or donor NK cells in combination with an anti- $CD33^{R69}$ antibody that induces ADCC. The $CD33^{R69}$-selective therapy will kill the subject's cancerous cells and spare the $CD33^{G69}$-expressing HSCT cells. The reverse mismatched combination would also be effective. The subject may then be monitored and, optionally, retreated with one or more of these selective therapies.

[00526] *Scenario 2: Prospective screening, screen patients upon relapse.* In this scenario, HSCT donors are prospectively screened to assess the donor's expression of a polymorphic

variant of a given target antigen, e.g., CD33, and identify a donor who expresses a different variant than the prospective recipient subject. This can be done by genotyping patient and donor using a (PCR) based genotyping approach. At this time, both HSC and immune effector cells (such as T cells, NK cells, and iNKT cells) may be harvested from the same donor and separated via leukapheresis. The HSC may be used for transplant into the target-mismatched recipient; and the immune effector cells may be transduced with a CAR that selectively binds the variant of the antigen (e.g., $CD33^{R69}$ or $CD33^{G69}$) expressed by the recipient's, but not the donor's cells, or stored for later use if needed.

[00527] The subject is conditioned and transplanted with HSC from a target-mismatched donor, e.g. a donor who expresses $CD33^{G69}$ and for a patient who expresses $CD33^{R69}$, or the reverse. The donor may be a related or unrelated histocompatible donor as above.

[00528] If relapse occurs, the subject is conditioned (e.g., cyclophosphamide/ fludarabine, 3 days) and treated with polymorphically selective treatment such as CAR-bearing immune effector cells (e.g., CAR-T, TCR-deleted CAR-T, CAR-NK, or CAR-iNKT), or NK cells in combination with an antibody that induces ADCC) that target the variant of the antigen expressed on the surface of the subject's malignant cells and not the variant expressed on the surface of the donor's cells. For example, the patient whose cells express $CD33^{R69}$ and whose HSCT graft expresses may be treated with $CD33^{G69}$ may be treated with TCR-deleted $CD33^{R69}$-CART, or $CD33^{R69}$-CAR-NK, or donor NK cells in combination with an anti-$CD33^{R69}$ antibody that induces ADCC. The $CD33^{R69}$-selective therapy will kill the subject's $CD33^{R69}$-expressing cancerous cells and spare the $CD33^{G69}$-expressing HSCT cells. The reverse mismatched combination would also be effective. The subject may then be monitored and, optionally, retreated with one or more of these selective therapies.

[00529] *Scenario 3: Prospective screening, treat patients upon relapse.* In this scenario, HSCT donors are prospectively screened to assess the donor's expression of a polymorphic variant of a given target antigen, e.g., CD33, and identify a donor who expresses a different variant than the prospective recipient subject. This can be done by genotyping patient and donor using a (PCR) based genotyping approach.

[00530] The subject is conditioned and transplanted with HSC from a target-mismatched donor, e.g. a donor who expresses $CD33^{G69}$ and for a patient who expresses $CD33^{R69}$, or the

reverse. The donor may be a related or unrelated histocompatible donor as above. If relapse occurs, the subject is conditioned (e.g., cyclophosphamide/ fludarabine, 3 days) and treated with polymorphically selective treatment such as CAR-bearing immune effector cells (e.g., TCR-deleted CAR-T or CAR-NK or CAR-iNKT), or NK cells in combination with an antibody that induces ADCC, or an antibody-drug conjugate comprising an antibody that induces ADCC, that target the variant of the antigen expressed on the surface of the subject's malignant cells and not the variant expressed on the surface of the donor's cells. For example, the patient whose cells express $CD33^{R69}$ and whose HSCT graft expresses may be treated with $CD33^{G69}$ may be treated with TCR-deleted $CD33^{R69}$-CART, or $CD33^{R69}$-CAR-NK, or donor NK cells in combination with an anti-$CD33^{R69}$ antibody that induces ADCC. The $CD33^{R69}$-selective therapy will kill the subject's $CD33^{R69}$-expressing cancerous cells and spare the $CD33^{G69}$-expressing HSCT cells. The reverse mismatched combination would also be effective. The subject may then be monitored and, optionally, retreated with one or more of these selective therapies.

[00531] *Scenario 4: Prospective screening, treat at time of transplant.* In this scenario, HSCT donors are prospectively screened to assess the donor's expression of a polymorphic variant of a given target antigen, e.g., CD33, and identify a donor who expresses a different variant than the prospective recipient subject. This can be done by genotyping patient and donor using a (PCR) based genotyping approach.

[00532] The subject is conditioned and transplanted with HSC from a target-mismatched donor, e.g. a donor who expresses $CD33^{G69}$ and for a patient who expresses $CD33^{R69}$, or the reverse. The donor may be a related or unrelated histocompatible donor as above. The conditioning may be as for standard HSCT (fully myeloablative), or reduced intensity conditioning (RIC); or alternatively, could be a T cell depleted transplant.

[00533] Nearly concurrently with transplant – that is, within 1 day, 2 days, 3 days, or 10 days, etc. of HSCT, but in any event, not requiring relapse – the subject is treated with polymorphically selective treatment such as CAR-bearing immune effector cells (e.g., CAR-T, TCR-deleted CAR-T, CAR-NK, or CAR-iNKT), or NK cells in combination with an antibody that induces ADCC) that target the variant of the antigen expressed on the surface of the subject's malignant cells and not the variant expressed on the surface of the donor's cells. For example, the patient whose cells express $CD33^{R69}$ and whose HSCT graft

expresses may be treated with $CD33^{G69}$ may be treated with TCR-deleted $CD33^{R69}$-CART, or $CD33^{R69}$-CAR-NK, or donor NK cells in combination with an anti-$CD33^{R69}$ antibody that induces ADCC. The $CD33^{R69}$-selective therapy will kill the subject's $CD33^{R69}$-expressing cancerous cells and spare the $CD33^{G69}$-expressing HSCT cells. The reverse mismatched combination would also be effective. The subject may then be monitored and, optionally, retreated with one or more of these selective therapies.

[00534] The foregoing methods may be adapted to demonstrate the binding and polymorphic selectivity of other scFvs, antibodies, antibody-drug conjugates, and CARs against antigens such as cancer antigens. For example, the methods are expected to demonstrate anti-FLT3 scFvs that selectively bind either the T227 or M227 variants. The methods are also expected to demonstrate anti-CLL-1 scFvs that selectively bind either the K244 or Q244 variant.

Example 17: Identification of Non-Selective Anti-Human CD33 scFv Clones

[00535] The methods above in Example 1 have been used to discover polymorphically non-selective anti-human CD33 scFv clones.

Table 16a. Sequences of Non-Selective Anti-CD33 Polypeptides (CDR Sequences)

Poly-peptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
89	YTFTNYYMH	705	GWINPNSGDTNYE	760	CARDDRIQLWVPLVFW	815	RASQGISNYLA	870	SASNLQS	925	CQQSFSTPFTF	980
90	FTFSNSDMN	706	SYISGTGSTIYYA	761	CAKDYDSSYGSGYYGMDVW	816	RASQSIYNYLN	871	AASNLQS	926	CQQYGNAPLTF	981
91	GTFSSYAIS	707	GWMNPNSGNTGYA	762	CAREDYYDSSGNFDYW	817	QASHDINIHLN	872	DASNLET	927	CQQAYSLPWTF	982
92	YTFTNHYMH	708	GIINPSGGSTSYA	763	CASAEVGATHYGMDVW	818	RSSQSLLHSNGYNYLD	873	AASSLQS	928	CMQALHPPTF	983
93	YSFTNYDIS	709	GWVNPNSGNTGYA	764	CAKDAPYYYDSSGYYGVFDYW	819	RSSQSLLHSNGYNYLD	874	AASSLQS	929	CMQALQTPLTF	984
94	YTFTTYDIN	710	GWISGYNGNTGYA	765	CAKDMGYGDYPDAFDIW	820	RSSQSLLHSNGYNYLD	875	AASTLQS	930	CMQALQIPITF	985
95	YSFTTYDIN	711	GRMNPNSGNTGYA	766	CARVVHGMDVW	821	RSSQSLLHSNGYNYLD	876	LGSLRAP	931	CMQALQTPWTF	986

96	GTFSS YAIS	712	GWMN PSSAN TGYA	767	CAKDE MELLT AFDIW	822	RASQSI GSWLA	877	GVSTL HS	932	CQQSY STPPTF	987
97	FTFRS YWMT	713	SVISGS GDNTY YA	768	CARET TWGM DVW	823	RASQSI SSYLN	878	DASNL ET	933	CQQSSI IPLTF	988
98	GSFSSS AIN	714	GWMN PNSGN TGYA	769	CARDR GIAVA GASPY YYYG MDVW	824	RASQD IGSYLA	879	AASSL QS	934	CHQSY STPFTF	989
99	YTFSD YHIH	715	GWMN PNSGN TGYA	770	CARTH SSGYY YWFDP W	825	RASQG ISNNLN	880	QASNK DT	935	CQQSY SSPPTF	990
100	ATRSW MH	716	GIINPS GDSTS YA	771	CAKEP YSSSP YYFDY W	826	RASQSI SSWLA	881	GASSL QS	936	CQQSY TTPITF	991
101	FTFSSY GVH	717	SAISGD GGDTY YA	772	CARDT WDYS NYGGI DYW	827	RASQN INTFLN	882	AASTL QS	937	CQQYD SFPLTF	992
102	FTFSN AWMS	718	SGIGGS GGTIY YA	773	CAREV AAPLH PFGYY YYMD VW	828	RSSQS LLHSN GYNYL D	883	LGSNR AS	938	CMQAL ETPITF	993
103	YTFTG YYMH	719	GWMN PDSGD TNYA	774	CATTR QPHYG MDVW	829	RSSQS LLHSN GYNYL D	884	LGSNR AS	939	CMQAT HWPTF	994

104	FTFSSS WMH	720	AVISY DGSEE YYA	775	CARLT DYGDY VLGRY LSDW	830	RASQG ISSYLA	885	AASSL QS	940	CQQSY SIPPTF	995
105	FTFNN AWMT	721	AVISY DGSNK YYA	776	CARM AVAGK GAFDI W	831	RASQSI YSWLA	886	AASTL QS	941	CQQTY STPVTF	996
106	YTFTG YYMH	722	GRIKP NSGGT DYA	777	CARGA YSGSY YGPIE YFQH W	832	RASQSI SWFLN	887	AASSL QN	942	CQQYG SFPPTF	997
107	YTFTD YYIH	723	GGIIPIF GTANY A	778	CAREP LWFGE SSPHD YYGM DVW	833	QASQD ISNYLN	888	AASTL QS	943	CQQSY SSPPTF	998
108	YTFTN YDIN	724	GWMN PNSGN TGLV	779	CARG WGHG YGDYK FDYW	834	RSSQS LLYSS NNLNY LA	889	WASTR ES	944	CQQYY SNPLTF	999
109	YTFTT YGIS	725	GWMN PNSGN TGYA	780	CAREG GDGDY PDYW	835	RASQSI SSSSLA	890	GASTR AT	945	CQQYE TAPYT F	1000
110	YTFTD YYVH	726	GWMN PNSGN TGYA	781	CARDF IWVEG YLASP PPRFD YW	836	RASQRI GNWL A	891	AASSL QS	946	CQQSY STPLTF	1001
111	GTFTS YGIS	727	GWINP NTGVT NYA	782	CANEQ GGFDY W	837	RASQS VAGSY LA	892	GASTR AT	947	CQQYY STPLTF	1002

112	STLTG YDIH	728	GGIIPF LGTAS YA	783	CARGG GSGYD LDYW	838	RSSESI SSWLA	893	SASTL QS	948	CQQSY STPVTF	1003
113	GTFSS YDIN	729	GGLIP VFGTT HYA	784	CATGL GVTTS NYYYG MDVW	839	RASQG IRNDIG	894	AASTL QS	949	CQQTY MMPYT F	1004
114	GTFSK YAIS	730	GWMN PNSGN TGYA	785	CARDQ GLTGY FDLW	840	RASQSI GNWL A	895	KASSL ES	950	CQQSY NTPPTF	1005
115	YTFTG YYMH	731	GIISPS GGSPT YA	786	CAREG NGGM DVW	841	RSSQS LLHSN GYNYL D	896	LGSNR AS	951	CMQAL QTPYT F	1006
116	FTFSN YAMA	732	SAISGS GGGTY YA	787	CAREG GYDPD YYYYG MDVW	842	RASQSI SSYLN	897	ATSRL QS	952	CQQGF NFPPTF	1007
117	FTFGD YPMS	733	AGISY DGLNE HYA	788	CARDR DSGPS GFQH W	843	RASQTI GTWLA	898	DASSL ES	953	CQQSY STPPTF	1008
118	FTISNA WMS	734	AHIWN DGSQK YYA	789	CARDG ALGVG PDDY W	844	RSSQS LLHSN GYNYL D	899	AASSL QS	954	CMQGL QTPHT F	1009
119	NTLTN DHIH	735	GWMN PNSGD TGYA	790	CARAG VDTA MVTY YYYG MDVW	845	RSSQS LLHSN GYNYL D	900	MGSNR AS	955	CMQAL ETPTF	1010

120	YTFTT YYMH	736	GWMN PNSGN TGYA	791	CARGH KVDSG YDPYG MDVW	846	RASQSI GTYLH	901	AISTLQ N	956	CQQSY SPPLTF	1011
121	DSFTD YYIH	737	GWMN PNSGN TGYA	792	CARDR EYSSSS RYFDL W	847	RASQN IGNWL A	902	AASTL QS	957	CQQSY NSITF	1012
122	YTFTD YWLH	738	GTINPS GGSTS YS	793	CAKEE EGFWS GYAFD YW	848	RASQSI SSYLN	903	AASSL QS	958	CQQSY STPLTF	1013
123	FILGNA WMH	739	ASVSG DGSDE NYA	794	CARDT HDYGD YAPFD YW	849	QASQD INNYL N	904	AASNL QS	959	CQQTY SFPLTF	1014
124	FTFSSY WMH	740	AVIWY DGSNK YYA	795	CVRDG ARSGM DVW	850	RASQS VSTYV A	905	GASTR AT	960	CQQYY DTPLTF	1015
125	YSFTT YDIH	741	GWMN PNSGN TGYA	796	CATDH WVLG GFDY W	851	QASQD ISNYLN	906	AASTL QS	961	CQQYS YLPVT F	1016
126	FTFTTY DMH	742	AGINW NSVIID YA	797	CAKDL LYYYD SIGAFD IW	852	RASQSI STWLA	907	AASSL QS	962	CQQSD TLPLTF	1017
127	YTFTN HHMH	743	GMINP SGGST SYA	798	CARGR PVDIV ATYYF DYW	853	QASQD IRNFLN	908	GASTL HS	963	CQQSY STPLTF	1018

128	YTFTN YYIH	744	GWTNP INGDT GSA	799	CAKEG QLAW ADYYY YMDV W	854	RASQG ISSALA	909	AASSL QS	964	CQQSY STPLTF	1019
129	FSLRN YWMH	745	SGISGS GGSTY YA	800	CARDY TGVVD YW	855	RASQSI SSYLN	910	AASSL QS	965	CQQSY STPLTF	1020
130	GTFSN YAIS	746	AWMN PNSGN TGYA	801	CARDG FIGFGE LFSAF DIW	856	RASQSI GTWLA	911	GATRL LS	966	CQQSY STPPTF	1021
131	GTFSN YAIN	747	GWINP NSGGT DSA	802	CARDS SLALS YGGNS EYYYG MDVW	857	QASQD ISDHLN	912	GASTL QS	967	CQQAY SFPWT F	1022
132	FTFNN YGMH	748	SAISGS GGSTY YA	803	CAREY MQQPH GGMD VW	858	RASQS VNSYL A	913	GASTR AT	968	CQQYG SSPLSF	1023
133	FTFSSS WMH	749	SAISSS GDATY YA	804	CAKFS DGGAG DSDY W	859	RASQG ISSYLA	914	TASSL QS	969	CQQYD NLPITF	1024
134	YTFDS YLLH	750	GMINP SGAGT TYA	805	CAKEG SIAAG YYFDS W	860	RASQSI DSWLA	915	AASSL QS	970	CQQSY TTPITF	1025
135	YSFTT YGIT	751	GWINP NSGNA GYA	806	CASDL AGYSS GYFDL W	861	KSSQS VLYGS NNKNY LA	916	WASTR ES	971	CQQYY STPLTF	1026

136	DTLTN HFVH	752	GWMN PNSGN TGYA	807	CARDP QMGA VAGGF DYW	862	RASQRI GNWL A	917	AASSL QS	972	CQQSY SPPLTF	1027
137	YTFTD YYIH	753	GMVNP SGGSA NYA	808	CAKDS AWQEP YYFDY W	863	RASQG ISSYLA	918	DASNL DT	973	CQQSY STPLTF	1028
138	YTFSS YDMH	754	GVINP GGGYT NYA	809	CARDE GWELL LDYW	864	RASQS VGSNL A	919	GASTR AT	974	CQQSH SLPPTF	1029
139	YTLSD HDIN	755	GWMN PSTGN TGYA	810	CERDQ LRFGA WFDP W	865	RASQG IRNYL A	920	AASSL QS	975	CQQSY SIPLTF	1030
140	ITVSSS WMH	756	SAIGT GGGTH YA	811	CARDQ GGQID HW	866	RASQSI SSWLA	921	DASTL QS	976	CQQSY SIPLTF	1031
141	GTFSS YAIS	757	GVISPN GDTTV YA	812	CARDR GVAHS YYYG MDVW	867	RASQSI SSYLN	922	AASSL HS	977	CQQSY SPPITF	1032
142	FTFSSY WMH	758	AVISY DGSDK YYA	813	CARGL GGTTG TADFD YW	868	RASQSI SSYLN	923	AASSL QS	978	CQQSY STPLTF	1033
143	YTFTG YYMH	759	GWMN ANSGN TGFA	814	CARDS SSWLS GGGW FDPW	869	RASQSI GTYLS	924	AASSL QS	979	CQQSY SSPITF	1034
191	GTFSS YAIS	1979	GWMN PNSGN TGYA	1982	CARED YYDSS GNFDY W	1985	QASHD INIHLN	1988	DASNL ET	1991	CQQAY SLPWT F	1994

192	YTFTN YYMH	1980	GWINP NSGDT NYE	1983	CARDD RIQLW VPLVF W	1986	RASQG ISNYLA	1989	SASNL QS	1992	CQQSF STPFTF	1995
193	FTFSNS DMN	1981	SYISGT GSTIY YA	1984	CAKDY DSSYG SGYYG MDVW	1987	RASQSI YNYLN	1990	AASNL QS	1993	CQQYG NAPLT F	1996

Table 16b. Sequences of Non-Selective Anti- CD33 Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
89	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGWINPNSGDTNY EQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDD RIQLWVPLVFWGQGTLVTVSS	1035	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYSASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSFSTPFTFGQGTKLE IKR	1090
90	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNSDMNWVRQAP GKGLEWVSYISGTGSTIYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKDYDSS YGSGYYGMDVWGQGTTVTV SS	1036	DIQMTQSPSSLSASVGDRVTI TCRASQSIYNYLNWYQQKPG KAPKLLIYAASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYGNAPLTFGQGTKV EIKR	1091
91	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAREDY YDSSGNFDYWGQGTLVTVSS	1037	DIQMTQSPSSLSASVGDRVTI TCQASHDINIHLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAYSLPWTFGQGTKV EIKR	1092
92	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNHYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCASAEVG ATHYGMDVWGQGTTVTVSS	1038	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASSLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALHPPTFG QGTKVEIKR	1093
93	QVQLVQSGAEVKKPGASVKV SCKASGYSFTNYDISWVRQAP GQGLEWMGWVNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDAP YYYDSSGYYGVFDYWGQGTL VTVSS	1039	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASSLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPLTFG QGTRLEIKR	1094
94	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYDINWVRQAP GQGLEWMGWISGYNGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDM GYGDYPDAFDIWGQGTMVTV SS	1040	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASTLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQIPITFG QGTKVEIKR	1095
95	QVQLVQSGAEVKKPGSSVKV SCKASGYSFTTYDINWVRQAP GQGLEWMGRMNPNSGNTGY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARVVHG MDVWGQGTTVTVSS	1041	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSLRAPGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPWTF GQGTKVEIKR	1096

