EXTENDED-RELEASE IMMUNE CELL ENGAGING PROTEINS AND METHODS OF TREATMENT

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/214,963, filed June 25, 2021; U.S. Provisional Patent Application No. 63/276,804, filed November 8, 2021; and U.S. Provisional Patent Application No. 63/328,603, filed April 7, 2022; each of which is incorporated herein by reference in its entirely.

INCORPORATION BY REFERENCE

[0002] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BACKGROUND

[0003] Cancer is the second leading cause of human death next to coronary disease. Worldwide, millions of people die from cancer every year. In the United States alone, cancer causes the death of well over a half-million people each year, with some 1.4 million new cases diagnosed per year. While deaths from heart disease have been declining significantly, those resulting from cancer generally are on the rise. In the early part of the next century, cancer is predicted to become the leading cause of death.

[0004] Moreover, even for those cancer patients that initially survive their primary cancers, common experience has shown that their lives are dramatically altered. Many cancer patients experience strong anxieties driven by the awareness of the potential for recurrence or treatment failure. Many cancer patients experience significant physical debilitations following treatment.

[0005] Generally speaking, the fundamental problem in the management of the deadliest cancers is the lack of effective and non-toxic systemic therapies. Cancer is a complex disease characterized by genetic mutations that lead to uncontrolled cell growth. Cancerous cells are present in all organisms and, under normal circumstances, their excessive growth is tightly regulated by various physiological factors. Controlling the toxicity of various cancer therapies remain an important and unsolved issue.

SUMMARY OF THE INVENTION

[0006] Provided here in is a pharmaceutical composition comprising an extended-release binding protein which comprises a half-life extended immune cell engaging protein, a masking peptide, and a cleavable linker, wherein the masking peptide is covalently linked to the N-

terminus or the C-terminus of the half-life-extended immune cell engaging protein through the cleavable linker, and wherein the cleavable linker is significantly cleaved in systemic circulation. In some embodiments, the extended-release binding protein has a higher therapeutic index than a corresponding half-life-extended immune cell engaging protein without the masking peptide. In some embodiments, administration of the extended-release binding protein results in a lower Cmax/Cmin ratio of an active version of the extended-release binding protein in systemic circulation than the Cmax/Cmin ratio when a corresponding half-life extended immune cell engaging protein without the masking peptide is administered. In some embodiments, multiple administration of the extended-release binding protein results in a more gradual increase of a level of an active version of the extended-release binding protein in systemic circulation than when a corresponding half-life-extended immune cell engaging protein without the masking peptide is administered. In some embodiments, administration of the extended-release binding protein results in a lower Cytokine release syndrome (CRS) level than the CRS observed when a corresponding half-life extended immune cell engaging protein without the masking peptide is administered.

[0007] In some embodiments, the half-life extended immune cell engaging protein comprises an immune cell engaging domain. In some embodiments, the immune cell engaging domain comprises a natural killer (NK) cell engaging domain, a T cell engaging domain, a NK-T cell engaging domain, a B cell engaging domain, a dendritic cell engaging domain, a macrophage cell engaging domain, or a combination thereof. In some embodiments, the immune cell engaging domain comprises the T cell engaging domain. In some embodiments, the T cell engaging domain binds a CD3 molecule. In some embodiments, the CD3 molecule is at least one of: a CD3γ molecule, a CD3δ molecule, or a CD3ε molecule.

[0008] In some embodiments, the half-life extended immune cell engaging protein comprises a first domain (A), a second domain (B), and a third domain (C), wherein (i) the first domain (A) is the T cell engaging domain and specifically binds to human CD3, (ii) the second domain (B) specifically binds to human serum albumin (HSA), and (iii) the third domain (C) specifically binds to a target antigen; and wherein the domains are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(B)-(A)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, H_2N-(B)-(C)-(A)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(B)-L1-(A)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH, H_2N-(B)-L1-(C)-L2-(A)-COOH. In some embodiments, the third domain comprises a single domain antibody (sdAb), a single-chain variable fragment (scFv), a variable heavy domain (VH), a variable light domain (VL), antigen-binding fragment (Fab), a DARPin or a peptide. In

some embodiments, the masking peptide inhibits or reduces the binding of the first domain (A) to the human CD3. In some embodiments, the masking peptide inhibits or reduces the binding of the first domain (A) to the N-terminus of human CD3ε. In some embodiments, the masking peptide comprises an amino acid sequence having at least 80% homology to QDGNEE (SEQ ID NO: 3633). In some embodiments, the masking peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 3633-3652. In some embodiments, the masking peptide inhibits or reduces the binding of the third domain (C) to the target antigen. In some embodiments, the cleavable linker comprises a cleavage site. In some embodiments, the cleavable site is recognized by a protease. In some embodiments, the protease is selected from the group consisting of a serine protease, a cysteine protease, an aspartate protease, a threonine protease, a glutamic acid protease, a metalloproteinase, a gelatinase, and an asparagine peptide lyase. In some embodiments, the protease is present in blood circulation. In some embodiments, the protease is selected from the group consisting of a Cathepsin, a Cathepsin B, a Cathepsin C, a Cathepsin D, a Cathepsin E, a Cathepsin H, a Cathepsin S, a Cathepsin K, a Cathepsin L, a kallikrein, a hK1, a hK10, a hK15, a plasmin, a collagenase, a Type IV collagenase, a stromelysin, a Factor Xa, a chymotrypsin-like protease, a trypsin-like protease, a elastase-like protease, a subtilisin-like protease, an actinidain, a bromelain, a calpain, a caspase, a caspase-3, a Mir1-CP, a papain, a HIV-1 protease, a HSV protease, a CMV protease, a chymosin, a renin, a pepsin, a matriptase, a legumain, a plasmepsin, a nepenthesin, a metalloexopeptidase, a metalloendopeptidase, a matrix metalloprotease (MMP), a MMP1, a MMP2, a MMP3, a MMP7, a MMP8, a MMP9, a MMP10, a MMP11, a MMP12, a MMP13, a MMP14, an ADAM10, an ADAM12, an urokinase plasminogen activator (uPA), an enterokinase, a prostate-specific target (PSA, hK3), an interleukin-1β converting enzyme, a thrombin, a FAP (FAP-α), a type II transmembrane serine protease (TTSP), a neutrophil elastase, a cathepsin G, a proteinase 3, a neutrophil serine protease 4, a mast cell chymase, a mast cell tryptase, a dipeptidyl peptidase, and a dipeptidyl peptidase IV (DPPIV/CD26).