96	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGWMNPSSANTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDE MELLTAFDIWGQGTMVTVSS	1042	DIQMTQSPSSLSASVGDRVTI TCRASQSIGSWLAWYQQKPG KAPKLLIYGVSTLHSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGQGTKLE IKR	1097
97	EVQLLESGGGLVQPGGSLRLS CAASGFTFRSYWMTWVRQAP GKGLEWVSVISGSGDNTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARETTW GMDVWGQGTTVTVSS	1043	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSSIIPLTFGGGTKVEI KR	1098
98	QVQLVQSGAEVKKPGASVKV SCKASGGSFSSSAINWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDR GIAVAGASPYYYYGMDVWG QGTTVTVSS	1044	DIQMTQSPSSLSASVGDRVTI TCRASQDIGSYLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCHQSYSTPFTFGQGTKLE IKR	1099
99	QVQLVQSGAEVKKPGSSVKV SCKASGYTFSDYHIHWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARTHSS GYYYWFDPWGQGTLVTVSS	1045	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLNWYQQKPG KAPKLLIYQASNKDTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSSPPTFGQGTKVE IKR	1100
100	QVQLVQSGAEVKKPGASVKV SCKASGATRSWMHWVRQAP GQGLEWMGIINPSGDSTSYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKEPYSS SPYYFDYWGQGTLVTVSS	1046	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYTTPITFGQGTRLE IKR	1101
101	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYGVHWVRQAP GKGLEWVSAISGDGGDTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDTW DYSNYGGIDYWGQGTLVTVS S	1047	DIQMTQSPSSLSASVGDRVTI TCRASQNINTFLNWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYDSFPLTFGGGTKV EIKR	1102
102	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNAWMSWVRQAP GKGLEWVSGIGGSGGTIYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAREVAAP LHPFGYYYYMDVWGKGTTV TVSS	1048	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALETPITFG QGTRLEIKR	1103

103	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGWMNPDSGDTN YAQNFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCATTR QPHYGMDVWGQGTTVTVSS	1049	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQATHWPTFG QGTRLEIKR	1104
104	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSSWMHWVRQAP GKGLEWVAVISYDGSEEYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARLTDY GDYVLGRYLSDWGQGTLVTV SS	1050	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPPTFGQGTKLEI KR	1105
105	EVQLLESGGGLVQPGGSLRLS CAASGFTFNNAWMTWVRQA PGKGLEWVAVISYDGSNKYY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCARMA VAGKGAFDIWGQGTMVTVSS	1051	DIQMTQSPSSLSASVGDRVTI TCRASQSIYSWLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYSTPVTFGQGTKV EIKR	1106
106	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGRIKPNSGGTDY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGA YSGSYYGPIEYFQHWGQGTLV TVSS	1052	DIQMTQSPSSLSASVGDRVTI TCRASQSISWFLNWYQQKPG KAPKLLIYAASSLQNGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYGSFPPTFGGGTKV EIKR	1107
107	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTDYYIHWVRQAP GQGLEWMGGIIPIFGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAREPLWFG ESSPHDYYGMDVWGQGTLVT VSS	1053	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSSPPTFGQGTKVE IKR	1108
108	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYDINWVRQAP GQGLEWMGWMNPNSGNTGL VEKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGW GHGYGDYKFDYWGQGTLVT VSS	1054	DIVMTQSPDSLAVSLGERATI NCRSSQSLLYSSNNLNYLAW YQQKPGQPPKLLIYWASTRES GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCQQYYSNPLTF GQGTKVEIKR	1109
109	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTTYGISWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCAREGGD GDYPDYWGQGTLVTVSS	1055	EIVMTQSPATLSVSPGERATL SCRASQSISSSSLAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYETAPYTFGQGTKLE IKR	1110

110	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYVHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDF IWVEGYLASPPPRFDYWGQGT LVTVSS	1056	DIQMTQSPSSLSASVGDRVTI TCRASQRIGNWLAWYQQKP GKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSTPLTFGQGTK LEIKR	1111
111	QVQLVQSGAEVKKPGASVKV SCKASGGTFTSYGISWVRQAP GQGLEWMGWINPNTGVTNY AQDFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCANEQ GGFDYWGQGTLVTVSS	1057	EIVMTQSPATLSVSPGERATL SCRASQSVAGSYLAWYQQKP GQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYYSTPLTFGGGTK VEIKR	1112
112	QVQLVQSGAEVKKPGSSVKV SCKASGSTLTGYDIHWVRQAP GQGLEWMGGIIPFLGTASYAQ EFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARGGGSGY DLDYWGQGTLVTVSS	1058	DIQMTQSPSSLSASVGDRVTI TCRSSESISSWLAWYQQKPG KAPKLLIYSASTLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPVTFGQGTRLEI KR	1113
113	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYDINWVRQAP GQGLEWMGGLIPVFGTTHYA QNFQGRVTITADESTSTAYME LSSLRSEDTAVYYCATGLGVT TSNYYYGMDVWGQGTLVTV SS	1059	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNDIGWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYMMPYTFGQGTK LEIKR	1114
114	QVQLVQSGAEVKKPGASVKV SCKASGGTFSKYAISWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDQ GLTGYFDLWGRGTLVTVSS	1060	DIQMTQSPSSLSASVGDRVTI TCRASQSIGNWLAWYQQKPG KAPKLLIYKASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYNTPPTFGPGTKVDI KR	1115
115	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGIISPSGGSPTYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAREGNG GMDVWGQGTTVTVSS	1061	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPYTF GQGTKLEIKR	1116
116	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNYAMAWVRQAP GKGLEWVSAISGSGGGTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAREGGY DPDYYYYGMDVWGQGTTVT VSS	1062	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYATSRLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQGFNFPPTFGGGTKV EIKR	1117

117	EVQLLESGGGLVQPGGSLRLS CAASGFTFGDYPMSWVRQAP GKGLEWVAGISYDGLNEHYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDRDS GPSGFQHWGQGTLVTVSS	1063	DIQMTQSPSSLSASVGDRVTI TCRASQTIGTWLAWYQQKPG KAPKLLIYDASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPPTFGQGTKVEI KR	1118
118	EVQLVESGGGLVKPGGSLRLS CAASGFTISNAWMSWVRQAP GKGLEWVAHIWNDGSQKYY ADSVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCARDGA LGVGPDDYWGQGTLVTVSS	1064	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASSLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGLQTPHTF GGGTKVEIKR	1119
119	QVQLVQSGAEVKKPGASVKV SCKASGNTLTNDHIHWVRQA PGQGLEWMGWMNPNSGDTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARA GVDTAMVTYYYYGMDVWG QGTTVTVSS	1065	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYMGSNRASG VPDRFSGSGSGTDFTLKISRV EAEDVGVYYCMQALETPTFG QGTRLEIKR	1120
120	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYYMHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARG HKVDSGYDPYGMDVWGQGT TVTVSS	1066	DIQMTQSPSSLSASVGDRVTI TCRASQSIGTYLHWYQQKPG KAPKLLIYAISTLQNGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSPPLTFGGGTKVEI KR	1121
121	QVQLVQSGAEVKKPGASVKV SCKASGDSFTDYYIHWVRQAP GQGLEWMGWMNPNSGNTGY AQQFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDRE YSSSSRYFDLWGRGTLVTVSS	1067	DIQMTQSPSSLSASVGDRVTI TCRASQNIGNWLAWYQQKP GKAPKLLIYAASTLQSGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQSYNSITFGPGTKV DIKR	1122
122	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYWLHWVRQA PGQGLEWMGTINPSGGSTSYS HKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAKEEEG FWSGYAFDYWGQGTLVTVSS	1068	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	1123
123	EVQLLESGGGLVQPGGSLRLS CAASGFILGNAWMHWVRQAP GKGLEWVASVSGDGSDENYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDTHD YGDYAPFDYWGQGTLVTVSS	1069	DIQMTQSPSSLSASVGDRVTI TCQASQDINNYLNWYQQKPG KAPKLLIYAASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYSFPLTFGGGTKV EIKR	1124

124	EVQLVESGGGLVKPGGSLRLS CAASGFTFSSYWMHWVRQAP GKGLEWVAVIWYDGSNKYY ADSVKGRFTISRDDSKNTLYL QMNSLKTEDTAVYYCVRDGA RSGMDVWGQGTTVTVSS	1070	EIVMTQSPATLSVSPGERATL SCRASQSVSTYVAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYYDTPLTFGGGTKVE IKR	1125
125	QVQLVQSGAEVKKPGASVKV SCKASGYSFTTYDIHWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCATDH WVLGGFDYWGQGTLVTVSS	1071	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYSYLPVTFGQGTKL EIKR	1126
126	EVQLLESGGGLVQPGGSLRLS CAASGFTFTTYDMHWVRQAP GKGLEWVAGINWNSVIIDYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAKDLLY YYDSIGAFDIWGQGTMVTVSS	1072	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSDTLPLTFGGGTKV EIKR	1127
127	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNHHMHWVRQA PGQGLEWMGMINPSGGSTSY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGRP VDIVATYYFDYWGQGTLVTV SS	1073	DIQMTQSPSSLSASVGDRVTI TCQASQDIRNFLNWYQQKPG KAPKLLIYGASTLHSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1128
128	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYIHWVRQAP GQGLEWLGWTNPINGDTGSA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAKEGQL AWADYYYYMDVWGKGTTVT VSS	1074	DIQMTQSPSSLSASVGDRVTI TCRASQGISSALAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1129
129	EVQLVESGGGLVKPGGSLRLS CAASGFSLRNYWMHWVRQA PGKGLEWVSGISGSGGSTYYA DSVKGRFTISRDDSKNTLYLQ MNSLKTEDTAVYYCARDYTG VVDYWGQGTLVTVSS	1075	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1130
130	QVQLVQSGAEVKKPGASVKV SCKASGGTFSNYAISWVRQAP GQGLEWMAWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDGF IGFGELFSAFDIWGQGTMVTV SS	1076	DIQMTQSPSSLSASVGDRVTI TCRASQSIGTWLAWYQQKPG KAPKLLIYGATRLLSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGQGTKLE IKR	1131

131	QVQLVQSGAEVKKPGASVKV SCKASGGTFSNYAINWVRQAP GQGLEWMGWINPNSGGTDSA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDSSL ALSYGGNSEYYYGMDVWGQ GTTVTVSS	1077	DIQMTQSPSSLSASVGDRVTI TCQASQDISDHLNWYQQKPG KAPKLLIYGASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAYSFPWTFGQGTKL EIKR	1132
132	EVQLLESGGGLVQPGGSLRLS CAASGFTFNNYGMHWVRQAP GKGLEWVSAISGSGGSTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAREYMQQ PHGGMDVWGQGTTVTVSS	1078	EIVMTQSPATLSVSPGERATL SCRASQSVNSYLAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYGSSPLSFGGGTKVEI KR	1133
133	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSSWMHWVRQAP GKGLEWVSAISSSGDATYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKFSDGG AGDSDYWGQGTLVTVSS	1079	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYTASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQYDNLPITFGQGTRLEI KR	1134
134	QVQLVQSGAEVKKPGASVKV SCKASGYTFDSYLLHWVRQA PGQGLEWMGMINPSGAGTTY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKEGS IAAGYYFDSWGQGTLVTVSS	1080	DIQMTQSPSSLSASVGDRVTI TCRASQSIDSWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYTTPITFGGGTKVE IKR	1135
135	QVQLVQSGAEVKKPGASVKV SCKASGYSFTTYGITWVRQAP GQGLEWMGWINPNSGNAGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCASDLA GYSSGYFDLWGRGTLVTVSS	1081	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYGSNNKNYLA WYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCQQYYSTPL TFGGGTKVEIKR	1136
136	QVQLVQSGAEVKKPGASVKV SCKASGDTLTNHFVHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARDP QMGAVAGGFDYWGQGTLVT VSS	1082	DIQMTQSPSSLSASVGDRVTI TCRASQRIGNWLAWYQQKP GKAPKLLIYAASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSPPLTFGPGTKV DIKR	1137
137	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYIHWVRQAP GQGLEWMGMVNPSGGSANY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDSA WQEPYYFDYWGQGTLVTVSS	1083	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYDASNLDTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1138

138	QVQLVQSGAEVKKPGASVKV SCKASGYTFSSYDMHWVRQA PGQGLEWMGVINPGGGYTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDEG WELLLDYWGQGTLVTVSS	1084	EIVMTQSPATLSVSPGERATL SCRASQSVGSNLAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQSHSLPPTFGQGTRLEI KR	1139
139	QVQLVQSGAEVKKPGASVKV SCKASGYTLSDHDINWVRQAP GQGLEWMGWMNPSTGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCERDQL RFGAWFDPWGQGTLVTVSS	1085	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNYLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPLTFGGGTKVE IKR	1140
140	EVQLVESGGGLVKPGGSLRLS CAASGITVSSSWMHWVRQAP GKGLEWVSAIGTGGGTHYAD SVKGRFTISRDDSKNTLYLQM NSLKTEDTAVYYCARDQGGQ IDHWGQGTLVTVSS	1086	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPLTFGGGTKVE IKR	1141
141	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGVISPNGDTTVYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDRGV AHSYYYGMDVWGQGTLVTV SS	1087	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLHSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSPPITFGQGTRLEI KR	1142
142	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYWMHWVRQAP GKGLEWVAVISYDGSDKYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARGLGG TTGTADFDYWGQGTLVTVSS	1088	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1143
143	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGWMNANSGNTG FAQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDSS SWLSGGGWFDPWGQGTLVTV SS	1089	DIQMTQSPSSLSASVGDRVTI TCRASQSIGTYLSWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSSPITFGQGTKLEI KR	1144
191	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAREDY YDSSGNFDYWGQGTLVTVSS	1997	DIQMTQSPSSLSASVGDRVTI TCQASHDINIHLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAYSLPWTFGQGTKV EIKR	2000

192	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGWINPNSGDTNY EQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDD RIQLWVPLVFWGQGTLVTVSS	1998	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYSASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSFSTPFTFGQGTKLE IKR	2001
193	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNSDMNWVRQAP GKGLEWVSYISGTGSTIYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKDYDSS YGSGYYGMDVWGQGTTVTV SS	1999	DIQMTQSPSSLSASVGDRVTI TCRASQSIYNYLNWYQQKPG KAPKLLIYAASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYGNAPLTFGQGTKV EIKR	2002

[00536] The polypeptides above were tested as disclosed above in Examples 4 and 5. Data is disclosed below in Table 16c, reporting FACS fold change over parental as (-), indicating < 2 fold; (+), indicating 2-10 fold; (++), indicating 10-30 fold; and (+++), indicating > 30 fold.

Table 16c. Polypeptide Activity (FACS and BLI)

Polypeptide No.	CD33 Mutant Geometric Mean Fold Change over Jurkat Parental	CD33 WT Geometric Mean Fold Change over Jurkat Parental	CD33 R69 BLI/Octet Binding Summary (Yes/No/ Ambiguous)	CD33 R69G BLI/Octet Binding Summary (Yes/No/ Ambiguous)
89	++	++	Yes	Yes
90	+++	+++	Yes	Yes
91	++	+++	Yes	Yes
92	+	+	Yes	Yes
93	+	+	Yes	Yes
94	++	+	Yes	Yes
95	+	+	Yes	Yes
96	+++	+++	Yes	Yes
97	+	++	Yes	Yes
98	+++	++	Yes	Yes
99	++	+++	Yes	Yes
100	++	++	Yes	Yes
101	+++	+++	Yes	Yes
102	++	++	Yes	Yes
103	++	++	Yes	Yes
104	+++	+++	Yes	Yes
105	++	++	Yes	Yes

106	+	+	Yes	Yes
107	++	++	Yes	Yes
108	++	++	Yes	Yes
109	++	++	Yes	Yes
110	+++	+++	Yes	Yes
111	++	+++	Yes	Yes
112	+	+	Yes	Yes
113	++	+++	Yes	Yes
114	++	+++	Yes	Yes
115	++	++	Yes	Yes
116	+++	+++	Yes	Yes
117	+	+	Yes	Yes
118	+	++	Yes	Yes
119	+++	++	Yes	Yes
120	+++	+++	Yes	Yes
121	++	++	Yes	Yes
122	+++	++	Yes	Yes
123	+++	+++	Yes	Yes
124	+++	+++	Yes	Yes
125	+++	+++	Yes	Yes
126	++	+++	Yes	Yes
127	++	++	Yes	Yes
128	++	++	Yes	Yes
129	++	++	Yes	Yes
130	++	++	Yes	Yes
131	++	+++	Yes	Yes
132	++	+	Yes	Yes
133	+	+	Yes	Yes
134	+++	+++	Yes	Yes
135	+++	++	Yes	Yes
136	++	++	Yes	Yes
137	+++	+++	Yes	Yes
138	++	++	Yes	Yes
139	+++	+++	Yes	Yes
140	+	+	Yes	Yes
141	+++	++	Yes	Yes
142	+	+	Yes	Yes
143	+	+	Yes	Yes
191	++	+++	Yes	Yes
192	++	++	Yes	Yes

193	+++	+++	Yes	Yes

Example 18: Identification of Non-Selective Anti-Human CLL-1 scFv Clones

[00537] The methods above in Example 1 have been used to discover non-selective anti-human CLL-1 scFv clones.

Table 17a. Sequences of Non-Selective Anti-CLL-1 Polypeptides (CDR Sequences)

Poly-peptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
144	YTFTAYYMH	1145	GIIDPSGGSTSYA	1192	CARGDYGDYHTLW	1239	RASQGISSYLA	1286	DASSLQS	1333	CQQSYSTPITF	1380
145	GTFSTSYMH	1146	GWIHPDDGNTDYA	1193	CARDLGDYDTFDIW	1240	RVSQGISSYLN	1287	DASNLQA	1334	CQQSYSTPPTF	1381
146	YTFSGHYMH	1147	GWIDPNSGGTNYA	1194	CARDYPFYGDNDAFDIW	1241	RVSQGISSYLN	1288	EASSLES	1335	CQQSYSIPFTF	1382
147	YTFTSYHIH	1148	GGIIPSGGSTSYA	1195	CARGTNDDHYDYW	1242	RASQGISNYLA	1289	DASNLET	1336	CQQSYSTPLTF	1383
148	GTFTTYGIS	1149	GWMNPFSDNTDYA	1196	CARGTGDDAFDIW	1243	RASQSISTWVA	1290	AASSLQS	1337	CQQSFSIPLTF	1384
149	YTFTSYDIN	1150	GWMNPNSGNTGYA	1197	CARELEGEWFDPW	1244	RASQSISSYLN	1291	SASNLQS	1338	CQQAISFPLTF	1385
150	YIFTSQYIH	1151	GWINPNSGGTNYA	1198	CARDPWGAYGGDAFDIW	1245	RASQGISNNLN	1292	DASHLDT	1339	CQQNYSPPPTF	1386
151	YTFTDYYIH	1152	GWMNPNSGNTGYA	1199	CARVDTADYMDVW	1246	RASQGISSWLA	1293	DASNLQT	1340	CQQSYSTPLTF	1387

152	GTFST NAIS	1153	GWMN PNSGN TGYA	1200	CAKED YGGNF DYW	1247	RASQSI GPWLA	1294	DASNL QA	1341	CQQSH SLPLTF	1388
153	GAFSS YALS	1154	GWMN PNSGN TGYA	1201	CAAD WMIGG DAFDI W	1248	RASQSI SSWLA	1295	DASRL QS	1342	CQQSY GIPLTF	1389
154	GTFSS YGVT	1155	GWINP NTGGT DYA	1202	CAGEV GVGGY DAFDI W	1249	RASQG ISNWL A	1296	AASSL QS	1343	CQQSY SIPLTF	1390
155	YTFTS YDIN	1156	GWMN PSSGD SGYA	1203	CARPE RSDAF DIW	1250	RASQSI GPWLA	1297	DASNL EA	1344	CQQSF SSPLTF	1391
156	YTFTG YFIH	1157	GWMN PNSGN TGYA	1204	CARGD YADW FDPW	1251	RASQSI STWLA	1298	DAFTL ET	1345	CQQSY STPLTF	1392
157	YTFSD YYIH	1158	GIINPS GGSTS YA	1205	CARG MTDD AFDIW	1252	RASQG ISSWL A	1299	DASNL ET	1346	CQQTY AIPLTF	1393
158	DSFSS YGIS	1159	GWINP KSGAT TSA	1206	CARST AFDAF DIW	1253	RASQSI SSWLA	1300	DASNL ET	1347	CQQSY STPLTF	1394
159	YSFTA NYIH	1160	GIINPS GGSTS YA	1207	CARGN YGDYV EDW	1254	RASQSI SSWLA	1301	DASNL ET	1348	CQQSY GTPLTF	1395
160	GTFTS YDIN	1161	GWINP HSGGT NYA	1208	CARLV GGDAF DIW	1255	RASQSI SSWLA	1302	AASSL QG	1349	CQQGY TTPLTF	1396

161	YTFTS YDIN	1162	GMINP NSGGT SYA	1209	CAREL LGESF DYW	1256	RASQG ISSYLA	1303	GASIL QS	1350	CQQSY STSFTF	1397
162	YTFTN YGIS	1163	GWINP NSGGT NFA	1210	CARGT NGDEL DYW	1257	RASQSI SSYLA	1304	AASTL QS	1351	CQQSY STPLTF	1398
163	YTFTS YYMQ	1164	GWMN PNSGN TGYA	1211	CARAL YGDYL DIW	1258	RASQPI ATWLA	1305	DTSSL QS	1352	CQQSY SLPLGF	1399
164	YTFTA HYIH	1165	GIINPN GGRTT YA	1212	CARDS DFWSG YYSDY YYGM DVW	1259	QASQD ISNFLN	1306	ATSTL QS	1353	CQQSY TTEWT F	1400
165	YTFTS YDIN	1166	GWMN PNSGN TGYA	1213	CARLS SGYYP DYW	1260	RASQFI ANWL A	1307	DASSL ES	1354	CQQSY STPLTF	1401
166	YTFES YDMN	1167	GWIDP HSGDT NFA	1214	CARAD YGGNA DYW	1261	RASQG ISNWL A	1308	DASNL ET	1355	CQQSY STPYTF	1402
167	YTFTS YYMH	1168	GWINP NSGGT NYA	1215	CARGT TGDDF DYW	1262	RASQD ISTWL A	1309	AASSL QS	1356	CQQSY SIPPTF	1403
168	YTFTN YGIS	1169	GWINP NSGGT NYA	1216	CARVR SDDFF DYW	1263	RASQS VNHW LA	1310	AASTL QS	1357	CQQSY SLPLTF	1404
169	YTFTN DYIH	1170	GWMS PNSGK TGFA	1217	CAKDN SSGWY FDLW	1264	RVSQG ISSYLA	1311	DASNL ET	1358	CQQYD TLPITF	1405

170	GSFSN HGVS	1171	GWMN PNSGD TGYA	1218	CARPR KDDAF AIW	1265	RASQSI SSWLA	1312	EASTL QS	1359	CQQSY STPLTF	1406
171	YTFTD YYIH	1172	GMVDP NTGNI NYA	1219	CTSGS TNDAF DIW	1266	RASQSI GPWLA	1313	EASNL AS	1360	CQQSY STPLTF	1407
172	YTFSD YYVH	1173	GWMN PNSGN TGYA	1220	CARGL TGDQF DYW	1267	RASQSI SSYLN	1314	AASSL QS	1361	CQQSY STPLTF	1408
173	YTFNG YNMH	1174	GWINP NSGDT NYA	1221	CASLD YGDYA VYW	1268	RASQSI STWLA	1315	DASSL RS	1362	CQQSY STPITF	1409
174	FIFRDH WMH	1175	SSIDFS TGYIY YA	1222	CARDP WGDG DFDY W	1269	RASQSI SSWLA	1316	AASSL QS	1363	CQQTY TTPYTF	1410
175	YTFTS YDIH	1176	GWINP NSGNT GYA	1223	CAGGP DVDAA MVLD YW	1270	QASQD ISNYLN	1317	DASNL ET	1364	CQQAD GFPPTF	1411
176	GSFTS YYIH	1177	GWMN PNSGN TGYA	1224	CARGA TDDAF DIW	1271	RASQN IDTWL A	1318	DGSNL EA	1365	CQQSY NTPITF	1412
177	YTFTS YYMH	1178	GWMN PNSGN TGYA	1225	CARST YSDSF DYW	1272	RASQSI SNWLA	1319	DASNL ET	1366	CQQSY STPLTF	1413
178	FTFSSS DMS	1179	SSITGS GDGTY YA	1226	CIRDW EGIYQ W	1273	RVSQG ISSYLN	1320	DASNL ET	1367	CQQGY STPWT F	1414

179	GTFSS YAIS	1180	GTINPS GGSTN YA	1227	CAIGG YDSPY MDVW	1274	QASQD ISNYLN	1321	DASNL ET	1368	CQQGY SPPWT F	1415
180	YTFTSL DIN	1181	GSMNP RSGST AYA	1228	CAKSD YGDYL DYW	1275	RASQSI SPWLA	1322	DASNL QS	1369	CQQSY STPLTF	1416
181	YTFTG YYMH	1182	GVINPS GGSTS YA	1229	CARGR TDDAF DIW	1276	RASQTI SSWLA	1323	AASTL QS	1370	CQQSY SIPLTF	1417
182	YTFTD YYMH	1183	GIINTG AGTTN YA	1230	CARGL TSDHF DYW	1277	RASQN IGPWL A	1324	EAFTL QS	1371	CQQSD NIPITF	1418
183	GTFSS YAIS	1184	GGIIPK FGPPN YA	1231	CARNS YGDDF DYW	1278	RASQSI SSWLA	1325	AASSL QR	1372	CQQSY STPLTF	1419
184	GTFGN YGIN	1185	GVINPS SGGTN LA	1232	CARSL GWPSP YMDV W	1279	RASQSI SRYLN	1326	DASNL ET	1373	CQQSY STPWT F	1420
185	FTFSNS DMY	1186	SAISGS DGTTY YA	1233	CARDD YGDQG FDLW	1280	RASQD IRNDL G	1327	DASNL QT	1374	CQQSY NMPYT F	1421
186	YTFTK YYMH	1187	GWINP NSGNT GYA	1234	CARDI AVAGS TYYYY GMDV W	1281	QASQD ISNYLN	1328	DATNL ET	1375	CQQSY STPPTF	1422
187	FTFSSY DMH	1188	SSISSS SSYIYY A	1235	CARDI DDVAG DYW	1282	QASQD ISNYLN	1329	GASSL QS	1376	CQQSY STPFTF	1423

188	FTFSSY GMH	1189	SYTSSS SSTIYY A	1236	CARGN VGDN WNDD EAFLG W	1283	QASQD ISNYLN	1330	DASNL ET	1377	CQQTY DTPYT F	1424
189	LTAGS NYMS	1190	SAISDD GHWT DYA	1237	CVKDD GEGSG IDW	1284	RASQG ISDYLA	1331	GASSL QS	1378	CQQSY STPWT F	1425
190	FTFSSS WMH	1191	STINTN GDAAY YA	1238	CARDT VLDDY GDYDD YGMD VW	1285	RASQS VSSSY LA	1332	GASTR AA	1379	CQQYG SSPFTF	1426
194	VTFSN SGIN	2003	GWMN PASGD TGYA	2010	CARGE YGAEY FQHW	2017	RASQSI SSWLA	2024	DASSL ES	2031	CQQSH SLPPTF	2038
195	YTFTN SYIH	2004	GIINPS GDSTT YA	2011	CAKPT TGDG MDVW	2018	RASQG ISNWL A	2025	DASNL ET	2032	CQQSY STPLTF	2039
196	YTLTN YYMH	2005	GWISP TDGKT KYA	2012	CTTDL LGDWF DPW	2019	RASRSI RSYLN	2026	DASNL ET	2033	CQQSY NTPWT F	2040
197	YTLTN NWMH	2006	GWMN PNSGN TGYA	2013	CATAT ADDAF DIW	2020	RASQSI STWLA	2027	GASSL QS	2034	CQQSY DIPITF	2041
198	FTFSTF WMS	2007	ATISY DGSNQ YYA	2014	CARLE LHEGR FDYW	2021	RASQSI SSYLN	2028	DASNL ET	2035	CQQAN SFPFTF	2042
199	DTFTG YHIH	2008	GWMN PDSGS TGYA	2015	CTTDR LYGDY FDYW	2022	RASQS VSSWL A	2029	DASSL QS	2036	CQQAN SFPFTF	2043

200	YTFTD YYMH	2009	GWMN PNSGN TGYA	2016	CAADD TKSPY GMDV W	2023	QASQD ISNYLN	2030	EASSL QS	2037	CQQTY SPPPTF	2044

Table 17b. Sequences of Non-Selective Anti-CLL-1 Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
144	QVQLVQSGAEVKKPGASVKV SCKASGYTFTAYYMHWVRQA PGQGLEWMGIIDPSGGSTSYA QQFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGDYG DYHTLWGQGTLVTVSS	1427	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYDASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPITFGPGTKVD IKR	1474
145	QVQLVQSGAEVKKPGASVKV SCKASGGTFSTSYMHWVRQA PGQGLEWMGWIHPDDGNTDY APKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDLG DYDTFDIWGQGTMVTVSS	1428	DIQMTQSPSSLSASVGDRVTI TCRVSQGISSYLNWYQQKPG KAPKLLIYDASNLQAGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGQGTKV EIKR	1475
146	QVQLVQSGAEVKKPGASVKV SCKASGYTFSGHYMHWVRQA PGQGLEWMGWIDPNSGGTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDYP FYGDNDAFDIWGQGTTVTVSS	1429	DIQMTQSPSSLSASVGDRVTI TCRVSQGISSYLNWYQQKPG KAPKLLIYEASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSIPFTFGPGTKVDI KR	1476
147	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYHIHWVRQAP GQGLEWVGGIIPSGGSTSYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARGTNDD HYDYWGQGTLVTVSS	1430	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1477
148	QVQLVQSGAEVKKPGASVKV SCKASGGTFTTYGISWVRQAP GQGLEWMGWMNPFSDNTDY AQNFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGTG DDAFDIWGQGTMVTVSS	1431	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWVAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSFSIPLTFGQGTKVEI KR	1478
149	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDINWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARELE GEWFDPWGQGTLVTVSS	1432	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYSASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAISFPLTFGQGTKVE IKR	1479
150	QVQLVQSGAEVKKPGASVKV SCKASGYIFTSQYIHWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDPWG AYGGDAFDIWGQGTMVTVSS	1433	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLNWYQQKPG KAPKLLIYDASHLDTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQNYSPPPTFGQGTRLE IKR	1480

151	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYIHWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARVDT ADYMDVWGKGTLVTVSS	1434	DIQMTQSPSSLSASVGDRVTI TCRASQGISSWLAWYQQKPG KAPKLLIYDASNLQTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	1481
152	QVQLVQSGAEVKKPGASVKV SCKASGGTFSTNAISWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKED YGGNFDYWGQGTLVTVSS	1435	DIQMTQSPSSLSASVGDRVTI TCRASQSIGPWLAWYQQKPG KAPKLLIYDASNLQAGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSHSLPLTFGPGTKV DIKR	1482
153	QVQLVQSGAEVKKPGASVKV SCKASGGAFSSYALSWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAADW MIGGDAFDIWGQGTTVTVSS	1436	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDASRLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYGIPLTFGGGTKVE IKR	1483
154	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYGVTWVRQA PGQGLEWMGWINPNTGGTDY AQNFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAGEV GVGGYDAFDIWGQGTTVTVS S	1437	DIQMTQSPSSLSASVGDRVTI TCRASQGISNWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPLTFGGGTKVE IKR	1484
155	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDINWVRQAP GQGLEWMGWMNPSSGDSGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARPER SDAFDIWGQGTTVTVSS	1438	DIQMTQSPSSLSASVGDRVTI TCRASQSIGPWLAWYQQKPG KAPKLLIYDASNLEAGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSFSSPLTFGGGTKVE IKR	1485
156	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYFIHWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGD YADWFDPWGQGTLVTVSS	1439	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYDAFTLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	1486
157	QVQLVQSGAEVKKPGASVKV SCKASGYTFSDYYIHWVRQAP GQGLEWMGIINPSGGSTSYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARGMTD DAFDIWGQGTMVTVSS	1440	DIQMTQSPSSLSASVGDRVTI TCRASQGISSWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYAIPLTFGGGTKLE IKR	1487

158	QVQLVQSGAEVKKPGASVKV SCKASGDSFSSYGISWVRQAP GQGLEWMGWINPKSGATTSA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARSTAF DAFDIWGQGTTVTVSS	1441	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	1488
159	QVQLVQSGAEVKKPGASVKV SCKASGYSFTANYIHWVRQAP GQGLEWMGIINPSGGSTSYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCARGNYG DYVEDWGQGTLVTVSS	1442	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYGTPLTFGGGTKV EIKR	1489
160	QVQLVQSGAEVKKPGASVKV SCKASGGTFTSYDINWVRQAP GQGLEWMGWINPHSGGTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARLVGG DAFDIWGQGTMVTVSS	1443	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYAASSLQGGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQGYTTPLTFGPGTKV DIKR	1490
161	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDINWVRQAP GQGLEWMGMINPNSGGTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARELLG ESFDYWGQGTLVTVSS	1444	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYGASILQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSTSFTFGPGTKVDI KR	1491
162	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYGISWVRQAP GQGLEWMGWINPNSGGTNFA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGTNG DELDYWGQGTLVTVSS	1445	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTRLE IKR	1492
163	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMQWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARAL YGDYLDIWGQGTTVTVSS	1446	DIQMTQSPSSLSASVGDRVTI TCRASQPIATWLAWYQQKPG KAPKLLIYDTSSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSLPLGFGQGTKVEI KR	1493
164	QVQLVQSGAEVKKPGASVKV SCKASGYTFTAHYIHWVRQAP GQGLEWMGIINPNGGRTTYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDSDF WSGYYSDYYYGMDVWGQGT TVTVSS	1447	DIQMTQSPSSLSASVGDRVTI TCQASQDISNFLNWYQQKPG KAPKLLIYATSTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYTTEWTFGQGTKV EIKR	1494

165	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDINWVRQAP GQGLEWMGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARLSS GYYPDYWGQGTLVTVSS	1448	DIQMTQSPSSLSASVGDRVTI TCRASQFIANWLAWYQQKPG KAPKLLIYDASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPLTFGGGTKVEI KR	1495
166	QVQLVQSGAEVKKPGASVKV SCKASGYTFESYDMNWVRQA PGQGLEWMGWIDPHSGDTNF AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARAD YGGNADYWGQGTLVTVSS	1449	DIQMTQSPSSLSASVGDRVTI TCRASQGISNWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKV EIKR	1496
167	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGTT GDDFDYWGQGTLVTVSS	1450	DIQMTQSPSSLSASVGDRVTI TCRASQDISTWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPPTFGPGTKVD IKR	1497
168	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYGISWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARVRSD DFFDYWGQGTLVTVSS	1451	DIQMTQSPSSLSASVGDRVTI TCRASQSVNHWLAWYQQKP GKAPKLLIYAASTLQSGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQSYSLPLTFGGGTK VEIKR	1498
169	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNDYIHWVRQAP GQGLEWMGWMSPNSGKTGF AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDNS SGWYFDLWGRGTLVTVSS	1452	DIQMTQSPSSLSASVGDRVTI TCRVSQGISSYLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYDTLPITFGQGTRLE IKR	1499
170	QVQLVQSGAEVKKPGASVKV SCKASGGSFSNHGVSWVRQA PGQGLEWMGWMNPNSGDTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARPR KDDAFAIWGQGTLVTVSS	1453	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYEASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	1500
171	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYIHWVRQAP GQGLEWMGMVDPNTGNINY AQTFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCTSGST NDAFDIWGQGTMVTVSS	1454	DIQMTQSPSSLSASVGDRVTI TCRASQSIGPWLAWYQQKPG KAPKLLIYEASNLASGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1501

172	QVQLVQSGAEVKKPGASVKV SCKASGYTFSDYYVHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARGL TGDQFDYWGQGTLVTVSS	1455	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	1502
173	QVQLVQSGAEVKKPGASVKV SCKASGYTFNGYNMHWVRQ APGQGLEWMGWINPNSGDTN YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCASLD YGDYAVYWGQGTLVTVSS	1456	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYDASSLRSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPITFGQGTKVE IKR	1503
174	EVQLLESGGGLVQPGGSLRLS CAASGFIFRDHWMHWVRQAP GKGLEWVSSIDFSTGYIYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARDPWGD GDFDYWGRGTLVTVSS	1457	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYTTPYTFGQGTRL EIKR	1504
175	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYDIHWVRQAP GQGLEWMGWINPNSGNTGYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAGGPDV DAAMVLDYWGQGTLVTVSS	1458	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQADGFPPTFGGGTKV EIKR	1505
176	QVQLVQSGAEVKKPGASVKV SCKASGGSFTSYYIHWVRQAP GQGLEWVGWMNPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGAT DDAFDIWGQGTMVTVSS	1459	DIQMTQSPSSLSASVGDRVTI TCRASQNIDTWLAWYQQKP GKAPKLLIYDGSNLEAGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQSYNTPITFGQGTRL EIKR	1506
177	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARST YSDSFDYWGQGTLVTVSS	1460	DIQMTQSPSSLSASVGDRVTI TCRASQSISNWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKLE IKR	1507
178	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSSDMSWVRQAPG KGLEWVSSITGSGDGTYYADS VKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCIRDWEGIYQ WGQGTLVTVSS	1461	DIQMTQSPSSLSASVGDRVTI TCRVSQGISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQGYSTPWTFGQGTKL EIKR	1508

179	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGTINPSGGSTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAIGGYD SPYMDVWGKGTTVTVSS	1462	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQGYSPPWTFGGGTKV EIKR	1509
180	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSLDINWVRQAP GQGLEWMGSMNPRSGSTAYA QSFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAKSDYG DYLDYWGQGTLVTVSS	1463	DIQMTQSPSSLSASVGDRVTI TCRASQSISPWLAWYQQKPG KAPKLLIYDASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKLE IKR	1510
181	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGVINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGRTD DAFDIWGQGTLVTVSS	1464	DIQMTQSPSSLSASVGDRVTI TCRASQTISSWLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSIPLTFGGGTKLE IKR	1511
182	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWLGIINTGAGTTNYA PKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGLTS DHFDYWGQGTLVTVSS	1465	DIQMTQSPSSLSASVGDRVTI TCRASQNIGPWLAWYQQKPG KAPKLLIYEAFTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSDNIPITFGQGTKVE IKR	1512
183	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGGIIPKFGPPNYAP KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARNSYGDD FDYWGQGTLVTVSS	1466	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYAASSLQRGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	1513
184	QVQLVQSGAEVKKPGASVKV SCKASGGTFGNYGINWVRQA PGQGLEWMGVINPSSGGTNL AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARSLG WPSPYMDVWGQGTMVTVSS	1467	DIQMTQSPSSLSASVGDRVTI TCRASQSISRYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKL EIKR	1514
185	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNSDMYWVRQAP GKGLEWVSAISGSDGTTYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDDYG DQGFDLWGRGTLVTVSS	1468	DIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPG KAPKLLIYDASNLQTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYNMPYTFGQGTKL EIKR	1515

186	QVQLVQSGAEVKKPGASVKV SCKASGYTFTKYYMHWVRQA PGQGLEWMGWINPNSGNTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDIA VAGSTYYYYGMDVWGQGTT VTVSS	1469	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYDATNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGGGTKV EIKR	1516
187	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYDMHWVRQAP GKGLEWVSSISSSSSYIYYADS VKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCARDIDDVA GDYWGQGTLVTVSS	1470	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPFTFGQGTKLE IKR	1517
188	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSYGMHWVRQAP GKGLEWVSYTSSSSSTIYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCARGNVGD NWNDDEAFLGWGQGTLVTVS S	1471	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYDTPYTFGQGTKL EIKR	1518
189	EVQLLESGGGLVQPGGSLRLS CAASGLTAGSNYMSWVRQAP GKGLEWVSAISDDGHWTDYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCVKDDGE GSGIDWGQGTLVTVSS	1472	DIQMTQSPSSLSASVGDRVTI TCRASQGISDYLAWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGPGTKV DIKR	1519
190	EVQLLESGGGLVQPGGSLRLS CAASGFTFSSSWMHWVRQAP GKGLEWVSTINTNGDAAYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARDTVL DDYGDYDDYGMDVWGQGTT VTVSS	1473	EIVMTQSPATLSVSPGERATL SCRASQSVSSSYLAWYQQKP GQAPRLLIYGASTRAAGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYGSSPFTFGPGTK VDIKR	1520
194	QVQLVQSGAEVKKPGASVKV SCKASGVTFSNSGINWVRQAP GQGLEWMGWMNPASGDTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGEY GAEYFQHWGQGTLVTVSS	2045	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYDASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSHSLPPTFGQGTRLEI KR	2052
195	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNSYIHWVRQAP GQGLEWMGIINPSGDSTTYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKPTTGD GMDVWGQGTTVTVSS	2046	DIQMTQSPSSLSASVGDRVTI TCRASQGISNWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	2053

196	QVQLVQSGAEVKKPGASVKV SCKASGYTLTNYYMHWVRQ APGQGLEWMGWISPTDGKTK YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCTTDL LGDWFDPWGQGTLVTVSS	2047	DIQMTQSPSSLSASVGDRVTI TCRASRSIRSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYNTPWTFGQGTKV EIKR	2054
197	QVQLVQSGAEVKKPGASVKV SCKASGYTLTNNWMHWVRQ APGQGLEWMGWMNPNSGNT GYAQKFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCAT ATADDAFDIWGQGTMVTVSS	2048	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYGASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYDIPITFGPGTKVDI KR	2055
198	EVQLLESGGGLVQPGGSLRLS CAASGFTFSTFWMSWVRQAP GKGLEWVATISYDGSNQYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARLELH EGRFDYWGQGTLVTVSS	2049	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPFTFGPGTKV DIKR	2056
199	QVQLVQSGAEVKKPGASVKV SCKASGDTFTGYHIHWVRQAP GQGLEWMGWMNPDSGSTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCTTDRL YGDYFDYWGQGTLVTVSS	2050	DIQMTQSPSSLSASVGDRVTI TCRASQSVSSWLAWYQQKP GKAPKLLIYDASSLQSGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQANSFPFTFGPGTK VDIKR	2057
200	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDYYMHWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAAD DTKSPYGMDVWGQGTMVTV SS	2051	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYEASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQTYSPPPTFGQGTKLEI KR	2058

[00538] The polypeptides above were tested as disclosed above in Example 4. Data is disclosed below in Table 17c, reporting FACS fold change over parental as (-), indicating < 2 fold; (+), indicating 2-10 fold; (++), indicating 10-30 fold; and (+++), indicating > 30 fold.