[0009] In some embodiments, the cleavable linker comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3688-3770 and SEQ ID No: 3878. In some embodiments, the cleavable linker comprises an amino acid sequence of SEQ ID Nos: 3688-3770 and SEQ ID No: 3878. In some embodiments, the target antigen is a tumor antigen. In some embodiments, the third domain specifically binds to a target antigen selected from the group consisting of: CD19 (B-lymphocyte antigen CD19, B-Lymphocyte Surface Antigen B4, T-Cell Surface Antigen Leu-12, CVID3), PSMA (prostate specific membrane antigen), MSLN (mesothelin), BCMA (B-cell maturation antigen), DLL3 (Delta-like ligand 3), FLT3 (FMS-like tyrosine kinase 3), CD20 (B-lymphocyte antigen CD20, MS4A1, B1, Bp35, CVID5, LEU-16, MS4A2,

S7, membrane spanning 4-domains A1), CD22 (SIGLEC-2, SIGLEC2), CD25 (IL2RA, interleukin-2 receptor alpha chain), CD27 (S152, S152. LPFS2, T14, TNFRSF7, Tp55), CD30 (TNFRSF8), CD33 (Siglec-3, sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67), CD37 (GP52-40, TSPAN26), CD38 (cyclic ADP ribose hydrolase, ADPRC1, ADPRC 1), CD40 (Bp50, CDW40, TNFRSF5, p50), CD44 (HCAM, homing cell adhesion molecule), Pgp-1 (phagocytic glycoprotein-1), Hermes antigen, lymphocyte homing receptor, ECM-III, and HUTCH-1), CD48 (BLAST-1, B-lymphocyte activation marker, SLAMF2, signaling lymphocytic activation molecule 2), CD52 (CAMPATH-1 antigen), CD70, CD73 (NT5E, ecto-5'-nucleotidase), CD39 (ENTPD1, Ectonucleoside triphosphate diphosphohydrolase-1), CD74 (HLA class II histocompatibility antigen gamma chain, HLA-DR antigens-associated invariant chain), CD79b (immunoglobulin-associated beta), CD80 (B7-1), CD86 (B7-2), CD123 (IL3RA, interleukin-3 receptor), CD133 (PROM1), CD137 (TNFRSF9, tumor necrosis factor receptor superfamily member 9, 4-1BB, ILA, induced by lymphocyte activation), CD138 (SDC1), alpha fetoprotein (AFP), c-Met; c-Kit; CD371 (CLEC12A, C-type lectin domain family 12 mem ber A, CLL1)); CD370 (CLEC9A, C-type lectin domain containing 9A); cadherin 3 (CDH3, p-cadherin, PCAD); carbonic anhydrase 6 (CA6); carbonic anhydrase 9 (CA9, CAIX); carcinoembryonic antigen related cell adhesion molecule 3 (CEACAM3); carcinoembryonic antigen related cell adhesion molecule 5 (CEACAM5); CD66c (CEACAM6, carcinoembryonic antigen related cell adhesion molecule 6); chorionic somatomammotropin hormone 1 (CSH1, CS1); coagulation factor III, tissue factor (F3, TF); collectin subfamily member 10 (COLEC10); delta like canonical Notch ligand 3 (DLL3); ectonucleotide pyrophosphatase/ phosphodiesterase 3 (ENPP3); ephrin A1 (EFNA1); epidermal growth factor receptor (EGFR); EGFR variant III (EGFRvIII); EPH receptor A2 (EPHA2); epithelial cell adhesion molecule (EPCAM); erb-b2 receptor tyrosine kinase 2 (ERBB2, HER2); fibroblast activation protein alpha (FAP); fibroblast growth factor receptor 2 (FGFR2); fibroblast growth factor receptor 3 (FGFR3); folate hydrolase 1 (FOLH1, PSMA); folate receptor 1 (FOLR1, FRa); GD2 ganglioside; glycoprotein NMB (GPNMB, osteoactivin); guanylate cyclase 2C (GUCY2C, GCC); human papillomavirus (HPV) E6; HPV E7; major histocompatibility complex (MHC) class I-presented neoantigens, major histocompatibility complex (MHC) class II-presented neoantigens, major histocompatibility complex, class I, E (HLA-E); major histocompatibility complex, class I, F (HLA-F); major histocompatibility complex, class I, G (HLA-G, MHC-G); integrin subunit beta 7 (ITGB7); leukocyte immunoglobulin like receptor B1 (LILRB1, ILT2); leukocyte immunoglobulin like receptor B2 (LILRB2, ILT4); LY6/PLAUR domain containing 3 (LYPD3, C4.4A); glypican 3 (GPC3); KRAS proto-oncogene, GTPase (KRAS); MAGE family member A1 (MAGEA1); MAGE family member A3 (MAGEA3); MAGE family member A4 (MAGEA4); MAGE family