Table 17c. Polypeptide Activity (FACS)

Polypeptide No.	CLL-1 K244 BLI/Octet Binding Summary (Yes/No/ Ambiguous)	CLL-1 Q244 BLI/Octet Binding Summary (Yes/No/ Ambiguous)
144	Yes	Yes
145	Yes	Yes
146	Yes	Yes
147	Yes	Yes

148	Yes	Yes
149	Yes	Yes
150	Yes	Yes
151	Yes	Yes
152	Yes	Yes
153	Yes	Yes
154	Yes	Yes
155	Yes	Yes
156	Yes	Yes
157	Yes	Yes
158	Yes	Yes
159	Yes	Yes
160	Yes	Yes
161	Yes	Yes
162	Yes	Yes
163	Yes	Yes
164	Yes	Yes
165	Yes	Yes
166	Yes	Yes
167	Yes	Yes
168	Yes	Yes
169	Yes	Yes
170	Yes	Yes
171	Yes	Yes
172	Yes	Yes
173	Yes	Yes
174	Yes	Yes
175	Yes	Yes
176	Yes	Yes
177	Yes	Yes
178	Yes	Yes
179	Yes	Yes
180	Yes	Yes
181	Yes	Yes
182	Yes	Yes
183	Yes	Yes
184	Yes	Yes
185	Yes	Yes
186	Yes	Yes
187	Yes	Yes

188	Yes	Yes
189	Yes	Yes
190	Yes	Yes
194	Yes	Yes
195	Yes	Yes
196	No	Yes
197	Yes	Yes
198	Yes	No
199	Yes	No
200	Yes	No

Example 19: Identification of Non-Selective Anti-Human FLT3 scFv Clones

[00539] The methods above in Example 1 have been used to discover non-selective anti-human FLT3 scFv clones. Anti-human FLT-3 scFv clones were discovered by standard screening methodologies of a human antibody library using two recombinant polymorphic forms of human FLT3 extracellular domain antigens (huFLT3-T227 and huFLT3-M227). Using these antigens various panning tactics were employed to encourage enrichment of thermostable clones of desired affinity range. The scFvs were screened for binding to two single nucleotide polymorphism (SNP) variants of human FLT-3 (Threonine 227 and Methionine 227) by flow cytometry and bio-layer interferometry (BLI).

Table 18a. Sequences of Non-Selective Anti-FLT3 Polypeptides (CDR Sequences)

Poly-peptide No.	HCDR1	SEQ ID NO	HCDR2	SEQ ID NO	HCDR3	SEQ ID NO	LCDR1	SEQ ID NO	LCDR2	SEQ ID NO	LCDR3	SEQ ID NO
201	GTFSS DGIS	2059	GWISA YHGHT NYA	2153	CARGG KHSGS HRSYY YGMD VW	2247	RASHN IGNKL A	2341	GATTL QS	2435	CQQAN SFPRTF	2529
202	YTFTN YYMH	2060	GVINPS GGSTN YA	2154	CARAG VGAFH IW	2248	RASQSI RSWLA	2342	DASNL ET	2436	CQQIY SLPRTF	2530
203	YTLTE LSMH	2061	GRIIPIS GTANY A	2155	CARAA RYCSS TSCYW RDGM DVW	2249	KSSQS VLYSS NNKNY LA	2343	WASTR AS	2437	CQQYY STPQTF	2531
204	FDFST YNMF	2062	SGISGS GRSKY YA	2156	CARVY YDSSG YYPYY FDYW	2250	RASQSI GSNLD	2344	DASSL QS	2438	CQQSY STPYTF	2532
205	GSFISH TFS	2063	GGIIPIS GTANY A	2157	CAKGR GQLVG GYFQH W	2251	RSSQS LLHSN GYNYL D	2345	AASSL QS	2439	CMQAL QTPLTF	2533
206	YTFTS YYLH	2064	GGIIPIF GKAEY S	2158	CARED FWSGP YGMD VW	2252	RASQA ISSYLA	2346	AASNL QG	2440	CQQSY STPLTF	2534
207	YTFTN YYMH	2065	GWMN PNSGN TGYA	2159	CAKSH YYYFY GMDV W	2253	QASHD ISKYLN	2347	AASIL QS	2441	CQQSY STPYTF	2535

208	GTFSS RSIS	2066	GIINPS GGGTL YA	2160	CAKD MDGW SDAFDI W	2254	RASQS LSNIYL A	2348	DVSSR AA	2442	CQQYA TSPLTF	2536
209	FAFSS YVLH	2067	AGIWV DGHNK DYA	2161	CAREF GAAGS FQHW	2255	RASQSI STWLA	2349	DASKL ET	2443	CQQSY TTPYTF	2537
210	YTLTE LSMH	2068	GGIIPIS GTTKY A	2162	CARAS PRYYM DVW	2256	KSSQS VFYSS NNKNY LA	2350	WASTR AS	2444	CHQYY SKPPTF	2538
211	FTFSN HYMS	2069	SAIGA GGGTY YA	2163	CAKSS GYSYG RRPFD YW	2257	RASQG ISNNLA	2351	AASTL HN	2445	CQQYG RSPKT F	2539
212	YTFTG YYMH	2070	GGIIPIL GTANN A	2164	CARAP WGTFD YW	2258	RASQS VSSSQ LA	2352	DTSTR AT	2446	CQQYD NSLWT F	2540
213	YTFSR YYMS	2071	GWMN PNSGN TGYA	2165	CARTR FAAQP HNWH FDLW	2259	RASQSI SSYLN	2353	DASNL KT	2447	CQQSY STPLTF	2541
214	YTFTT YYMH	2072	GIINPS GGSTS YA	2166	CARDR AARPR GGFDY W	2260	RASQG IRNHL A	2354	AASSL QS	2448	CQQSY STPTF	2542
215	YTFTG YRMH	2073	GWINP NSGGT NYA	2167	CAKGG LDWR NWYF DLW	2261	RASQG ISSYLA	2355	AASTL QS	2449	CQQSY STPLTF	2543
216	NTFTM YYMH	2074	GAIIPIS GTVIY A	2168	CARLS GGRM YDAFD IW	2262	RSSQS LLHSN GYNYL D	2356	LGSNR AS	2450	CMQAL QTPLTF	2544

217	YTFTTF YLH	2075	GGIIPM SGTAN YA	2169	CASGG ENGM DVW	2263	KSSQS VLYSV NNKNY LA	2357	WASTR ES	2451	CQQYY SAPPTF	2545
218	YSFTT HYMH	2076	GIINPS GGSTR YA	2170	CARGS SYYYY GVDV W	2264	RASQSI STWLA	2358	AASSL QS	2452	CQQAI SFPLTF	2546
219	YTFTN YYMH	2077	GIINPS SGSAS YT	2171	CARDR STLVP LDYW	2265	RASQG IRSELS	2359	KASSL ES	2453	CLQHN SYPLTF	2547
220	YTFTG YYMY	2078	GIINPR GGITS YA	2172	CARGS TSSGW PNGDM DVW	2266	RASQG IRNDL G	2360	AASSL QS	2454	CQQAN RFPPTF	2548
221	YTFTD NYMH	2079	GWMT PDSNN TGFA	2173	CALGD GPFGM DVW	2267	RSSQS LLHSN GYNYL D	2361	GASYL QS	2455	CMQAL QGPITF	2549
222	YSFTA YYMH	2080	GIINPS GGSTS YA	2174	CARVA GINGE MAYW	2268	RASQD ISNYLA	2362	AASTL QS	2456	CQQSY RTPYT F	2550
223	YTFTN SFIH	2081	GIINPS GGSTS YA	2175	CAKAL ERRYY YGMD VW	2269	RASQG ISNYLA	2363	DGSNL ET	2457	CQQSY STPLTF	2551
224	YTFTG YYMH	2082	GVINPI YGTAN YA	2176	CAKAI SSGWS NDAFD IW	2270	RASQS VSSDF LA	2364	DTSSR AS	2458	CQQYA GPPTF	2552
225	YTLTE LSIH	2083	GGIVP MSGTA SYA	2177	CARRR DGYNS W	2271	KSSQS LLYGS KNYIS	2365	SSSTRE S	2459	CQQYY TTPYTF	2553

226	YTFTG YYMH	2084	GIIDPS GGSTS YA	2178	CARDR SLLWS GVGG MDVW	2272	RASQG ISNYLA	2366	GASNL QS	2460	CQQSY GTPYT F	2554
227	YTLNE LFMH	2085	GGIIPM SGTTF YA	2179	CAKGV RQYSY GRYYY GMDV W	2273	RASQS VSSYL N	2367	GASNL QS	2461	CQQSY TTPWT F	2555
228	GTFSS HAIS	2086	GWINP GSGGT NYA	2180	CAKDS YDFWS GYYID YW	2274	RASQSI YTHLN	2368	AASRL QT	2462	CQQSY SFPFTF	2556
229	YTFTN YYMH	2087	GIINPS GGSTS YA	2181	CARGV GYSGY GADL W	2275	RASQG ISNSLA	2369	AASSL QS	2463	CQQSH SPPYTF	2557
230	GTFSS NAIN	2088	GGIIPL FGTTN YA	2182	CARVL SGWY GTYYF DYW	2276	RASQS VSADY IA	2370	DVSTR AS	2464	CQHYG SSQVT F	2558
231	YTFTS YYIH	2089	GLINPS GGSTT YA	2183	CARGL GWGV VVPAA ELDYW	2277	RASQSI STYLN	2371	AASNL QS	2465	CQQSY SSPLTF	2559
232	YTFTS YGIH	2090	GGIIPIF GTASY A	2184	CTRSN GIAAA GTHW YFDLW	2278	RASQN IANSLN	2372	AASSL QS	2466	CQQYS SYPPTF	2560
233	YTFTS YYLH	2091	GVINPS GGSTT YA	2185	CARGI GYGGY FDYW	2279	RSSQS LLHSN GYNYL D	2373	AASSL QS	2467	CMQGL RTPHT F	2561

234	HTFTAYYMH	2092	GWMSPYSGNTGYA	2186	CARATRGTIQHW	2280	KSSQSVLYSSNNKNYLA	2374	WASIRES	2468	CQQYYTTPITF	2562
235	YTFTGYYMH	2093	GIINPSGGSTSYA	2187	CARDPGRLGELDYW	2281	RASQSVSSNLA	2375	GASTRAT	2469	CQQYGSSPLTF	2563
236	GTFSSYAIS	2094	GGIIPILGIANYA	2188	CAHVDGYGMDVW	2282	RASQSVSSNLA	2376	DVSSRAT	2470	CQQLDAYPLTF	2564
237	YTFTSYYMH	2095	GLINPSSGSTSYA	2189	CARSGSGGSYFLFDYW	2283	RSSQSLLHSNGYNYLD	2377	AASTLQS	2471	CMQALQTPLTF	2565
238	YTFTIYYMH	2096	GIINPSGGSTVYA	2190	CARGIGSKGAFDIW	2284	RSSQSLLHSNGYNYLD	2378	LGSNRAS	2472	CMQGLQTPYTF	2566
239	GTFSSYAIS	2097	GGIIPILGTANYA	2191	CARTMTTVTYYDAFDIW	2285	RASQSVGSSYLA	2379	DVSTRAA	2473	CHQYGSSPYTF	2567
240	YTFTSYYMH	2098	GIINPSSGSTTYA	2192	CARGLGKSAIDYW	2286	RASQSISSYLN	2380	AASSLQS	2474	CQQSYSTPLTF	2568
241	YTFTRHYVH	2099	GIINPSGGSTSYA	2193	CARSYHHYYYGMDVW	2287	RASQSISNYLA	2381	AASSLQG	2475	CQQSYSTPWTF	2569
242	GTFSSATIS	2100	GGIIPMFGTANYA	2194	CARDAYGDSTW	2288	RASESVSSALA	2382	GASTRAT	2476	CQQYGNSVTF	2570

243	GTFSS HAFN	2101	GGISP MFGTP NYA	2195	CARAP DYGDD WYFDL W	2289	RASQT LTGGL LA	2383	DTSSR AA	2477	CHHYG SSPYTF	2571
244	YTFTS YYMH	2102	GRINPS GGSTS YA	2196	CARVP GLYGG AIDYW	2290	RASQD IRNDL G	2384	AASSL QS	2478	CQQSY SSPFTF	2572
245	YTFTG FYIH	2103	GGVIPF FSRTIY A	2197	CAYGA NGHLY GMDA W	2291	RASQS VSSSY LA	2385	GASTR AT	2479	CQQYS SSPLTF	2573
246	GTFTS YFMH	2104	GGIIPM FGAPV YA	2198	CAAGL DFWSG PDNYY MDVW	2292	QATQD ISNYLN	2386	GASNL PS	2480	CQQSY SDLLTF	2574
247	GTLMS YAIS	2105	GIINPR GGTTR YA	2199	CARSE DSGYD YLDY W	2293	RGSQSI SGNYL A	2387	DTSAR AA	2481	CQQYN SYPLTF	2575
248	YTFTG YYMH	2106	GVINP NGGSIS YA	2200	CAREG WFGED GMDV W	2294	RASQD LDRYL A	2388	AASSL QT	2482	CQQYY STPYTF	2576
249	YTFTS DGIS	2107	GWMN PNSGN AGYA	2201	CATAV AGTDA FDIW	2295	RASQSI GNNLK A	2389	DTSAH TT	2483	CQHYG NSLTF	2577
250	YTLTSF AMH	2108	GRIIPM SGTAN YA	2202	CASTS PDQYY YGMD VW	2296	RASQS VGSSS LA	2390	GASTR AT	2484	CQQYG SSPYTF	2578
251	GTFSS DAIN	2109	GGIIPI VGTPT YA	2203	CAKGL AFGVF DGLDV W	2297	RASQS VSSNY LA	2391	DVSTR AT	2485	CQQYG SSTLTF	2579

252	YTLTD LSIH	2110	GGIIPM SGTAN YA	2204	CARSS SSWPK YFQH W	2298	RASQSI SSYLN	2392	AASSL QS	2486	CQQSY STPLTF	2580
253	YTFTT YFMH	2111	GGIVP VFGTT KYA	2205	CASSA VGWF DPW	2299	RASQD ISRWL A	2393	AASSL QS	2487	CQQYD NFPLTF	2581
254	YTFTS HYMH	2112	GWISP YNGNT NYA	2206	CARGE SNSGW INFDY W	2300	RASQS VSSSSL A	2394	DTSTR AT	2488	CQQYG TSPITF	2582
255	YTLTE LSMH	2113	GGIIPIS GTVTY A	2207	CANKG QQLVR GYFQH W	2301	QASHD IRNSV N	2395	ATSSL QS	2489	CQQSY NTPFTF	2583
256	YTFAT YYLH	2114	GMINP SGGSTI YA	2208	CARSS GYDFF DYW	2302	RASHD INNYL N	2396	DASNL ET	2490	CQQAD SFPLTF	2584
257	YTFTN YFMH	2115	GIINPS GGSTS YA	2209	CARAH TVYYY GMDV W	2303	RASQSI SSWLA	2397	AASTL QS	2491	CQQSY STPWT F	2585
258	GTFGS YAIS	2116	GWINP NTGGA HYA	2210	CARVG AAAGY QHW	2304	RASQSI KGALA	2398	SASNL QS	2492	CQQYN SYPLTF	2586
259	YTFTSS EIN	2117	GGIHP MFGTT NYA	2211	CARAR LMVY APSDY W	2305	KSSQS LFYSS NNRNY LA	2399	WASTR ES	2493	CQQYY SIPYTF	2587
260	YTFTN YYVH	2118	GMINP SGGST NYA	2212	CARVS GWKR GWFDP W	2306	RSSQSI STYLN	2400	GASNL QS	2494	CQQVI SYPITF	2588

261	YTFTR YYMH	2119	GIINPS GGSAS YA	2213	CARDL GGAAA GYFDY W	2307	KSSQSI SHSPN TRDYL A	2401	WASTR ES	2495	CQQYY SSPFTF	2589
262	FTFSD YGYY MH	2120	GWMD PSSGH TGYA	2214	CAKDI GWGA FDIW	2308	RASQR VGNTY LA	2402	DVSAR AS	2496	CQQYL SPPLTF	2590
263	GTFSS YAIS	2121	GGIIPI VGVAN YA	2215	CAKDI GGYPS DAFDI W	2309	RASQS VSSSY LA	2403	DVSTR AT	2497	CQQYG SSPITF	2591
264	YTLTE LSMH	2122	GGIIPIS SATSIP	2216	CARGA LYSSSP VRVVA GTKG WFDP W	2310	RASQD ISNYLA	2404	AASSL QS	2498	CQQYY SYPLTF	2592
265	HTFTS DYMH	2123	GRIIPIF GTADY A	2217	CARDD SSGIFD YW	2311	RASQS VNSEH LA	2405	DTSSR AT	2499	CQQYG SSPVTF	2593
266	YSLTE LSIH	2124	GGINPI SGTAN YA	2218	CARGT VRLN WFDP W	2312	RASQS VGSQL G	2406	GASTR AT	2500	CQQSF STPLTF	2594
267	YTLTSF GIS	2125	GMIIPL SGTTH YA	2219	CANLY GGNAY YYYG MDVW	2313	RASQD ISNFVA	2407	AASSL QS	2501	CQQSF DTPYT F	2595
268	GTFST YALS	2126	GGVIP VFGTT DYA	2220	CASMII FGAGG WDAY YFQEW	2314	RASQS VNNNQ LA	2408	DTSSR AT	2502	CQQYD TSPYTF	2596