member A11 (MAGEA11); MAGE family member C1 (MAGEC1); MAGE family member C2 (MAGEC2); MAGE family member D1 (MAGED1); MAGE family member D2 (MAGED2); mesothelin (MSLN); mucin 1 (MUC1) and splice variants thereof (*e.g.*, MUC1/C, D, and Z); mucin 16 (MUC16); necdin (NDN); nectin cell adhesion molecule 4 (NECTIN4); SLIT and NTRK like family member 6 (SLITRK6); promyelocytic leukemia (PML, TRIM19); protein tyrosine kinase 7 (inactive) (PTK7); CD352 (SLAMF6, SLAM family member 6); CD319 (SLAMF7, SLAM family member 7, 19A, CRACC, CS1); sialic acid binding Ig like lectin 7 (SIGLEC7); sialic acid binding Ig like lectin 9 (SIGLEC9); solute carrier family 34 (sodium phosphate), member 2 (SLC34A2); solute carrier family 39 member 6 (SLC39A6, LIV1); STEAP family member 1 (STEAP1); STEAP family member 2 (STEAP2); CD134 (TNFRSF4, TNF receptor superfamily member 4, OX40); CD137L (TNFSF9, TNF superfamily member 9, 4-1BB-L); CD261 (TNFRSF10A, TNF receptor superfamily member 10a, DR4, TRAILR1); CD262 (TNFRSF10B, TNF receptor superfamily member 10b, DR5, TRAILR2); CD267 (TNFRSF13B, TNF receptor superfamily member 13B, TACI, IGAD2); CD269 (TNFRSF17, TNF receptor superfamily member 17, BCMA,); CD357 (TNFRSF18, TNF receptor superfamily member 18 GITR); transferrin (TF); transforming growth factor beta 1 (TGFB1); trophoblast glycoprotein (TPBG, 5T4); trophinin (TRO, MAGED3); tumor associated calcium signal transducer 2 (TACSTD2, TROP2, EGP1); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ROR1; CD30; and Lewis Y antigen.

[0010] In some embodiments, the third domain specifically binds to CD19. In some embodiments, the third domain comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3771-3792. In some embodiments, the third domain comprises an amino acid sequence having at least 90% homology to SEQ ID Nos: 3771-3792. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID Nos: 3771-3792. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID No: 3771. In some embodiments, the domains of the half-life extended immune cell engaging protein are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(C)-(A)-(B)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2-(A)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3839-3843. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3839-3843.

[0011] In some embodiments, the third domain specifically binds to CD20. In some embodiments, the third domain comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3793-3808 and 3880. In some embodiments, the third domain

comprises an amino acid sequence having at least 90% homology to SEQ ID Nos: 3793-3808 and 3880. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID Nos: 3793-3808 and 3880. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID No: 3793. In some embodiments, the domains of the half-life extended immune cell engaging protein are linked in the following order: H_2N-(A)-(B)-(C)-COOH, or by linkers L1 and L2 in the following order: H_2N-(A)-L1-(B)-L2-(C)-COOH.

[0012] In some embodiments, the third domain specifically binds to CD33. In some embodiments, the third domain comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3809-3823. In some embodiments, the third domain comprises an amino acid sequence having at least 90% homology to SEQ ID Nos: 3809-3823. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID Nos: 3809-3823. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID No: 3809. In some embodiments, the domains of the half-life extended immune cell engaging protein are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3833-3837. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3834-3837.

[0013] In some embodiments, the third domain specifically binds to FLT3. In some embodiments, the third domain is a single domain antibody that specifically binds to FLT3. In some embodiments, the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1080-1155 and 3497-3498, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1156-1231, and 3499-3500, a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1232-1307, and 3501-3502. In some embodiments, the CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1150, 1152, 3497, and 3498; the CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1226, 1228, 3499, and 3500; the CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1302, 1304, 3501, and 3502. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1004-1079 and 3495-3496. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of: SEQ ID Nos: 1074, 1076, 3495, and 3496. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID No: 1074. In some embodiments, the

domains of the half-life extended immune cell engaging protein are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3844-3849. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3846-3849. In some embodiments, the third domain comprises an amino acid sequence of SEQ ID No: 1076. In some embodiments, the domains of the half-life extended immune cell engaging protein are linked in the following order: H_2N-(C)-(B)-(A)-COOH, or by linkers L1 and L2 in the following order: H_2N-(C)-L1-(B)-L2(A)-COOH. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3850-3855. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID No: 3854.

[0014] In some embodiments, the third domain is a single domain antibody that specifically binds to PSMA. In some embodiments, the third domain comprises a CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 462-465, a CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 466-472, and a CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 474-475. In some embodiments, the CDR1 comprises the amino acid sequence of SEQ ID No: 462, the CDR2 comprises the amino acid of SEQ ID No: 473, the CDR3 comprises the amino acid sequence of SEQ ID No: 474. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 476-489. In some embodiments, the third domain comprises the amino acid sequence of SEQ ID Nos: 489. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID No: 3824-3831.

[0015] In some embodiments, the third domain is a single domain antibody that specifically binds to MSLN. In some embodiments, the third domain comprises a CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 490-528, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 529-567, and a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 568-606. In some embodiments, the CDR1 comprises the amino acid sequence of SEQ ID No: 523, the CDR2 comprises the amino acid of SEQ ID No: 562, the CDR3 comprises the amino acid sequence of SEQ ID No: 601. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 607-650. In some embodiments,

the third domain comprises the amino acid sequence of SEQ ID No: 647. In some embodiments, the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID No: 3856-3858.

[0016] In some embodiments, the third domain is a single domain antibody that specifically binds to BCMA. In some embodiments, the third domain CDR1 comprises comprising an amino acid selected from the group consisting of SEQ ID Nos: 1-115, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 116-230, and a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 231-345. In some embodiments, the CDR1 comprises the amino acid sequence of SEQ ID No: 73, the CDR2 comprises the amino acid of SEQ ID No: 188, the CDR3 comprises the amino acid sequence of SEQ ID No: 303. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 346-461. In some embodiments, the third domain comprises the amino acid sequence of SEQ ID No: 383.

[0017] In some embodiments, the third domain is a single domain antibody that specifically binds to DLL3. In some embodiments, the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1751-2193, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 2194-2636, and a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 2637-3080. In some embodiments, the CDR1 comprises the amino acid sequence of SEQ ID No: 2182, the CDR2 comprises the amino acid of SEQ ID No: 2625, the CDR3 comprises the amino acid sequence of SEQ ID No: 3069. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1308-1750. In some embodiments, the third domain comprises the amino acid sequence of SEQ ID No: 1739.

[0018] In some embodiments, the third domain is a single domain antibody that specifically binds to EGFR. In some embodiments, the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 651-699, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 700-748, a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 479-797. In some embodiments, the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 798-846.

[0019] In some embodiments, the third domain is a single domain antibody that specifically binds to EpCAM. In some embodiments, the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 847-884, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 885-922, a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 923-960. In some embodiments,

the CDR1 comprises the amino acid sequence of SEQ ID No: 874 or 863, the CDR2 comprises the amino acid of SEQ ID No: 885 or 901, the CDR3 comprises the amino acid sequence of SEQ ID No: 923 or 939. In some embodiments, the third domain comprises a sequence selected from the group consisting of SEQ ID Nos: 961-1003. In some embodiments, the third domain comprises the amino acid sequence of SEQ ID No: 999 or 1003.

[0020] In some embodiments, the first domain comprises a single-chain variable fragment (scFv) specific to human CD3. In some embodiments, the scFv specific to human CD3 comprises a variable heavy chain region (VH), a variable light chain region (VL), and a linker, wherein VH comprises complementarity determining regions HC CDR1, HC CDR2, and HC CDR3, and wherein VL comprises complementarity determining regions LC CDR1, LC CDR2, and LC CDR3. In some embodiments, the HC CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3081, and 3087-3098, the HC CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3082, and 3099-3109, the HC CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3083, and 3110-3119. In some embodiments, the HC CDR1 comprises the amino acid sequence of SEQ ID No: 3097, the HC CDR2 comprises the amino acid sequence of SEQ ID No: 3108, the HC CDR3 comprises the amino acid sequence of SEQ ID No: 3110. In some embodiments, the LC CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3084, and 3120-3132, the LC CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3085, and 3099-3109, the LC CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3086, and 3146-3152. In some embodiments, the LC CDR1 comprises the amino acid sequence of SEQ ID No: 3120, the LC CDR2 comprises the amino acid sequence of SEQ ID No: 3145, the LC CDR3 comprises the amino acid sequence of SEQ ID No: 3146. In some embodiments, the first domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3153-3169. In some embodiments, the first domain comprises the amino acid sequence of SEQ ID No: 3153. In some embodiments, the linker comprises an amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 3868).

[0021] In some embodiments, the second domain comprises a single domain antibody (sdAb) which specifically binds to HSA. In some embodiments, the sdAb which specifically binds to HSA comprises complementarity determining regions CDR1, CDR2, and CDR3, wherein the CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3170, and 3173-3175, the CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3171, and 3176-3181, the CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3172, and 8182-3183. In some embodiments,

the CDR1 comprises an amino acid sequence of SEQ ID No: 3174, the CDR2 comprises an amino acid of SEQ ID No: 3178, the CDR3 comprises an amino acid sequence of SEQ ID No: 3183. In some embodiments, the second domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3184-3193. In some embodiments, the second domain comprises the amino acid sequence of SEQ ID No: 3190. In some embodiments, linkers L1 and L2 are each independently selected from $(GS)_n$ (SEQ ID No. 3859), $(GGS)_n$ (SEQ ID No. 3860), $(GGGS)_n$ (SEQ ID No. 3861), $(GGSG)_n$ (SEQ ID No. 3862), $(GGSGG)_n$ (SEQ ID No. 3863), $(GGGGS)_n$ (SEQ ID No. 3864), $(GGGGG)_n$ (SEQ ID No. 3865), or $(GGG)_n$ (SEQ ID No. 3866), wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, (GGGGSGGGGSGGGGSGGGGS)(SEQ ID No. 3867), (GGGGSGGGGSGGGGS) (SEQ ID No. 3868), LPETG (SEQ ID NO. 3869), (GGGGSGGGS) (SEQ ID No. 3871) or SGGG (SEQ ID NO. 3872). In some embodiments, linkers L1 and L2 are each independently GGGGSGGGS (SEQ ID NO: 3871).