269	GSFSS YALH	2127	GLINPS GGRTS YA	2221	CARDE GYATF DYW	2315	RASQSI SSSYL A	2409	DVSAR AT	2503	CQQYY STPLTF	2597
270	GTFSS YYMH	2128	GWISA YNGNT NYA	2222	CAKD MGYY YDSSG GFDY W	2316	RASQSI SSYLN	2410	DASNL ET	2504	CQQTY TTPLTF	2598
271	GTFSS YAIS	2129	GGIIPIF GTANY A	2223	CARDL SIGYY GDAFD IW	2317	RASQS VSYNQ LA	2411	DISSRA A	2505	CQQYG GLPAT F	2599
272	YIFTNY YIQ	2130	GGIIPIF GTVGY A	2224	CARGR IGGGN DYW	2318	QASQY ISNYLN	2412	DASSL ES	2506	CQQSY STPYTF	2600
273	DTFNS YAVN	2131	GGIIPS FGTPT YA	2225	CASVS YGSFD YW	2319	RASQS VSSSSL A	2413	DASTR AS	2507	CQQYN RLPYT F	2601
274	YTFTY RYLH	2132	GRITPI SGTTN YA	2226	CAKDS GQLAH YGMD VW	2320	KSSQS VLYSS NNKNY LA	2414	WASTR ES	2508	CQQYY KTPLTF	2602
275	YTFTS YYMH	2133	GWMN PYSGN TGYA	2227	CARVG SGWYS DYW	2321	RASQSI SSYLN	2415	AASSL QS	2509	CQQSY STPLTF	2603
276	YTFTR FNIH	2134	GWLNP FTGNT GYA	2228	CASSSS WYGW FDPW	2322	RASQS VSSYL A	2416	DTSTR AT	2510	CQQYH SSPWT F	2604
277	YTFTG YYMH	2135	GWIDP NSGGT NYA	2229	CARDV DTAM VTDY W	2323	RASQS VDNLV G	2417	DISSRA T	2511	CQQYG RSPITF	2605

278	YTFTS YYMH	2136	GIINPS SGSTT YA	2230	CARSV GATSA FDIW	2324	KSSQS VLYSS NNENY LA	2418	WASTR ES	2512	CQQYY SLPVTF	2606
279	YTFTK YYMH	2137	GIINPS GGSTS YA	2231	CARGR GYSYG YLDY W	2325	RASQSI SSSLN	2419	KASSL ES	2513	CQQYY SYPPTF	2607
280	YTFTR YYMH	2138	GIINPS GGSTS YA	2232	CARGE TRSYA PYGMD VW	2326	QASQD ISNYLN	2420	QASNK DT	2514	CQQSY STPPTF	2608
281	YTFNS YGIS	2139	GIINPT GGSTT YA	2233	CAKDP FVMDV W	2327	RASQS VSSSY LA	2421	DASAR AA	2515	CQQYY STPYTF	2609
282	GTFSS YAIS	2140	GWMN PNSGD TGYA	2234	CARDF EGGG WFDP W	2328	RASRSI SDYLA	2422	DASSR AT	2516	CQQYY TTPLTF	2610
283	YTFTS YYMD	2141	GRINPS SGSTT YV	2235	CARTP SGSYS DFDY W	2329	RASQSI SSYLN	2423	AASSL QS	2517	CQQSY STPWT F	2611
284	YTFTS YYMH	2142	GVINPS GGSTT YA	2236	CARVP GVSPG DYGM DVW	2330	RASHN ISTWL A	2424	AASSL QS	2518	CQQSY STPPTF	2612
285	YSFTN YYMH	2143	GGIIPV FGTTT YS	2237	CARES QDGDF DYW	2331	KSSQS VLYSS NNKNY LA	2425	WASTR ES	2519	CQQYY SSPLTF	2613
286	YTFTS YGIS	2144	GWISP NSGVT NYA	2238	CVSDD YGAFD YW	2332	RASQS VSSSY LA	2426	DVSTR AS	2520	CQQYN NWPYT F	2614

287	YTFTR HYVH	2145	GIINPS SGSAS YA	2239	CARDR LRSRF DYW	2333	RASQSI SSSLA	2427	AASSL QS	2521	CQQSY TIPPTF	2615
288	YTFTT YDIN	2146	GWMN PSSGN SGFA	2240	CARED YYDSS GYYN W	2334	RASQG ISNNLN	2428	KASTL ES	2522	CQQSY STPITF	2616
289	YTFTS YGIS	2147	GWMN PISGNT DYA	2241	CVVER RREVG MDVW	2335	QASQG ITSYLN	2429	KASSL ES	2523	CQQGY STPLTF	2617
290	GTFTS YYMH	2148	GWISA YNGKT DYA	2242	CARDQ GYYYD SSGAF DIW	2336	RASQSI SSYLN	2430	DASNL ET	2524	CQQTY SAPPTF	2618
291	YTFTS YYMH	2149	GIINPS GGSTV YA	2243	CARGI GSKGA FDIW	2337	RSSQS LLHSN GYNYL D	2431	LGSNR AS	2525	CMQGL QTPYT F	2619
292	YTFTS YGIS	2150	GWINP NSGGT NYA	2244	CARQG GLRDF DYW	2338	RASQSI STYVN	2432	DTSSL QS	2526	CQQSFI TPPTF	2620
293	YMFTT PYIH	2151	GVINPI SGTTT YA	2245	CANDR HYDF WSGY YKEEW EYFQH W	2339	RSSQS LLHSN GYNYL D	2433	LGSNR AS	2527	CMQAL QTPTF	2621
294	YTFTS NNMH	2152	GWINL NSGGT NYA	2246	CAKAI DYYY MDVW	2340	RASQG IRNDL G	2434	QASSL EN	2528	CQQAY SLPWT F	2622

Table 18b. Sequences of Non-Selective Anti-FLT3 Polypeptides (VH and VL Sequences)

Polypeptide No.	Full VH	SEQ ID NO	Full VL	SEQ ID NO
201	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSDGISWVRQAP GQGLEWMGWISAYHGHTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGG KHSGSHRSYYYGMDVWGQG TTVTVSS	2623	DIQMTQSPSSLSASVGDRVTI TCRASHNIGNKLAWYQQKPG KAPKLLIYGATTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANSFPRTFGPGTKV DIKR	2717
202	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGVINPSGGSTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARAG VGAFHIWGQGTMVTVSS	2624	DIQMTQSPSSLSASVGDRVTI TCRASQSIRSWLAWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQIYSLPRTFGQGTKVE IKR	2718
203	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTELSMHWVRQA PGQGLEWMGRIIPISGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARAARYC SSTSCYWRDGMDVWGQGTT VTVSS	2625	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYSSNNKNYLAW YQQKPGQPPKLLIYWASTRA SGVPDRFSGSGSGTDFTLTISS LQAEDVAVYYCQQYYSTPQT FGQGTKLEIKR	2719
204	EVQLLESGGGLVQPGGSLRLS CAASGFDFSTYNMFWVRQAP GKGLEWVSGISGSGRSKYYA DSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCARVYYD SSGYYPYYFDYWGQGTLVTV SS	2626	DIQMTQSPSSLSASVGDRVTI TCRASQSIGSNLDWYQQKPG KAPKLLIYDASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPYTFGQGTKL EIKR	2720
205	QVQLVQSGAEVKKPGSSVKV SCKASGGSFISHTFSWVRQAP GQGLEWMGGIIPISGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAKGRGQL VGGYFQHWGQGTLVTVSS	2627	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASSLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPLTFG QGTRLEIKR	2721
206	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTSYYLHWVRQA PGQGLEWMGGIIPIFGKAEYS QRFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAREDFWS GPYGMDVWGQGTTVTVSS	2628	DIQMTQSPSSLSASVGDRVTI TCRASQAISSYLAWYQQKPG KAPKLLIYAASNLQGGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	2722
207	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGWMNPNSGNTG YAQRFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCAKSH YYYFYGMDVWGQGTTVTVSS	2629	DIQMTQSPSSLSASVGDRVTI TCQASHDISKYLNWYQQKPG KAPKLLIYAASILQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPYTFGQGTKLEI KR	2723

208	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSRSISWVRQAP GQGLEWMGIINPSGGGTLYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDMDG WSDAFDIWGQGTTVTVSS	2630	EIVMTQSPATLSVSPGERATL SCRASQSLSNIYLAWYQQKP GQAPRLLIYDVSSRAAGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYATSPLTFGGGTK VEIKR	2724
209	EVQLLESGGGLVQPGGSLRLS CAASGFAFSSYVLHWVRQAP GKGLEWVAGIWVDGHNKDY ADSVKGRFTISRDNSKNTLYL QMNSLRAEDTAVYYCAREFG AAGSFQHWGQGTLVTVSS	2631	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYDASKLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYTTPYTFGQGTKV EIKR	2725
210	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTELSMHWVRQA PGQGLEWMGGIIPISGTTKYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARASPRY YMDVWGKGTTVTVSS	2632	DIVMTQSPDSLAVSLGERATI NCKSSQSVFYSSNNKNYLAW YQQKPGQPPKLLIYWASTRA SGVPDRFSGSGSGTDFTLTISS LQAEDVAVYYCHQYYSKPPT FGQGTKVEIKR	2726
211	EVQLLESGGGLVQPGGSLRLS CAASGFTFSNHYMSWVRQAP GKGLEWVSAIGAGGGTYYAD SVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAKSSGYS YGRRPFDYWGQGTLVTVSS	2633	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLAWYQQKPG KAPKLLIYAASTLHNGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYGRSPKTFGQGTKV EIKR	2727
212	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGGIIPILGTANNA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARAPWGT FDYWGQGTLVTVSS	2634	EIVMTQSPATLSVSPGERATL SCRASQSVSSSQLAWYQQKP GQAPRLLIYDTSTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYDNSLWTFGQGT RLEIKR	2728
213	QVQLVQSGAEVKKPGASVKV SCKASGYTFSRYYMSWVRQA PGQGLEWMGWMNPNSGNTG YAQKFQGRVTMTRDTSTSTV YMELSSLRSEDTAVYYCARTR FAAQPHNWHFDLWGRGTLVT VSS	2635	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYDASNLKTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGPGTKV DIKR	2729
214	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDRAA RPRGGFDYWGQGTLVTVSS	2636	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNHLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPTFGQGTKVEI KR	2730

215	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYRMHWVRQA PGQGLEWMGWINPNSGGTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKGG LDWRNWYFDLWGRGTLVTV SS	2637	DIQMTQSPSSLSASVGDRVTI TCRASQGISSYLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	2731
216	QVQLVQSGAEVKKPGSSVKV SCKASGNTFTMYYMHWVRQ APGQGLEWVGAIIPISGTVIYA RKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARLSGGR MYDAFDIWGQGTTVTVSS	2638	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPLTFG QGTKVEIKR	2732
217	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTTFYLHWVRQAP GQGLEWIGGIIPMSGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCASGGENG MDVWGQGTTVTVSS	2639	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYSVNNKNYLA WYQQKPGQPPKLLIYWASTR ESGVPDRFSGSGSGTDFTLTIS SLQAEDVAVYYCQQYYSAPP TFGQGTKVEIKR	2733
218	QVQLVQSGAEVKKPGASVKV SCKASGYSFTTHYMHWVRQA PGQGLEWMGIINPSGGSTRYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGSSY YYYGVDVWGKGTTVTVSS	2640	DIQMTQSPSSLSASVGDRVTI TCRASQSISTWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAISFPLTFGGGTKVE IKR	2734
219	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGIINPSSGSASYT QKLQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDRST LVPLDYWGQGTLVTVSS	2641	DIQMTQSPSSLSASVGDRVTI TCRASQGIRSELSWYQQKPG KAPKLLIYKASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCLQHNSYPLTFGGGTKVEI KR	2735
220	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMYWVRQA PGQGLEWMGIINPRGGITSYA QRFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGSTS SGWPNGDMDVWGKGTTVTV SS	2642	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQANRFPPTFGQGTKV EIKR	2736
221	QVQLVQSGAEVKKPGASVKV SCKASGYTFTDNYMHWVRQA PGQGLEWMGWMTPDSNNTG FAQNFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCALGD GPFGMDVWGQGTTVTVSS	2643	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYGASYLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQGPITFG QGTKVEIKR	2737

222	QVQLVQSGAEVKKPGASVKV SCKASGYSFTAYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARVAGI NGEMAYWGQGTLVTVSS	2644	DIQMTQSPSSLSASVGDRVTI TCRASQDISNYLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYRTPYTFGQGTKV EIKR	2738
223	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNSFIHWVRQAP GQGLEWMGIINPSGGSTSYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKALERR YYYGMDVWGQGTTVTVSS	2645	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYDGSNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTKV EIKR	2739
224	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGVINPIYGTANY ALKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCAKAISSG WSNDAFDIWGQGTMVTVSS	2646	EIVMTQSPATLSVSPGERATL SCRASQSVSSDFLAWYQQKP GQAPRLLIYDTSSRASGIPARF SGSGSGTEFTLTISSLQSEDFA VYYCQQYAGPPTFGQGTRLE IKR	2740
225	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTELSIHWVRQAP GQGLEWMGGIVPMSGTASYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARRRDGY NSWGQGTLVTVSS	2647	DIVMTQSPDSLAVSLGERATI NCKSSQSLLYGSKNYISWYQ QKPGQPPKLLIYSSSTRESGVP DRFSGSGSGTDFTLTISSLQAE DVAVYYCQQYYTTPYTFGQ GTKVEIKR	2741
226	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGIIDPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDRSL LWSGVGGMDVWGQGTTVTV SS	2648	DIQMTQSPSSLSASVGDRVTI TCRASQGISNYLAWYQQKPG KAPKLLIYGASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYGTPYTFGQGTKL EIKR	2742
227	QVQLVQSGAEVKKPGSSVKV SCKASGYTLNELFMHWVRQA PGQGLEWVGGIIPMSGTTFYA QTFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAKGVRQ YSYGRYYYGMDVWGQGTLV TVSS	2649	DIQMTQSPSSLSASVGDRVTI TCRASQSVSSYLNWYQQKPG KAPKLLIYGASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYTTPWTFGQGTRL EIKR	2743
228	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSHAISWVRQAP GQGLEWMGWINPGSGGTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAKDSYD FWSGYYIDYWGQGTLVTVSS	2650	DIQMTQSPSSLSASVGDRVTI TCRASQSIYTHLNWYQQKPG KAPKLLIYAASRLQTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSFPFTFGPGTKVD IKR	2744

229	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGVGY SGYGADLWGRGTLVTVSS	2651	DIQMTQSPSSLSASVGDRVTI TCRASQGISNSLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSHSPPYTFGQGTKL EIKR	2745
230	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSNAINWVRQAP GQGLEWMGGIIPLFGTTNYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARVLSGW YGTYYFDYWGQGTLVTVSS	2652	EIVMTQSPATLSVSPGERATL SCRASQSVSADYIAWYQQKP GQAPRLLIYDVSTRASGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQHYGSSQVTFGQGTK VEIKR	2746
231	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYIHWVRQAP GQGLEWMGLINPSGGSTTYA QSFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGLG WGVVVPAAELDYWGQGTLV TVSS	2653	DIQMTQSPSSLSASVGDRVTI TCRASQSISTYLNWYQQKPG KAPKLLIYAASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSSPLTFGPGTKVD IKR	2747
232	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGIHWVRQAP GQGLEWMGGIIPIFGTASYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCTRSNGIA AAGTHWYFDLWGRGTLVTVS S	2654	DIQMTQSPSSLSASVGDRVTI TCRASQNIANSLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYSSYPPTFGPGTKV DIKR	2748
233	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYLHWVRQA PGQGLEWIGVINPSGGSTTYA QRFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGIGY GGYFDYWGQGTLVTVSS	2655	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASSLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGLRTPHTF GGGTKVEIKR	2749
234	QVQLVQSGAEVKKPGSSVKV SCKASGHTFTAYYMHWVRQA PGQGLEWMGWMSPYSGNTG YAQNFQGRVTITADESTSTAY MELSSLRSEDTAVYYCARATR GTIQHWGQGTLVTVSS	2656	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYSSNNKNYLAW YQQKPGQPPKLLIYWASIRES GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCQQYYTTPITF GQGTRLEIKR	2750
235	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDPGR LGELDYWGQGTLVTVSS	2657	EIVMTQSPATLSVSPGERATL SCRASQSVSSNLAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYGSSPLTFGGGTKVEI KR	2751

236	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGGIIPILGIANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAHVDGYG MDVWGQGTTVTVSS	2658	EIVMTQSPATLSVSPGERATL SCRASQSVSSNLAWYQQKPG QAPRLLIYDVSSRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQLDAYPLTFGGGTKVE IKR	2752
237	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGLINPSSGSTSYA RNFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARSGSG GSYFLFDYWGQGTLVTVSS	2659	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYAASTLQSGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPLTFG GGTKVEIKR	2753
238	QVQLVQSGAEVKKPGASVKV SCKASGYTFTIYYMHWVRQA PGQGLEWMGIINPSGGSTVYA QTFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGIGS KGAFDIWGQGTMVTVSS	2660	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGLQTPYTF GQGTRLEIKR	2754
239	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGGIIPILGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARTMTTVT YYDAFDIWGQGTMVTVSS	2661	EIVMTQSPATLSVSPGERATL SCRASQSVGSSYLAWYQQKP GQAPRLLIYDVSTRAAGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCHQYGSSPYTFGQGTK VEIKR	2755
240	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIINPSSGSTTYA LKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGLGK SAIDYWGQGTLVTVSS	2662	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGQGTRLE IKR	2756
241	QVQLVQSGAEVKKPGASVKV SCKASGYTFTRHYVHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARSYHH YYYGMDVWGQGTTVTVSS	2663	DIQMTQSPSSLSASVGDRVTI TCRASQSISNYLAWYQQKPG KAPKLLIYAASSLQGGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKV EIKR	2757
242	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSATISWVRQAP GQGLEWMGGIIPMFGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARDAYG DSTWGQGTLVTVSS	2664	EIVMTQSPATLSVSPGERATL SCRASESVSSALAWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYGNSVTFGGGTKVEI KR	2758

243	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSHAFNWVRQAP GQGLEWMGGISPMFGTPNYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARAPDYG DDWYFDLWGRGTLVTVSS	2665	EIVMTQSPATLSVSPGERATL SCRASQTLTGGLLAWYQQKP GQAPRLLIYDTSSRAAGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCHHYGSSPYTFGQGTK VEIKR	2759
244	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGRINPSGGSTSYA QSFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARVPGL YGGAIDYWGQGTLVTVSS	2666	DIQMTQSPSSLSASVGDRVTI TCRASQDIRNDLGWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSSPFTFGQGTKVE IKR	2760
245	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTGFYIHWVRQAP GQGLEWMGGVIPFFSRTIYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAYGANGH LYGMDAWGQGTTVTVSS	2667	EIVMTQSPATLSVSPGERATL SCRASQSVSSSYLAWYQQKP GQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYSSSPLTFGQGTK VEIKR	2761
246	QVQLVQSGAEVKKPGSSVKV SCKASGGTFTSYFMHWVRQA PGQGLEWMGGIIPMFGAPVY AQDFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCAAGLDF WSGPDNYYMDVWGKGTTVT VSS	2668	DIQMTQSPSSLSASVGDRVTI TCQATQDISNYLNWYQQKPG KAPKLLIYGASNLPSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSDLLTFGPGTKV DIKR	2762
247	QVQLVQSGAEVKKPGASVKV SCKASGGTLMSYAISWVRQAP GQGLEWMGIINPRGGTTRYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARSEDS GYDYLDYWGQGTLVTVSS	2669	EIVMTQSPATLSVSPGERATL SCRGSQSISGNYLAWYQQKP GQAPRLLIYDTSARAAGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYNSYPLTFGGGTK VEIKR	2763
248	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGVINPNGGSISYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCAREGWF GEDGMDVWGQGTTVTVSS	2670	DIQMTQSPSSLSASVGDRVTI TCRASQDLDRYLAWYQQKP GKAPKLLIYAASSLQTGVPSR FSGSGSGTDFTLTISSLQPEDF ATYYCQQYYSTPYTFGQGTK LEIKR	2764
249	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSDGISWVRQAP GQGLEWMGWMNPNSGNAGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCATAV AGTDAFDIWGQGTMVTVSS	2671	EIVMTQSPATLSVSPGERATL SCRASQSIGNNLKAWYQQKP GQAPRLLIYDTSAHTTGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQHYGNSLTFGQGTK VEIK	2765