[0022] Provided herein is method for the treatment or amelioration of a disease comprising administrating to a subject in need thereof a pharmaceutical composition according to the description herein. In some embodiments, the disease is a cancer. Provided herein is method for increasing survival in a subject suffering from a cancer, the method comprising administering to the subject a pharmaceutical composition according to the description herein. Provided herein is method of reducing tumor size, the method comprising administering to a subject from a cancer a pharmaceutical composition according to the description herein. In some embodiments, the cancer is selected from the group consisting of: mesothelioma, a prostate cancer, a breast cancer, a brain cancer, a bladder cancer, a pancreatic carcinoma, a renal cancer, a solid tumor, a liver cancer, a leiomyosarcoma, an endometrium cancer, a breast cancer, a female reproductive system cancer, an ovarian carcinoma, a soft tissue sarcoma, a gastric cancer, a digestive/gastrointestinal cancer, a colorectal cancer, a glioblastoma multiforme, a head and neck cancer, a squamous cell carcinoma, a colon cancer, a gastric cancer, a rhabdomyosarcoma, an adrenal cancer, a lung cancer, an esophageal cancer, a colon cancer, a lung cancer, a non-small cell lung carcinoma (NSCLC), a neuroblastoma, a melanoma, glioblastoma multiforme, an ovarian cancer, an endocrine cancer, a respiratory/thoracic cancer, an anal cancer, a gastro-esophageal cancer, a thyroid cancer, a cervical cancer, an endometrial cancer, a hematological cancer, a leukemia, a lymphocytic leukemia, a multiple myeloma, a lymphoma, a Hodgkin's lymphoma, a non-Hodgkin's lymphoma, a lymphocytic leukemia, an anaplastic large-cell lymphoma (ALCL), or a myeloid leukemia. In some embodiments, the cancer is the prostate cancer. In some embodiments, the cancer is the ovarian carcinoma. In some embodiments, the cancer is the pancreatic carcinoma. In some embodiments, the cancer is the mesothelioma. In some embodiments, the cancer is the lung cancer.

[0023] Provided herein is a pharmaceutical composition comprising an extended-release binding protein which comprises an antigen binding protein, a masking peptide, and a cleavable linker, wherein upon administering to a subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation. In some embodiments, the antigen binding protein comprises an antigen binding domain that binds to a target antigen. In some embodiments, the masking peptide inhibits or reduces the binding of the antigen binding protein to the target antigen. In some embodiments, the antigen binding protein comprises an immune cell engaging domain. In some embodiments, the immune cell engaging domain comprises a T cell engaging domain. In some embodiments, the T cell engaging domain binds a CD3 molecule. In some embodiments, the masking peptide inhibits or reduces the binding of the antigen binding protein to the CD3 molecule. In some embodiments, the antigen binding protein comprises a half-life extension domain. In some embodiments, the half-life extension domain binds a human serum albumin (HSA). In some embodiments, the cleavable linker comprises a cleavage site. In some embodiments, the cleavable site is recognized by a protease. In some embodiments, wherein the masking peptide is covalently linked to the N-terminus or the C-terminus of the antigen binding protein through the cleavable linker.

[0024] Provided herein is a method of making an extended-release binding protein comprising adding a cleavable linker and a masking peptide to an antigen binding protein, wherein upon administering to a subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation. In some embodiments, the antigen binding protein comprises an antigen binding domain that binds to a target antigen. In some embodiments, the masking peptide inhibits or reduces the binding of the antigen binding protein to the target antigen. In some embodiments, the antigen binding protein comprises an immune cell engaging domain. In some embodiments, the immune cell engaging domain comprises a T cell engaging domain. In some embodiments, the T cell engaging domain binds a CD3 molecule. In some embodiments, the masking peptide inhibits or reduces the binding of the antigen binding protein to the CD3 molecule. In some embodiments, the antigen binding protein comprises a half-life extension domain. In some embodiments, the half-life extension domain binds a human serum albumin (HSA). In some embodiments, the cleavable linker comprises a cleavage site. In some embodiments, the cleavable site is recognized by a protease. In some embodiments, the masking peptide is covalently linked to the N-terminus or the C-terminus of the antigen binding protein through the cleavable linker.

[0025] Provided herein is a method of increasing the therapeutic index of an antigen binding protein, comprising adding a cleavable linker and a masking peptide to the antigen binding protein to form an extended-release binding protein, wherein upon administering to a subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation. Provided herein is method of decreasing the CRS level in a subject, comprising adding a cleavable linker and a masking peptide to an antigen binding protein to form an extended-release binding protein, wherein upon administering to the subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation. Provided herein is method of gradually increase an active drug's concentration in a subject's systemic circulation comprising administering an extended-release binding protein to the subject, wherein the extended-release binding protein comprises an antigen binding protein, a masking peptide, and a cleavable linker, wherein the extended-release binding protein releases the active drug upon cleavage of the cleavable linker in systemic circulation.

[0026] Provided herein is a pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker, wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, and wherein the cleavable linker is significantly cleaved in systemic circulation.

[0027] Provided herein is a pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker, wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, and wherein a half-life of the protein in systemic circulation is longer than a comparable protein without the masking peptide.

[0028] Provided herein is a pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker, wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, and wherein a comparable protein without the masking peptide has a nonlinear pharmacokinetics (PK) across a dose range evaluated, and wherein the protein has an improved linearity of PK across the dose range evaluated compared to the comparable protein.

[0029] Provided herein is a pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker, wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, wherein the binding moiety specifically binds to a target in a subject, and wherein a molar amount of the protein's binding moiety bound to the target when administered to the subject is lower compared to a molar

amount of a binding moiety of a comparable protein without the masking peptide when administered to the subject at a same dose level.

[0030] Provided herein is a pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker, wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, wherein the binding moiety specifically binds to a target in a subject, and wherein a first binding rate between the protein's binding moiety and the target when administered to the subject is lower compared to a second binding rate between a binding moiety of a comparable protein without the masking peptide and the target.

[0031] In some embodiments, the binding moiety specifically binds to ICOS (inducible T cell co-stimulator, CD278), OX40 (CD134, TNFRSF4, tumor necrosis factor receptor superfamily member 4), CD40 (TNFRSF5, tumor necrosis factor receptor superfamily member 5), DR5 (death receptor 5, TRAIL receptor 2), GITR (glucocorticoid-induced TNFR-related protein, TNFRSF18, tumor necrosis factor receptor superfamily member 18), 4-1BB (CD137, TNFRSF9, tumor necrosis factor receptor superfamily member 9) or any combinations thereof. In some embodiments, the protein comprises an antibody selected from the group consisting of GSK3359609, PF-8600, JNJ-64457107, CP-870,893, SGN-40 (Dacetuzumab), MEDI3039, ABBV-621, MEDI1873, AMG 228, PF-05082566 (Utomilumab), and urelumab.

[0032] Provided herein is a method of treating or ameliorating a disease comprising administrating to a subject in need thereof a pharmaceutical composition described herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0034] **FIG. 1A** shows an exemplary construct of an extended-release binding protein. **FIG. 1B** shows an exemplary construct of the active version of the extended-release binding protein. **FIG. 1C** shows the predicted concentrations of the intact version and the active version in systemic circulation after multiple administration events. **FIG. 1D** shows the predicted concentration of the active version of a corresponding antigen binding protein without the masking peptide in systemic circulation after multiple administration events.

[0035] **FIG. 2** illustrates additional extended-release binding protein constructs with various configurations of the anti-target, anti-albumin and anti-CD3 binding domains. **Figs. 2A-2C and**

Figs. 2G-2I illustrate the intact versions and **Figs. 2D-2F and Figs. 2J-2L** illustrate the active versions after cleavage of the linker that contain linker amino acids left after protease cleavage (as described herein, these remaining amino acids are referred to as "stub").

[0036] FIG. 3 Analytical cation exchange chromatography demonstrates the purity of three PSMA binding proteins.

[0037] FIG. 4 demonstrates slow activation of peptide masked PSMA targeting extended-release binding proteins in TDCC assay measured in the presence of HSA.

[0038] FIG. 5 demonstrates the masking effects of various peptide masks engineered into PSMA binding proteins measured in the presence of HSA.

[0039] FIGS. 6A-B demonstrates the masking effects of various peptide masks engineered into MSLN binding proteins.

[0040] FIG. 7 demonstrates the TDCC assay results of various CD19 targeting proteins measured in the presence of HSA.

[0041] FIG. 8 demonstrates the TDCC assay results of various FLT3 targeting proteins measured in the presence of HSA.

[0042] FIG. 9 demonstrates the TDCC assay results of various FLT3 targeting protein measured in the presence of HSA.

[0043] FIG. 10 demonstrates the TDCC assay results of various CD33 targeting proteins measured in the presence of HSA.

[0044] FIG. 11 demonstrates the TDCC assay results of CD19 targeting proteins in the T:C:A or T:A:C configuration measured in the presence of HSA.

[0045] FIG. 12 demonstrates the TDCC assay results of FLT3 targeting proteins in the T:C:A configuration measured in the presence of HSA.

[0046] Fig. 13A illustrates the binding of TriTAC-XR non-cleavable prodrug, cleavable prodrug, and active drug to human CD3ε by ELISA. **Fig. 13B** illustrates the binding of TriTAC-XR non-cleavable prodrug, cleavable prodrug, and active drug to human T cells as measured by flow cytometry.

[0047] FIG. 14 illustrates the pharmacokinetics of FLT3 TriTAC-XR-L001 in cynomolgus monkeys after single i.v. doses of 300 (**Fig. 14A**) and 1000 μg/kg (**Fig. 14B**), and FLT3 TriTAC-XR-L085 after a single i.v. doses of 1000 μg/kg (**Fig. 14C**). Two assays were used to quantify the Intact, Active, and Total amount of TriTAC-XR. Plotted are mean values measured in plasma samples collected from two test subjects per dose group.

[0048] FIG. 15 illustrates the amount of soluble FLT3L present in serum samples collected from cynomolgus monkeys after single i.v. doses of FLT3 TriTAC-XR-L001 (SEQ ID NO:

3873) or TriTAC-XR-L085 (SEQ ID NO: 3874). Data are plotted each individual test subject in each dose group.