250	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTSFAMHWVRQA PGQGLEWMGRIIPMSGTANY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCASTSPD QYYYGMDVWGQGTTVTVSS	2672	EIVMTQSPATLSVSPGERATL SCRASQSVGSSSLAWYQQKP GQAPRLLIYGASTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYGSSPYTFGQGTK VEIKR	2766
251	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSDAINWVRQAP GQGLEWMGGIIPIVGTPTYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAKGLAFGV FDGLDVWGQGTTVTVSS	2673	EIVMTQSPATLSVSPGERATL SCRASQSVSSNYLAWYQQKP GQAPRLLIYDVSTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYGSSTLTFGGGTK VEIKR	2767
252	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTDLSIHWVRQAP GQGLEWVGGIIPMSGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARSSSSW PKYFQHWGQGTLVTVSS	2674	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	2768
253	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTTYFMHWVRQA PGQGLEWMGGIVPVFGTTKY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCASSAVG WFDPWGQGTLVTVSS	2675	DIQMTQSPSSLSASVGDRVTI TCRASQDISRWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYDNFPLTFGGGTKL EIKR	2769
254	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSHYMHWVRQA PGQGLEWMGWISPYNGNTNY AQKLQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARGES NSGWINFDYWGQGTLVTVSS	2676	EIVMTQSPATLSVSPGERATL SCRASQSVSSSSLAWYQQKP GQAPRLLIYDTSTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYGTSPITFGQGTR LEIKR	2770
255	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTELSMHWVRQA PGQGLEWMGGIIPISGTVTYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCANKGQQL VRGYFQHWGQGTLVTVSS	2677	DIQMTQSPSSLSASVGDRVTI TCQASHDIRNSVNWYQQKPG KAPKLLIYATSSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYNTPFTFGQGTKLEI KR	2771
256	QVQLVQSGAEVKKPGASVKV SCKASGYTFATYYLHWVRQA PGQGLEWMGMINPSGGSTIYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARSSGY DFFDYWGQGTLVTVSS	2678	DIQMTQSPSSLSASVGDRVTI TCRASHDINNYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQADSFPLTFGGGTKV EIKR	2772

257	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYFMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARAHTV YYYGMDVWGQGTMVTVSS	2679	DIQMTQSPSSLSASVGDRVTI TCRASQSISSWLAWYQQKPG KAPKLLIYAASTLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKL EIKR	2773
258	QVQLVQSGAEVKKPGASVKV SCKASGGTFGSYAISWVRQAP GQGLEWMGWINPNTGGAHY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARVG AAAGYQHWGQGTLVTVSS	2680	DIQMTQSPSSLSASVGDRVTI TCRASQSIKGALAWYQQKPG KAPKLLIYSASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYNSYPLTFGGGTKV EIKR	2774
259	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTSSEINWVRQAP GQGLEWMGGIHPMFGTTNYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARARLM VYAPSDYWGQGTLVTVSS	2681	DIVMTQSPDSLAVSLGERATI NCKSSQSLFYSSNNRNYLAW YQQKPGQPPKLLIYWASTRES GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCQQYYSIPYTF GQGTKVEIKR	2775
260	QVQLVQSGAEVKKPGASVKV SCKASGYTFTNYYVHWVRQA PGQGLEWMGMINPSGGSTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARVSG WKRGWFDPWGQGTLVTVSS	2682	DIQMTQSPSSLSASVGDRVTI TCRSSQSISTYLNWYQQKPG KAPKLLIYGASNLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQVISYPITFGGGTKVE IKR	2776
261	QVQLVQSGAEVKKPGASVKV SCKASGYTFTRYYMHWVRQA PGQGLEWMGIINPSGGSASYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDLGG AAAGYFDYWGQGTLVTVSS	2683	DIVMTQSPDSLAVSLGERATI NCKSSQSISHSPNTRDYLAWY QQKPGQPPKLLIYWASTRESG VPDRFSGSGSGTDFTLTISSLQ AEDVAVYYCQQYYSSPFTFG PGTKVDIKR	2777
262	QVQLVQSGAEVKKPGASVKV SCKASGFTFSDYGYYMHWVR QAPGQGLEWMGWMDPSSGH TGYAQRFQGRVTMTRDTSTST VYMELSSLRSEDTAVYYCAK DIGWGAFDIWGQGTTVTVSS	2684	EIVMTQSPATLSVSPGERATL SCRASQRVGNTYLAWYQQK PGQAPRLLIYDVSARASGIPA RFSGSGSGTEFTLTISSLQSED FAVYYCQQYLSPPLTFGGGT KVEIKR	2778
263	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGGIIPIVGVANYAQ KLQGRVTITADESTSTAYMEL SSLRSEDTAVYYCAKDIGGYP SDAFDIWGQGTTVTVSS	2685	EIVMTQSPATLSVSPGERATL SCRASQSVSSSYLAWYQQKP GQAPRLLIYDVSTRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYGSSPITFGQGTK VEIKR	2779

264	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTELSMHWVRQA PGQGLEWMGGIIPISSATSIPQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARGALYSS SPVRVVAGTKGWFDPWGQGT LVTVSS	2686	DIQMTQSPSSLSASVGDRVTI TCRASQDISNYLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQYYSYPLTFGGGTKV EIKR	2780
265	QVQLVQSGAEVKKPGSSVKV SCKASGHTFTSDYMHWVRQA PGQGLEWMGRIIPIFGTADYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARDDSSG IFDYWGQGTLVTVSS	2687	EIVMTQSPATLSVSPGERATL SCRASQSVNSEHLAWYQQKP GQAPRLLIYDTSSRATGIPARF SGSGSGTEFTLTISSLQSEDFA VYYCQQYGSSPVTFGQGTKV EIKR	2781
266	QVQLVQSGAEVKKPGSSVKV SCKASGYSLTELSIHWVRQAP GQGLEWMGGINPISGTANYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARGTVRL NWFDPWGQGTLVTVSS	2688	EIVMTQSPATLSVSPGERATL SCRASQSVGSQLGWYQQKPG QAPRLLIYGASTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQSFSTPLTFGGGTKVEI KR	2782
267	QVQLVQSGAEVKKPGSSVKV SCKASGYTLTSFGISWVRQAP GQGLEWVGMIIPLSGTTHYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCANLYGGN AYYYYGMDVWGQGTTVTVS S	2689	DIQMTQSPSSLSASVGDRVTI TCRASQDISNFVAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSFDTPYTFGQGTKL EIKR	2783
268	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSTYALSWVRQAP GQGLEWMGGVIPVFGTTDYA HKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCASMIIFGA GGWDAYYFQEWGQGTLVTV SS	2690	EIVMTQSPATLSVSPGERATL SCRASQSVNNNQLAWYQQK PGQAPRLLIYDTSSRATGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYDTSPYTFGQGTK VEIKR	2784
269	QVQLVQSGAEVKKPGASVKV SCKASGGSFSSYALHWVRQAP GQGLEWMGLINPSGGRTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDEGY ATFDYWGQGTLVTVSS	2691	EIVMTQSPATLSVSPGERATL SCRASQSISSSYLAWYQQKPG QAPRLLIYDVSARATGIPARF SGSGSGTEFTLTISSLQSEDFA VYYCQQYYSTPLTFGPGTKV DIKR	2785
270	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYYMHWVRQA PGQGLEWMGWISAYNGNTNY AQKLQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKDM GYYYDSSGGFDYWGQGTLVT VSS	2692	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYTTPLTFGQGTKV EIKR	2786

271	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGGIIPIFGTANYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARDLSIGY YGDAFDIWGQGTMVTVSS	2693	EIVMTQSPATLSVSPGERATL SCRASQSVSYNQLAWYQQKP GQAPRLLIYDISSRAAGIPARF SGSGSGTEFTLTISSLQSEDFA VYYCQQYGGLPATFGQGTRL EIKR	2787
272	QVQLVQSGAEVKKPGSSVKV SCKASGYIFTNYYIQWVRQAP GQGLEWMGGIIPIFGTVGYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCARGRIGGG NDYWGQGTLVTVSS	2694	DIQMTQSPSSLSASVGDRVTI TCQASQYISNYLNWYQQKPG KAPKLLIYDASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYSTPYTFGQGTKLEI KR	2788
273	QVQLVQSGAEVKKPGSSVKV SCKASGDTFNSYAVNWVRQA PGQGLEWMGGIIPSFGTPTYA WKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCASVSYGS FDYWGQGTLVTVSS	2695	EIVMTQSPATLSVSPGERATL SCRASQSVSSSSLAWYQQKP GQAPRLLIYDASTRASGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYNRLPYTFGQGTK LEIKR	2789
274	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTYRYLHWVRQA PGQGLEWMGRITPISGTTNYA QKFQGRVTITADESTSTAYME LSSLRSEDTAVYYCAKDSGQL AHYGMDVWGQGTTVTVSS	2696	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYSSNNKNYLAW YQQKPGQPPKLLIYWASTRES GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCQQYYKTPLTF GGGTKLEIKR	2790
275	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGWMNPYSGNTG YAQKFQGRVTITADESTSTAY MELSSLRSEDTAVYYCARVGS GWYSDYWGQGTLVTVSS	2697	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPLTFGGGTKV EIKR	2791
276	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTRFNIHWVRQAP GQGLEWMGWLNPFTGNTGY ARKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCASSSSW YGWFDPWGQGTLVTVSS	2698	EIVMTQSPATLSVSPGERATL SCRASQSVSSYLAWYQQKPG QAPRLLIYDTSTRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYHSSPWTFGQGTKVE IKR	2792
277	QVQLVQSGAEVKKPGSSVKV SCKASGYTFTGYYMHWVRQA PGQGLEWMGWIDPNSGGTNY AQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARDVDT AMVTDYWGRGTLVTVSS	2699	EIVMTQSPATLSVSPGERATL SCRASQSVDNLVGWYQQKP GQAPRLLIYDISSRATGIPARF SGSGSGTEFTLTISSLQSEDFA VYYCQQYGRSPITFGQGTRLE IKR	2793

278	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIINPSSGSTTYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARSVGA TSAFDIWGQGTMVTVSS	2700	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYSSNNENYLAW YQQKPGQPPKLLIYWASTRES GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCQQYYSLPVTF GQGTKLEIKR	2794
279	QVQLVQSGAEVKKPGASVKV SCKASGYTFTKYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGRGY SYGYLDYWGQGTLVTVSS	2701	DIQMTQSPSSLSASVGDRVTI TCRASQSISSSLNWYQQKPGK APKLLIYKASSLESGVPSRFSG SGSGTDFTLTISSLQPEDFATY YCQQYYSYPPTFGGGTKVEI KR	2795
280	QVQLVQSGAEVKKPGASVKV SCKASGYTFTRYYMHWVRQA PGQGLEWMGIINPSGGSTSYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGETR SYAPYGMDVWGQGTTVTVSS	2702	DIQMTQSPSSLSASVGDRVTI TCQASQDISNYLNWYQQKPG KAPKLLIYQASNKDTGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGQGTKLE IKR	2796
281	QVQLVQSGAEVKKPGASVKV SCKASGYTFNSYGISWVRQAP GQGLEWMGIINPTGGSTTYAQ KFQGRVTMTRDTSTSTVYME LSSLRSEDTAVYYCAKDPFVM DVWGQGTTVTVSS	2703	EIVMTQSPATLSVSPGERATL SCRASQSVSSSYLAWYQQKP GQAPRLLIYDASARAAGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYYSTPYTFGQGTK LEIKR	2797
282	QVQLVQSGAEVKKPGASVKV SCKASGGTFSSYAISWVRQAP GQGLEWMGWMNPNSGDTGY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDFE GGGWFDPWGQGTLVTVSS	2704	EIVMTQSPATLSVSPGERATL SCRASRSISDYLAWYQQKPG QAPRLLIYDASSRATGIPARFS GSGSGTEFTLTISSLQSEDFAV YYCQQYYTTPLTFGQGTKVE IKR	2798
283	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMDWVRQA PGQGLEWMGRINPSSGSTTYV QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARTPSG SYSDFDYWGQGTLVTVSS	2705	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPWTFGQGTKV EIKR	2799
284	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGVINPSGGSTTY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARVPG VSPGDYGMDVWGQGTTVTVS S	2706	DIQMTQSPSSLSASVGDRVTI TCRASHNISTWLAWYQQKPG KAPKLLIYAASSLQSGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPPTFGQGTRLE IKR	2800

285	QVQLVQSGAEVKKPGSSVKV SCKASGYSFTNYYMHWVRQA PGQGLEWMGGIIPVFGTTTYS QTFQGRVTITADESTSTAYME LSSLRSEDTAVYYCARESQDG DFDYWGQGTLVTVSS	2707	DIVMTQSPDSLAVSLGERATI NCKSSQSVLYSSNNKNYLAW YQQKPGQPPKLLIYWASTRES GVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCQQYYSSPLTF GGGTKVEIKR	2801
286	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGISWVRQAP GQGLEWMGWISPNSGVTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCVSDDYG AFDYWGQGTLVTVSS	2708	EIVMTQSPATLSVSPGERATL SCRASQSVSSSYLAWYQQKP GQAPRLLIYDVSTRASGIPAR FSGSGSGTEFTLTISSLQSEDF AVYYCQQYNNWPYTFGQGT KLEIKR	2802
287	QVQLVQSGAEVKKPGASVKV SCKASGYTFTRHYVHWVRQA PGQGLEWVGIINPSSGSASYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARDRLR SRFDYWGQGTLVTVSS	2709	DIQMTQSPSSLSASVGDRVTI TCRASQSISSSLAWYQQKPGK APKLLIYAASSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSYTIPPTFGQGTKLEI KR	2803
288	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYDINWVRQAP GQGLEWMGWMNPSSGNSGF AQQFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAREDY YDSSGYYNWGQGTLVTVSS	2710	DIQMTQSPSSLSASVGDRVTI TCRASQGISNNLNWYQQKPG KAPKLLIYKASTLESGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQSYSTPITFGQGTKVE IKR	2804
289	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGISWVRQAP GQGLEWMGWMNPISGNTDY APNFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCVVERR REVGMDVWGQGTTVTVSS	2711	DIQMTQSPSSLSASVGDRVTI TCQASQGITSYLNWYQQKPG KAPKLLIYKASSLESGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQGYSTPLTFGGGTKVEI KR	2805
290	QVQLVQSGAEVKKPGASVKV SCKASGGTFTSYYMHWVRQA PGQGLEWMGWISAYNGKTDY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCARDQ GYYYDSSGAFDIWGQGTLVT VSS	2712	DIQMTQSPSSLSASVGDRVTI TCRASQSISSYLNWYQQKPG KAPKLLIYDASNLETGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQTYSAPPTFGQGTKL EIKR	2806
291	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYYMHWVRQA PGQGLEWMGIINPSGGSTVYA QTFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARGIGS KGAFDIWGQGTMVTVSS	2713	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQGLQTPYTF GQGTRLEIKR	2807

292	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGISWVRQAP GQGLEWMGWINPNSGGTNYA QKFQGRVTMTRDTSTSTVYM ELSSLRSEDTAVYYCARQGGL RDFDYWGQGTLVTVSS	2714	DIQMTQSPSSLSASVGDRVTI TCRASQSISTYVNWYQQKPG KAPKLLIYDTSSLQSGVPSRFS GSGSGTDFTLTISSLQPEDFAT YYCQQSFITPPTFGQGTKLEIK R	2808
293	QVQLVQSGAEVKKPGSSVKV SCKASGYMFTTPYIHWVRQAP GQGLEWMGVINPISGTTTYAQ KFQGRVTITADESTSTAYMEL SSLRSEDTAVYYCANDRHYDF WSGYYKEEWEYFQHWGQGT LVTVSS	2715	DIVMTQSPLSLPVTPGEPASIS CRSSQSLLHSNGYNYLDWYL QKPGQSPQLLIYLGSNRASGV PDRFSGSGSGTDFTLKISRVE AEDVGVYYCMQALQTPTFG GGTKVEIKR	2809
294	QVQLVQSGAEVKKPGASVKV SCKASGYTFTSNNMHWVRQA PGQGLEWMGWINLNSGGTNY AQKFQGRVTMTRDTSTSTVY MELSSLRSEDTAVYYCAKAID YYYMDVWGKGTTVTVSS	2716	DIQMTQSPSSLSASVGDRVTI TCRASQGIRNDLGWYQQKPG KAPKLLIYQASSLENGVPSRF SGSGSGTDFTLTISSLQPEDFA TYYCQQAYSLPWTFGQGTKL EIKR	2810

[00540] The polypeptides above were tested as disclosed above in Examples 4 and 5. Data is disclosed below in Table 18c, reporting FACS fold change over parental as (-), indicating < 2 fold; (+), indicating 2-10 fold; (++), indicating 10-30 fold; and (+++), indicating > 30 fold.

Table 18c. Polypeptide Activity (FACS & BLI)

Polypeptide No.	FLT3 Mutant Geometric Mean Fold Change over Jurkat Parental	FLT3 WT Geometric Mean Fold Change over Jurkat Parental	FLT3 Mutant BLI/Octet Binding Summary (Yes/No/ Ambiguous)	FLT3 WT BLI/Octet Binding Summary (Yes/No/ Ambiguous)
201	-	-	Yes	Yes
202	+	-	Yes	No
203	-	-	Yes	No
204	-	-	Ambiguous	Ambiguous
205	-	-	Yes	Yes
206	-	-	Yes	Yes
207	++	++	Yes	Yes
208	++	++	Yes	Yes
209	-	-	Yes	Yes
210	+	-	Yes	Yes
211	-	-	Ambiguous	Ambiguous

212	++	++	Yes	Yes
213	++	++	Yes	Yes
214	+++	+++	Yes	Yes
215	++	++	Yes	Yes
216	-	-	Yes	Yes
217	-	-	Yes	Yes
218	++	++	Yes	Yes
219	++	++	Yes	Yes
220	-	-	Yes	No
221	+	-	Yes	No
222	+++	+++	Yes	Yes
223	+++	+++	Yes	Yes
224	+	-	Yes	Yes
225	+	-	Yes	Yes
226	+	-	Yes	Yes
227	-	-	Yes	Yes
228	+++	+++	Yes	Yes
229	+++	+++	Yes	Yes
230	-	-	Yes	Yes
231	+++	+++	Yes	Yes
232	-	-	Yes	Yes
233	+++	+++	Yes	Yes
234	-	-	Yes	Yes
235	+++	+++	Yes	Yes
236	-	-	Yes	Yes
237	+++	+++	Yes	Yes
238	+++	+++	Yes	Yes
239	-	-	Yes	Yes
240	+++	+++	Yes	Yes
241	++	++	Yes	Yes
242	+++	+++	Yes	Yes
243	+	+	Yes	Yes
244	+++	+++	Yes	Yes
245	+	-	Yes	Yes
246	+	++	Yes	Yes
247	+	+	Yes	Yes
248	+	+	Yes	Yes
249	+	+	Yes	Yes
250	+	-	Yes	Yes
251	-	-	Yes	Yes

252	-	-	Yes	Yes
253	+	+	Yes	Yes
254	+	++	Yes	Yes
255	-	-	Yes	Yes
256	+++	+++	Yes	Yes
257	++	++	Yes	Yes
258	-	-	Ambiguous	Ambiguous
259	++	++	Yes	Yes
260	+++	+++	Yes	Yes
261	+++	+++	Yes	Yes
262	++	++	Yes	Yes
263	+	-	Yes	Yes
264	-	-	Yes	Yes
265	++	++	Yes	Yes
266	-	-	Yes	Yes
267	-	-	Yes	Yes
268	+	-	Yes	Yes
269	++	++	Yes	Yes
270	++	++	Yes	Yes
271	-	-	Yes	Yes
272	-	-	Yes	Yes
273	++	++	Yes	Yes
274	-	-	Yes	Yes
275	-	-	Yes	Yes
276	+	-	Yes	Yes
277	-	-	Yes	Yes
278	+++	+++	Yes	Yes
279	+++	+++	Yes	Yes
280	+++	+++	Yes	Yes
281	+	-	Yes	Yes
282	+	-	Yes	Yes
283	+++	+++	Yes	Yes
284	+++	+++	Yes	Yes
285	-	-	Yes	Yes
286	+	-	Yes	Yes
287	+	++	Yes	Yes
288	++	+	Yes	Yes
289	-	-	Yes	Yes
290	++	++	Yes	Yes
291	+++	+++	Yes	Yes

292	+	+	Yes	Yes
293	+	+	Yes	Yes
294	++	++	Yes	Yes

[00541] The detailed description set-forth above is provided to aid those skilled in the art in practicing the present disclosure. However, the disclosure described and claimed herein is not to be limited in scope by the specific embodiments herein disclosed because these embodiments are intended as illustration of several aspects of the disclosure. Any equivalent embodiments are intended to be within the scope of this disclosure. Indeed, various modifications of the disclosure in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description, which do not depart from the spirit or scope of the present inventive discovery. Such modifications are also intended to fall within the scope of the appended claims.