[0049] FIG. 16 illustrates the amount of FLT3 transcript present in RNA prepared from bone marrow collected from cynomolgus monkeys after single i.v. doses of FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) or TriTAC-XR-L085 (SEQ ID NO: 3874). Plotted are technical replicates. Data are plotted each individual test subject in each dose group.

[0050] FIG. 17 illustrates the pharmacokinetics of FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) or a constitutively active FLT3 TriTAC (SEQ ID NO: 3875) in non-human primates (NHP).

[0051] FIG. 18 illustrates the amount of FLT3 transcript present in RNA prepared from bone marrow collected from cynomolgus monkeys after single i.v. doses of 1000 μg/kg FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) or a constitutively active FLT3 TriTAC (SEQ ID NO: 3875). Plotted are technical replicates. Data are plotted each individual test subject in each dose group.

[0052] FIG. 19 illustrates the predicted pharmacokinetics of repeat dosing of TriTAC-XR or TriTAC in NHP.

[0053] FIG. 20 shows the empirical pharmacokinetics of repeat dosing of CD20 TriTAC-XR in cyno monkeys.

[0054] FIG. 21 illustrates the peak cytokine levels (IL-2 in **Fig. 21A**, IL-6 in **Fig. 21B**) after i.v. dosing of FLT3 TriTAC-XR (FLT3 TriTAC-XR-L001, SEQ ID NO: 3873) at 300 and 1000 μg/kg or a constitutively active FLT3 TriTAC (SEQ ID NO: 3875) at 10, 100, and 1000 μg/kg. Plotted are mean values measured in serum samples collected from two test subjects per dose group.

[0055] FIG. 22 illustrates the amount of soluble FLT3L present in serum samples collected from cynomolgus monkeys after single i.v. doses of FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) at 300 and 1000 μg/kg, or a constitutively active FLT3 TriTAC (SEQ ID NO: 3875) at 10, 100 and 1000 μg/kg. Plotted are mean values measured in serum samples collected from two test subjects per dose group.

[0056] FIG. 23 illustrates the efficacy of an a FLT3 TriTAC-XR in a mouse tumor model.

[0057] FIG. 24 illustrates the pharmacokinetics of CD19 TriTAC-XR or a constitutively active CD19 TriTAC in NHP.

[0058] FIG. 25 illustrates the peak cytokine levels (IL-2 in **Fig. 25A**, IL-6 in **Fig. 25B**) after i.v. dosing of CD19 TriTAC-XR or a constitutively active CD19 TriTAC.

[0059] FIG. 26 illustrates that target cell depletion is comparable between CD19 TriTAC and CD19 TriTAC-XR.

[0060] FIG. 27 illustrates the pharmacokinetics of CD20 TriTAC-XR or a constitutively active CD20 TriTAC in NHP.

[0061] FIG. 28 illustrates the peak cytokine levels (IL-2 in **Fig. 28A**, IL-6 in **Fig. 28B**) after i.v. dosing of CD20 TriTAC-XR or a constitutively active CD20 TriTAC.

[0062] FIG. 29 illustrates that target cell depletion is comparable between CD20 TriTAC and CD20 TriTAC-XR.

[0063] FIG. 30 illustrates exemplary constructs of a protein with masking peptide as described herein.

DETAILED DESCRIPTION OF THE INVENTION

Certain definitions

[0064] The terminology used herein is for the purpose of describing particular cases only and is not intended to be limiting. As used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the terms "including", "includes", "having", "has", "with", or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term "comprising."

[0065] The term "about" or "approximately" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, *e.g.*, the limitations of the measurement system. For example, "about" can mean within 1 or more than 1 standard deviation, per the practice in the given value. Where particular values are described in the application and claims, unless otherwise stated the term "about" should be assumed to mean an acceptable error range for the particular value.

[0066] The terms "individual," "patient," or "subject" are used interchangeably. None of the terms require or are limited to situation characterized by the supervision (*e.g.* constant or intermittent) of a health care worker (*e.g.* a doctor, a registered nurse, a nurse practitioner, a physician's assistant, an orderly, or a hospice worker).

[0067] An "antibody" typically refers to a Y-shaped tetrameric protein comprising two heavy (H) and two light (L) polypeptide chains held together by covalent disulfide bonds and non-covalent interactions. Human light chains comprise a variable domain (VL) and a constant domain (CL) wherein the constant domain may be readily classified as kappa or lambda based on amino acid sequence and gene loci. Each heavy chain comprises one variable domain (VH) and a constant region, which in the case of IgG, IgA, and IgD, comprises three domains termed CH1, CH2, and CH3 (IgM and IgE have a fourth