CLAIMS

What is claimed is:

1. A polypeptide which selectively binds a first polymorphic variant of a human cancer cell antigen over a second polymorphic variant of the human cancer cell antigen; or selectively binds the second polymorphic variant of the antigen over the first polymorphic variant of the antigen.
2. The polypeptide of claim 1, wherein the antigen is chosen from CD33, CLL-1, and FLT3.
3. The polypeptide of claim 2, wherein the antigen is CD33.
4. A polypeptide which selectively binds a first polymorphic variant of CD33 over a second polymorphic variant of CD33; or selectively binds the second polymorphic variant of CD33 over the first polymorphic variant of CD33; wherein the binding is at least 2-fold selective.
5. The polypeptide of claim 4, wherein the binding is at least 10-fold selective.
6. The polypeptide of claim 5, wherein the binding is at least 30-fold selective.
7. The polypeptide of any of claims 3-6, wherein the first polymorphic variant of CD33 is R69 and the second polymorphic variant of CD33 is G69; or the first polymorphic variant of CD33 is G69 and the second polymorphic variant of CD33 is R69.
8. The polypeptide of claim 7, comprising six complementarity-determining regions (CDRs).
9. The polypeptide of claim 8, comprising:
   three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and
   three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3.
10. The polypeptide of any of claims 7-9, wherein:
   HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:1-25 and 201-217,
   HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:26-50 and 218-234, and
   HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:51-75 and 235-251.
11. The polypeptide of any of claims 7-9, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:1-25,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:26-50, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:51-75.

12. The polypeptide of any of claims 7-9, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 201-217,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 218-234, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 235-251.

13. The polypeptide of any of claims 10-12, wherein the HCDR1, HCDR2, and HCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

14. The polypeptide of any of claims 10-12, wherein the HCDR1, HCDR2, and HCDR3 have the recited amino acid sequences.

15. The polypeptide of any of claims any of claims 7-14, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:76-100 and 252-268,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:101-125 and 269-285, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:126-150 and 286-302.

16. The polypeptide of any of claims any of claims 7-14, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 76-100,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:101-125, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:126-150.

17. The polypeptide of any of claims any of claims 7-14, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 252-268,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 269-285, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 286-302.

18. The polypeptide of any of claims 15-17, wherein the LCDR1, LCDR2, and LCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

19. The polypeptide of any of claims 15-17, wherein the LCDR1, LCDR2, and LCDR3 have the recited amino acid sequences.

20. The polypeptide of claim 7, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175 and 303-319.

21. The polypeptide of claim 7, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175.

22. The polypeptide of claim 7, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 303-319.

23. The polypeptide of any of claims 20-22, wherein the V_H domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

24. The polypeptide of any of claims 20-22, wherein the V_H domain has one of the recited amino acid sequences.

25. The polypeptide of any of claims 7 and 20-24, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200 and 320-336.

26. The polypeptide of any of claims 7 and 20-24, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200.

27. The polypeptide of any of claims 7 and 20-24, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 320-336.

28. The polypeptide of any of claims 25-27, wherein the V_L domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

29. The polypeptide of any of claims 25-27, wherein the V_L domain has one of the recited amino acid sequences.

30. The polypeptide of any of claims 20-29, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 1-42.

31. The polypeptide of any of claims 20-29, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 1-25.

32. The polypeptide of any of claims 20-29, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 26-42.

33. The polypeptide of any of claims 29-32, wherein the V_H and V_L domains have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequence pairs.

34. The polypeptide of claim 2, wherein the antigen is FLT3.

35. A polypeptide which selectively binds a first polymorphic variant of FLT3 over a second polymorphic variant of FLT3; or selectively binds the second polymorphic variant of FLT3 over the first polymorphic variant; wherein the binding is at least 2-fold selective.

36. The polypeptide of claim 35, wherein the binding is at least 10-fold selective.

37. The polypeptide of claim 36, wherein the binding is at least 30-fold selective.

38. The polypeptide of any of claims 34-37, wherein the first polymorphic variant of FLT3 is T227 and the second polymorphic variant of FLT3 is M227; or first polymorphic variant of FLT3 is M227 and the second polymorphic variant of FLT3 is T227.

39. The polypeptide of claim 2, wherein the antigen is CLL-1.

40. A polypeptide which selectively binds a first polymorphic variant of CLL-1 over a second polymorphic variant of CLL-1; or selectively binds the second polymorphic variant of CLL-1 over the first polymorphic variant; wherein the binding is at least 2-fold selective.

41. The polypeptide of claim 40, wherein the binding is at least 10-fold selective.

42. The polypeptide of claim 40, wherein the binding is at least 30-fold selective.

43. The polypeptide of any of claims 39-42, wherein the first polymorphic variant of CLL-1 is K224 and the second polymorphic variant of CLL-1 is Q244; or first polymorphic variant of CLL-1 is Q224 and the second polymorphic variant of CLL-1 is K244.

44. The polypeptide of claim 43, comprising six complementarity-determining regions (CDRs).

45. The polypeptide of claim 44, comprising:

three heavy chain variable (V_H) domain CDRs: HCDR1, HCDR2, and HCDR3; and

three light chain variable (V_L) domain CDRs: LCDR1, LCDR2, and LCDR3.

46. The polypeptide of any of claims 43-45, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:337-360- and 529-550,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:361-384 and 551-572, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:385-408 and 573-594.

47. The polypeptide of any of claims 43-45, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 337-360,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 361-384, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 385-408.

48. The polypeptide of any of claims 43-45, wherein:

HCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 529-550,

HCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 551-572, and

HCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 573-594.

49. The polypeptide of any of claims 46-48, wherein the HCDR1, HCDR2, and HCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

50. The polypeptide of any of claims 46-48, wherein the HCDR1, HCDR2, and HCDR3 have the recited amino acid sequences.

51. The polypeptide of any of claims any of claims 43-50, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:409-432 and 595-616,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:433-456 and 617-638, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs:457-480 and 639-660.

52. The polypeptide of any of claims any of claims 43-50, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 409-432,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 433-456, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 457-480.

53. The polypeptide of any of claims any of claims 43-50, wherein:

LCDR1 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 595-616,

LCDR2 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 617-638, and

LCDR3 comprises an amino acid sequence with at least 95% sequence identity to an amino acid sequence chosen from SEQ ID NOs: 639-660.

54. The polypeptide of any of claims 51-53, wherein the LCDR1, LCDR2, and LCDR3 have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

55. The polypeptide of any of claims 51-53, wherein the LCDR1, LCDR2, and LCDR3 have the recited amino acid sequences.

56. The polypeptide of claim 44, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175 and 303-319.

57. The polypeptide of claim 44, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 151-175.

58. The polypeptide of claim 44, comprising a V_H domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 303-319.

59. The polypeptide of any of claims 56-58, wherein the V_H domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

60. The polypeptide of any of claims 56-58, wherein the V_H domain has one of the recited amino acid sequences.

61. The polypeptide of any of claims 44 and 56-60, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200 and 320-336.

62. The polypeptide of any of claims 44 and 56-60, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 176-200.

63. The polypeptide of any of claims 44 and 56-60, comprising a V_L domain having an amino acid sequence exhibiting at least 95% sequence identity to a sequence chosen from any of SEQ ID NOs 320-336.

64. The polypeptide of any of claims 61-63, wherein the V_L domain has at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequences.

65. The polypeptide of any of claims 61-63, wherein the V_L domain has one of the recited amino acid sequences.

66. The polypeptide of any of claims 56-65, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 43-88.

67. The polypeptide of any of claims 56-65, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 43-66.

68. The polypeptide of any of claims 56-65, comprising a combination of a V_H domain and a V_L domain, wherein the combination is chosen from those recited in Polypeptide No.s 67-88.

69. The polypeptide of any of claims 66-68, wherein the V_H and V_L domains have at least 97%, 98% or 99% sequence identity to one of the recited amino acid sequence pairs.

70. A single-chain variable fragment (scFv) comprising the polypeptide of any of claims 1-69.

71. A monoclonal antibody (mAb), or an antigen-binding fragment thereof, comprising the polypeptide of any of claims 1-69.

72. The mAb, or antigen-binding fragment thereof, of claim 71, wherein the mAb is of the IgG, IgM, or IgA isotype.

73. The mAb, or antigen-binding fragment thereof, of claim 72, wherein the mAb is of the IgG1 isotype.

74. The mAb, or antigen-binding fragment thereof, of claim 72, wherein the mAb is of the IgG3 isotype.

75. The mAb, or antigen-binding fragment thereof, of claim 72, wherein the mAb is of the IgG4 isotype.

76. The mAb, or antigen-binding fragment thereof, of claim 72, wherein the mAb is human or humanized.

77. The mAb, or antigen-binding fragment thereof, of any of claims 45-50, wherein the mAb comprises a sequence chosen from SEQ ID NOs: 1627-1978.

78. An antibody-drug conjugate (ADC) comprising the mAb, or antigen-binding fragment thereof, of any of claims 71-78.

79. The ADC of claim 52, having Formula I:

$$Ab\text{-}(L\text{-}D)_p$$

(I)

wherein:

Ab is an antibody comprising the polypeptide of any of claims 1-43, or the antibody of any of claims 45-51, or an antigen-binding fragment of either of the foregoing;

L is a linker;

D is a drug; and

p is about 1 to about 20.

80. The ADC of claim 79, wherein D is chosen from saporin, MMAE, MMAF, DM1, and DM4.

81. A chimeric antigen receptor (CAR) comprising an extracellular ligand binding domain comprising a polypeptide of any one of claims 1-69.

82. The CAR of claim 81, additionally comprising:
    a. a hinge domain;
    b. a transmembrane domain;
    c. optionally, one or more co-stimulatory domains; and
    d. a cytoplasmic signaling domain.
83. The CAR of claim 82, wherein the hinge domain is chosen from FcγRIIIa, CD8α, CD28 and IgG1.
84. The CAR of claim 83, wherein the hinge domain is CD8α.
85. The CAR of any of claims 82-84, wherein the transmembrane domain is chosen from alpha, beta or zeta chain of the T-cell receptor, CD28, CD3 epsilon, CD45, CD4, CD5, CD9, CD16, CD22, CD33, CD37, CD64, CDS0, CD86, CD134, CD137 and CD154
86. The CAR of claim 85, wherein the transmembrane domain is CD28.
87. The CAR of any of claims 82-86, wherein the cytoplasmic signaling domain is chosen from CD8, CD3ζ, CD3δ, CD3γ, CD3ε, CD22, CD32, DAP10, DAP12, CD66d, CD79a, CD79b, FcγRIγ, FcγRIIIγ, FcεRIβ, FcεRIγ (FCERIG), FcRγ, FcRβ, and FcRε.
88. The CAR of claim 87, wherein the cytoplasmic signaling domain is CD3ζ.
89. The CAR of any of claims 82-88, wherein one co-stimulatory domain is chosen from 4-1BB, CD28, and ICOS.
90. The CAR of claim 89, wherein the costimulatory domain is CD28.
91. The CAR of claim 89, wherein the costimulatory domain is 4-1BB.
92. The CAR of claim 89, comprising two or more costimulatory domains.
93. The CAR of claim 89, wherein two of the costimulatory domains are CD28 and 4-1BB.
94. The CAR of claim 82, comprising a sequence chosen from SEQ ID NOs: 1539-1598.
95. A nucleotide sequence encoding any of the polypeptides, scFvs, mAbs, or CARs of any of claims 1-94.
96. A vector comprising the nucleotide sequence of claim 95.
97. The vector of claim 96, wherein the vector is a lentiviral vector.
98. The vector of claim 97, wherein the lentiviral vector comprises a VSVG domain.
99. An engineered immune effector cell expressing at the cell surface a CAR of any one of claim 81-94.

100. The engineered immune effector cell of claim 99, wherein the engineered immune effector cell expresses at the cell surface:
a first polymorphic variant of a human cancer cell antigen; and
a CAR that is selective for a second polymorphic over the first polymorphic variant of the antigen.

101. The engineered immune effector cell of claim 99, wherein the cell is a primary cell.

102. The engineered immune effector cell of claim 99, wherein the cell is derived from:
- an induced pluripotent stem cell (iPSC);
- cord blood;
- peripheral blood; or
- an immortalized cell line.

103. The engineered immune effector cell of claim 102, wherein the immortalized cell line is NK-92.

104. The engineered immune cell of any of claims 99-103, wherein the cell is chosen from a T cell, an natural killer (NK) cell, an invariant natural killer T (iNKT) cell, a macrophage, and a dendritic cell.

105. The engineered immune effector cell of claim 104, wherein the cell is a T cell.

106. The engineered immune effector cell of claim 105, wherein the T cell is chosen from an inflammatory T-lymphocyte, a cytotoxic T-lymphocyte, a regulatory T-lymphocyte, or a helper T-lymphocyte.

107. The engineered immune effector cell of claim 105, wherein the engineered immune effector cell is deficient in a subunit of the T cell receptor complex.

108. The engineered immune effector cell of claim 107, wherein the subunit of the T cell receptor complex is chosen from TCRα (TRAC), TCRβ, TCRδ, TCRγ, CD3ε, CD3γ, CD3δ, and CD3ζ.

109. The engineered immune effector cell of any of claims 105-108, wherein the engineered immune effector cell is deficient in a cell surface protein that is the target of the CAR.

110. The engineered immune effector cell of claim 104, wherein the engineered immune effector cell is an NK cell.

111. The engineered immune effector cell of claim 110, wherein the engineered immune effector cell is a memory-like (ML) NK cell.

112. The engineered immune effector cell of claim 111, wherein the engineered immune effector cell is a cytokine-induced memory-like (CIML) NK cell.

113. The engineered immune effector cell of claim 104, wherein the engineered immune effector cell is an iNKT cell.

114. A method of treatment of a subject in need thereof, who has a first polymorphic variant of an antigen on the surface of a target cell, comprising:

b. optionally, treating the subject with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen;

c. administering to the subject either:

- a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
- a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
- an antibody-drug conjugate (ADC) comprising monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; and

d. administering to the subject a population of donor hematopoietic cells, a plurality of which comprise a second polymorphic variant of the antigen;

wherein the administering of the hematopoietic cells, and the administering of the CAR-expressing cells, mAb, or ADC, may be done concurrently, or sequentially in either order.

115. A method of immunotherapy of a human subject in need thereof, who has a first polymorphic variant of an antigen on the surface of a target cell, comprising:

a. optionally, treating the subject with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen;

b. administering to the subject a population of donor hematopoietic cells, a plurality of which comprise a second polymorphic variant of the antigen; and

c. administering to the subject:

- a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that specifically binds the first polymorphic variant of an antigen on the surface of a target cell; or

- a monoclonal antibody (mAb) or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
- an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

116. A method of treatment of a subject in need thereof, who has a first polymorphic variant of an antigen on the surface of a target cell, comprising:

a. administering to the subject:
   - a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) which binds the antigen on the surface of the target cell; or
   - a monoclonal antibody (mAb) which binds the antigen on the surface of the target cell; or
   - an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb) which binds the antigen on the surface of the target cell; and
b. optionally, treating the subject with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen;
c. administering to the subject either:
   - a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
   - a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; or
   - an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell; and
d. administering to the subject a population of donor hematopoietic cells, a plurality of which comprise a second polymorphic variant of the antigen;

wherein the administering of the hematopoietic cells, and the administering of the CAR-expressing cells, mAb, or ADC, may be done concurrently, or sequentially in either order.

117. The method of any of claims 114-116, wherein the subject is a human.

118. The method of any of claims 114-117, wherein the binding is at least 2-fold selective.

119. The method of claim 118, wherein the binding is at east 10-fold selective.

120. The method of claim 119, wherein the binding is at least 30-fold selective.

121. The method of any of claims 114-120, wherein the antigen is chosen from CD33, CLL-1, and FLT3.

122. The method of claim 121, wherein the antigen is CD33.

123. The method of claim 122, wherein the first polymorphic variant of CD33 is R69 and the second polymorphic variant of CD33 is G69; or the first polymorphic variant of CD33 is G69 and the second polymorphic variant of CD33 is R69.

124. The method of claim 121, wherein the antigen is FLT3.

125. The method of claim 124, wherein the first polymorphic variant of FLT3 is T227 and the second polymorphic variant of FLT3 is M227; or first polymorphic variant of FLT3 is M227 and the second polymorphic variant of FLT3 is T227.

126. The method of claim 121, wherein the antigen is CLL-1.

127. The method of claim 126, wherein the first polymorphic variant of CLL-1 is K224 and the second polymorphic variant of CLL-1 is Q244; or first polymorphic variant of CLL-1 is Q224 and the second polymorphic variant of CLL-1 is K244.

128. The method of any of claims 114-127, wherein the subject is concurrently administered both the population of engineered immune effector cells and the population of hematopoietic cells.

129. The method of any of claims 114-127, wherein the subject is sequentially administered the population of hematopoietic cells, and the population of engineered immune effector cells, mAb, or ADC.

130. The method of any of claims 114-127, wherein the subject is sequentially administered the population of engineered immune effector cells, mAb, or ADC, and the population of hematopoietic cells.

131. The method of any of claims 114-130, wherein the subject is treated with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen before administering of the hematopoietic cells.

132. The method of any of claims 114-130, wherein the subject has already been conditioned with one or more conditioning regimens to deplete the subject of target cells bearing the first polymorphic variant of the antigen.

133. The method of any of claims 114-132, wherein the hematopoietic cells are hematopoietic stem cells and/or hematopoietic progenitor cells.

134. The method of any of claims 114-133, wherein the subject is administered a population of engineered immune effector cells that express a chimeric antigen receptor (CAR) that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

135. The method of claim 134, wherein the engineered immune effector cells are derived from the subject (i.e., autologous) and the hematopoietic cells are derived from a donor (i.e., allogeneic).

136. The method of claim 134, wherein the engineered immune effector cells and hematopoietic cells are derived from a single donor.

137. The method of claim 108, wherein the engineered immune cells are derived from a first donor and hematopoietic cells are derived from a second donor.

138. The method of any of claims 134-137, wherein the chimeric antigen receptor (CAR) comprises a polypeptide of any of claims 1-69.

139. The method of claim any of claims 134-137, wherein the chimeric antigen receptor (CAR) comprises the scFv of claim 70.

140. The method of any of claims 134-137, wherein the chimeric antigen receptor (CAR) is a CAR of any of claims 81-94.

141. The method of any of claims 134-137, wherein the engineered immune effector cell is one of any of any of claims 99-113.

142. The method of any of claims 114-133, wherein the subject is administered a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

143. The method of claim 142, wherein the monoclonal antibody (mAb) comprises a polypeptide of any of claims 1-69.

144. The method of claim 142, wherein the monoclonal antibody (mAb) is a mAb of any of claims 71-77.

145. The method of any of claims 114-133, wherein the subject is administered an antibody-drug conjugate (ADC) comprising a monoclonal antibody (mAb), or antigen-binding fragment thereof, that selectively binds the first polymorphic variant of the antigen on the surface of the target cell.

146. The method of any of claims 142-145, wherein the mAb or ADC is administered prophylactically after transplant to prevent relapse.

147. The method of any of claims 114-146, additionally comprising genotyping the subject and donor to ensure the HSC donor and patient express different variants of the target antigen.

148. The method of claim 147, wherein the genotyping is done using either a protein- (FACS) or DNA- (PCR) based assay.

149. The method of claim 147, wherein the patient is genotyped after relapse from transplant.

150. The method of claim 147, wherein the patient is genotyped before transplant.

151. The method of claim 147, wherein the hematopoietic cell donor is genotyped before hematopoietic cell transplant.

152. The method of any of claims 137-147, wherein the immune effector cell donor is genotyped before transplant of the population of engineered immune effector cells that express the CAR .

153. The method of any of claims 137-147, wherein the immune effector cell donor is genotyped before hematopoietic cell transplant.

FIG. 1

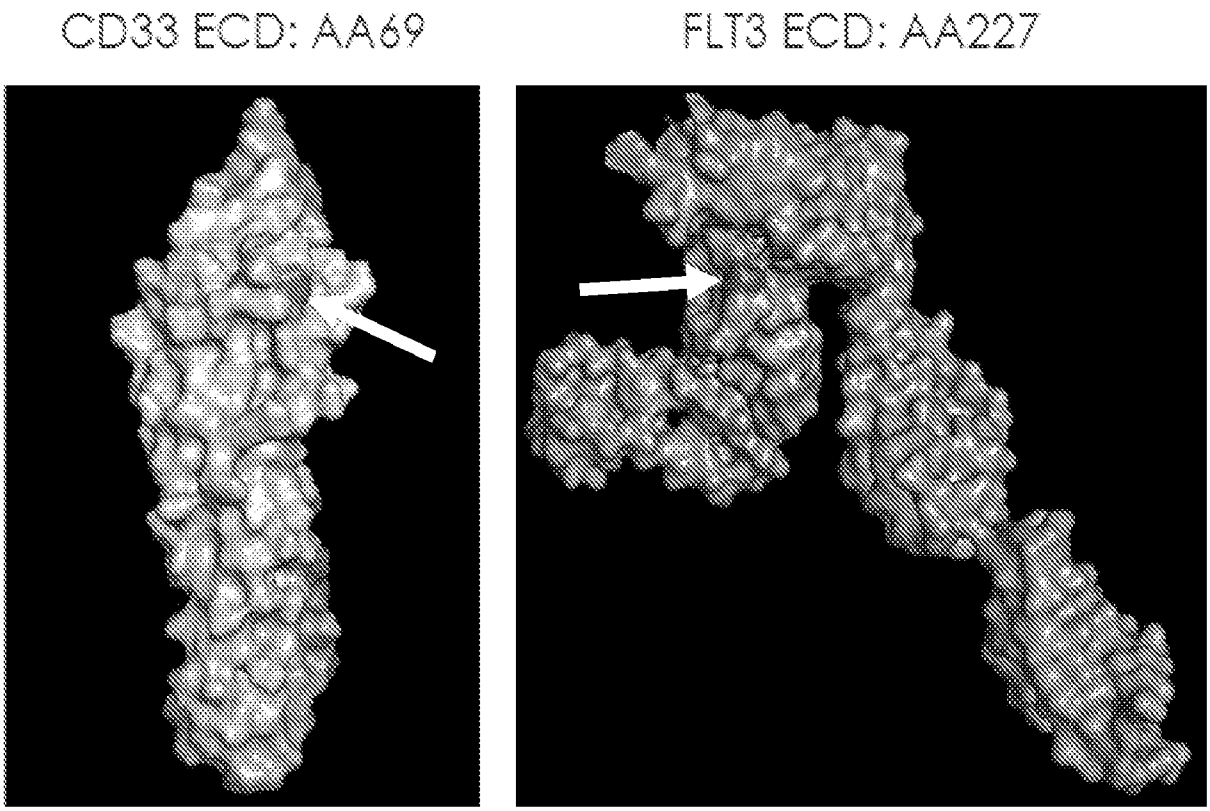


FIG. 2

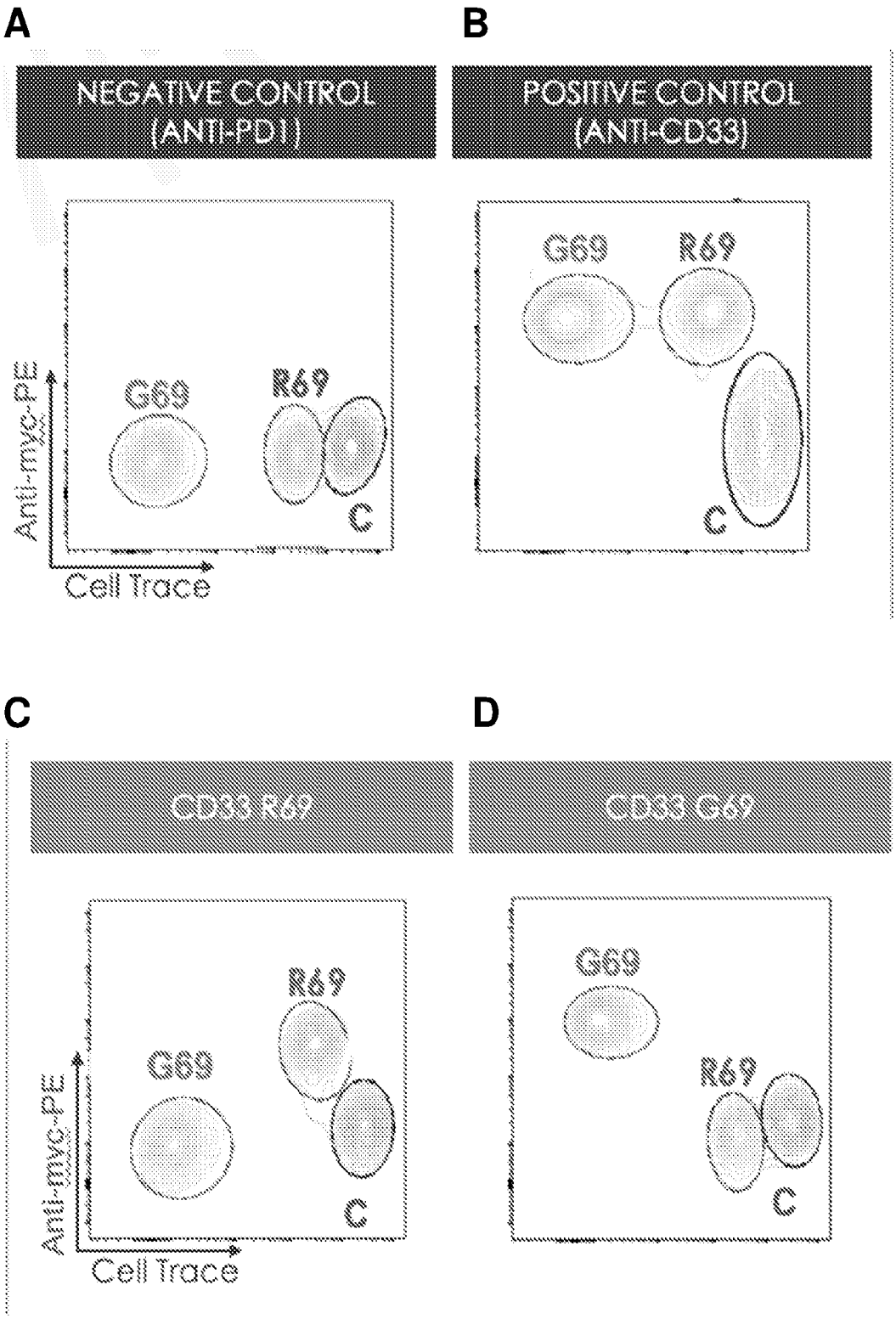

A
NEGATIVE CONTROL (ANTI-PD1)
G69
R69
C
Anti-myc-PE
Cell Trace
B
POSITIVE CONTROL (ANTI-CD33)
G69
R69
C
C
CD33 R69
R69
G69
C
Anti-myc-PE
Cell Trace
D
CD33 G69
G69
R69
C

FIG. 3

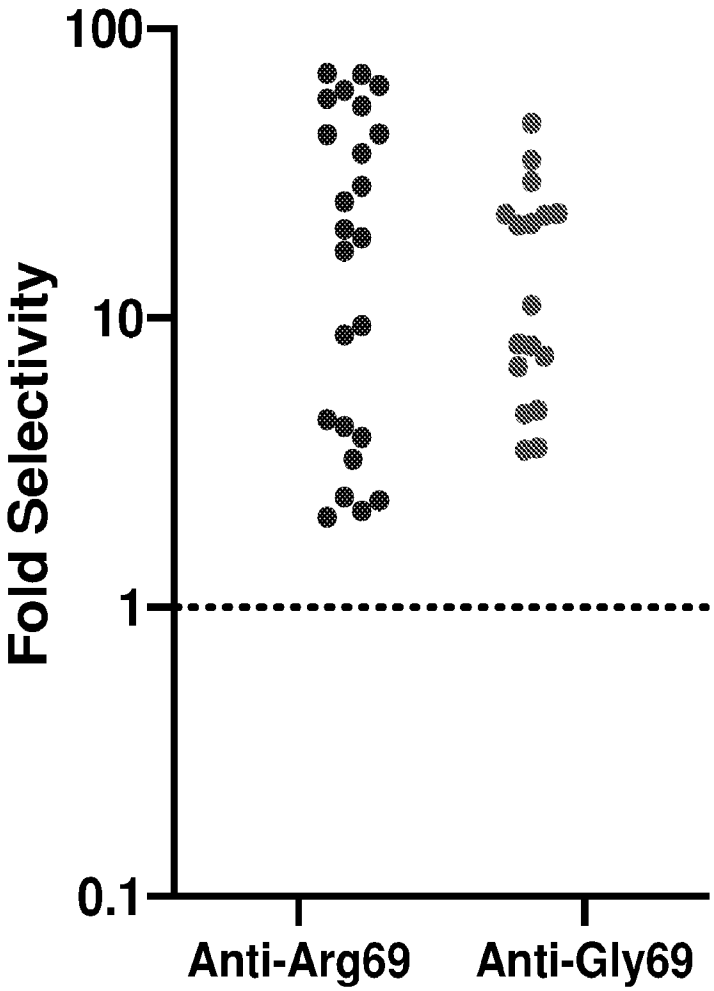


FIG. 4

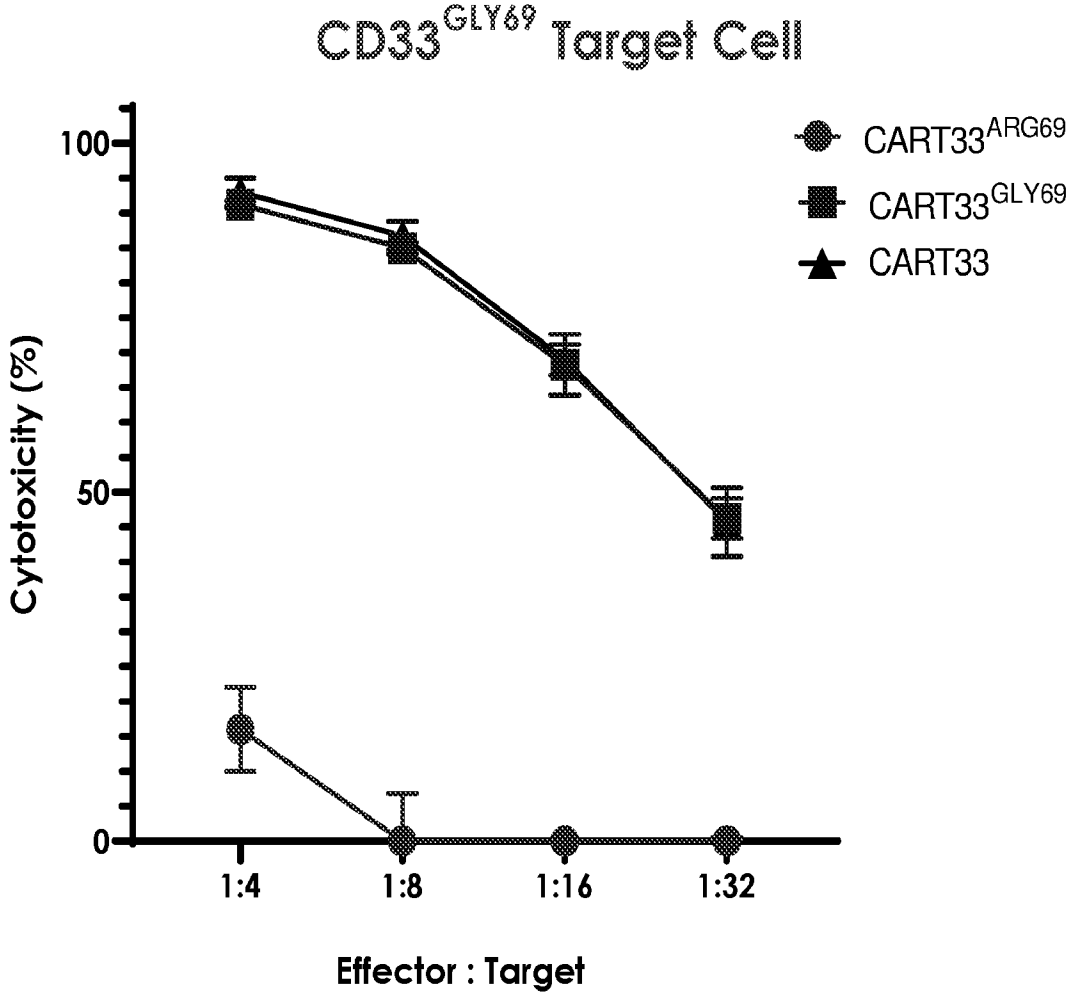
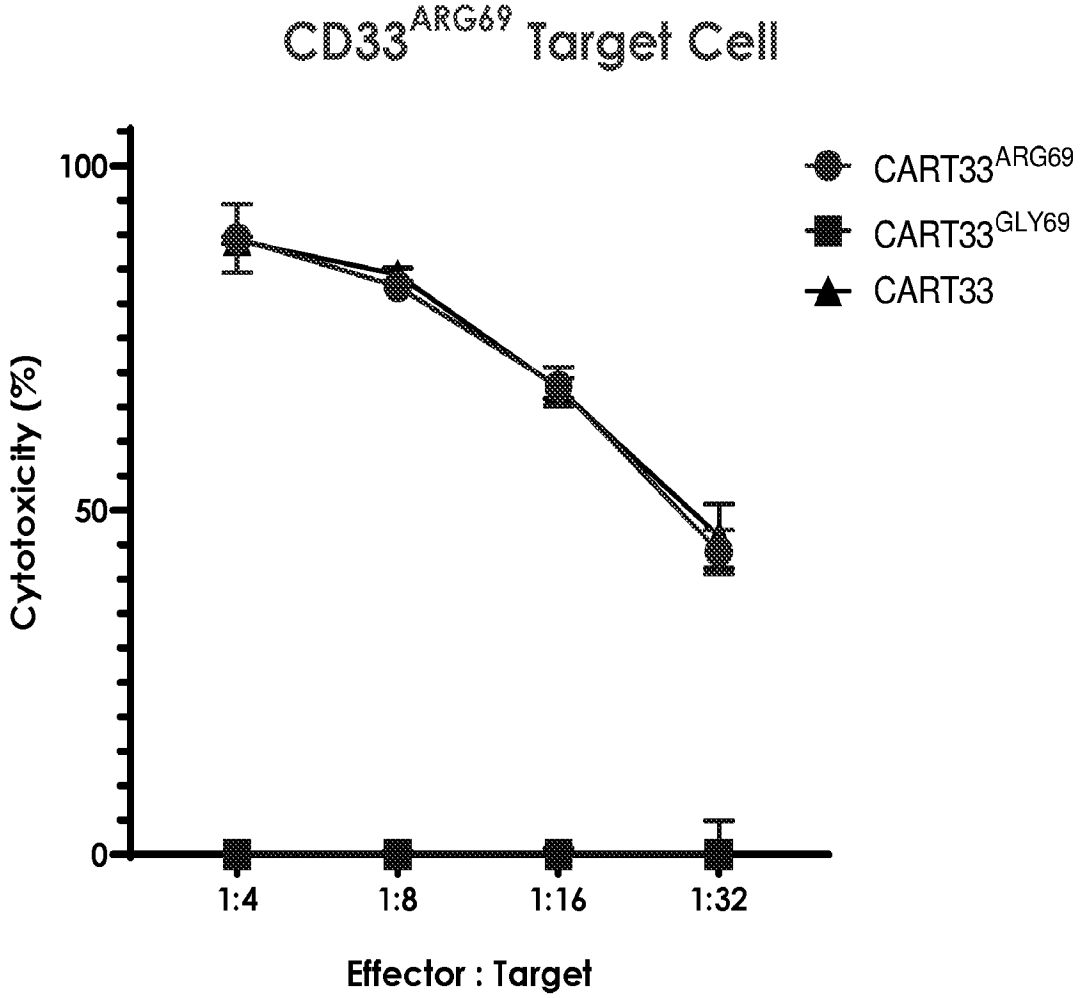

CD33GLY69 Target Cell
CART33ARG69
CART33GLY69
CART33
Cytotoxicity (%)
100
50
0
1:4
1:8
1:16
1:32
Effector : Target

FIG. 5


CD33ARG69 Target Cell
CART33ARG69
CART33GLY69
CART33
Cytotoxicity (%)
100
50
0
1:4
1:8
1:16
1:32
Effector : Target

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/015980

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - A61K 39/395; C07K 16/28; C12N 5/00 (2022.01)
CPC - A61K 2035/124; C07K 16/2803; C07K 16/2851; C07K 16/2866; C12N 5/0647 (2022.02)

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)

see Search History document

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

see Search History document

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

see Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2020/0376034 A1 (DRAGONFLY THERAPEUTICS INC.) 03 December 2020 (03.12.2020) entire document	1-9
X	US 2020/0316120 A1 (IMMPACT-BIO LTD.) 08 October 2020 (08.10.2020) entire document	1, 2, 34, 39
X	US 2018/0280502 A1 (MILTENYI BIOTEC GMBH) 04 October 2018 (04.10.2018) entire document	114-117
X	US 2017/0037149 A1 (AMGEN RESEARCH (MUNICH) GMBH) 09 February 2017 (09.02.2017) entire document	35-38
X	US 2020/0148774 A1 (GENENTECH INC.) 14 May 2020 (14.05.2020) entire document	40-45
P, X	WO 2021/226163 A2 (DRAGONFLY THERAPEUTICS INC.) 11 November 2021 (11.11.2021) entire document	1-9, 34-45, 114-117
P, X	WO 2021/076554 A1 (DRAGONFLY THERAPEUTICS INC.) 22 April 2021 (22.04.2021) entire document	1-9, 34-45, 114-117

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

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"D" document cited by the applicant in the international application
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 April 2022	MAY 03 2022
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Harry Kim Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/015980

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:

      ☐ in the form of an Annex C/ST.25 text file.

      ☐ 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:

      ☒ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

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:

On 25 March 2022, the ISA/US issued Form PCT/ISA/225 requiring the applicant to furnish a nucleotide and/or amino acid sequence listing in the form of an Annex C/ST.25 text file, accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.

A timely response to the form was not received by the ISA/US. Consequently, the international search was not established taking into account a sequence listing.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2022/015980

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

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

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 20-22, 56-58
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claims 20-22 and 56-58 are held unsearchable as a meaningful opinion could not be formed without the sequence listing; the applicant did not, within the prescribed time limit, furnish a sequence listing in the form of an Annex C/ST.25 text file, and such listing was not available to the International Searching Authority in the form and manner acceptable to it; or the sequence listing furnished did not comply with the standard provided for in Annex C of the Administrative Instructions.

3. ☒ Claims Nos.: 10-19, 23-33, 46-55, 59-113, 118-153
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.