domain, CH4). In IgG, IgA, and IgD classes the CH1 and CH2 domains are separated by a flexible hinge region, which is a proline and cysteine rich segment of variable length (generally from about 10 to about 60 amino acids in IgG). The variable domains in both the light and heavy chains are joined to the constant domains by a "J" region of about 12 or more amino acids and the heavy chain also has a "D" region of about 10 additional amino acids. Each class of antibody further comprises inter-chain and intra-chain disulfide bonds formed by paired cysteine residues. There are two types of native disulfide bridges or bonds in immunoglobulin molecules: interchain and intrachain disulfide bonds. The location and number of interchain disulfide bonds vary according to the immunoglobulin class and species. Interchain disulfide bonds are located on the surface of the immunoglobulin, are accessible to solvent and are usually relatively easily reduced. In the human IgG1 isotype there are four interchain disulfide bonds, one from each heavy chain to the light chain and two between the heavy chains. The interchain disulfide bonds are not required for chain association. As is well known the cysteine rich IgG1 hinge region of the heavy chain has generally been held to consist of three parts: an upper hinge, a core hinge, and a lower hinge. Those skilled in the art will appreciate that that the IgG1 hinge region contain the cysteines in the heavy chain that comprise the interchain disulfide bonds (two heavy/heavy, two heavy/light), which provide structural flexibility that facilitates Fab movements. The interchain disulfide bond between the light and heavy chain of IgG1 are formed between C214 of the kappa or lambda light chain and C220 in the upper hinge region of the heavy chain. The interchain disulfide bonds between the heavy chains are at positions C226 and C229 (all numbered per the EU index according to Kabat, *et al.*, infra.)

[0068] As used herein the term "antibody" includes polyclonal antibodies, multiclonal antibodies, monoclonal antibodies, chimeric antibodies, deimmunized, humanized and primatized antibodies, CDR grafted antibodies, human antibodies, recombinantly produced antibodies, intrabodies, multispecific antibodies, bispecific antibodies, monovalent antibodies (*e.g.*, a monovalent IgG), multivalent antibodies, anti-idiotypic antibodies, synthetic antibodies, including muteins and variants thereof, immunospecific antibody fragments such as: hcIgG, a V-NAR, Fv, Fd, Fab, F(ab')2, F(ab'), Fab2, Fab3 fragments, single-chain fragments (*e.g.*, di-scFv, scFv, scFvFc, scFv-zipper, scFab), disulfide-linked Fvs (sdFv), a Fd fragment consisting of the VH and CH1 domains, linear antibodies, single domain antibodies such as nanobodies or single variable domain antibodies comprising merely one variable domain such as sdAb (VH, VL, or VHH domains), "r IgG" ("half antibody"), diabodies, single chain diabodies, tandem diabodies

(Tandab's), tandem di-scFv, tandem tri-scFv, "minibodies" are in some instances exemplified by a structure which is as follows: (VH-VL-CH3)2, (scFv-CH3)2, ((scFv)2-CH3+CH3), ((scFv)2-CH3) or (scFv-CH3-scFv)2, multibodies such as triabodies or tetrabodies,; and derivatives thereof including Fc fusions and other modifications, and any other immunoreactive molecule so long as it comprises a domain having a binding site for preferential association or binding with an FLT3protein. Moreover, unless dictated otherwise by contextual constraints the term further comprises all classes of antibodies (*i.e.* IgA, IgD, IgE, IgG, and IgM) and all subclasses (*i.e.*, IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2). Heavy-chain constant domains that correspond to the different classes of antibodies are typically denoted by the corresponding lower case Greek letter alpha, delta, epsilon, gamma, and mu, respectively. Light chains of the antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (kappa) and lambda (lambda), based on the amino acid sequences of their constant domains.

[0069] As used herein, "Variable region" or "variable domain" refers to the fact that certain portions of the variable domains differ extensively 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 evenly distributed throughout the variable domains of antibodies. It is 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 variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a β-sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the βsheet 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 (*see* Kabat *et al.*, Sequences of Proteins of Immunological Interest, Fifth Edition, National Institute of Health, Bethesda, Md. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity. The assignment of amino acids to each domain, framework region and CDR is, in some embodiments, in accordance with one of the numbering schemes provided by Kabat *et al.* (1991) Sequences of Proteins of Immunological Interest (5th Ed.), US Dept. of Health and Human Services, PHS, NIH, NIH Publication no. 91-3242; Chothia *et al.*, 1987, PMID: 3681981; Chothia *et al.*, 1989, PMID: 2687698; MacCallum

et al., 1996, PMID: 8876650; or Dubel, Ed. (2007) Handbook of Therapeutic Antibodies, 3rd Ed., Wily-VCH Verlag GmbH and Co or AbM (Oxford Molecular/MSI Pharmacopeia) unless otherwise noted.

[0070] "Variable domain residue numbering as in Kabat" or "amino acid position numbering as in Kabat," and variations thereof, refers to the numbering system used for heavy chain variable domains or light chain variable domains of the compilation of antibodies in Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991). Using this numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or CDR of the variable domain. For example, a heavy chain variable domain may include a single amino acid insert (residue 52a according to Kabat) after residue 52 of H2 and inserted residues (*e.g.*, residues 82a, 82b, and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence. It is not intended that CDRs of the present disclosure necessarily correspond to the Kabat numbering convention.

[0071] The term "Framework" or "FR" residues (or regions) refer to variable domain residues other than the CDR or hypervariable region residues as herein defined. A "human consensus framework" is a framework which represents the most commonly occurring amino acid residue in a selection of human immunoglobulin VL or VH framework sequences.

[0072] The term "epitope," as used herein, refers to an antigenic determinant that interacts with a specific antigen binding site in the variable region of an antibody molecule known as a paratope. A single antigen may have more than one epitope. Thus, different antibodies may bind to different areas on an antigen and may have different biological effects. Epitopes may be either conformational or linear. A conformational epitope is produced by spatially juxtaposed amino acids from different segments of the linear polypeptide chain. A linear epitope is one produced by adjacent amino acid residues in a polypeptide chain. In certain circumstance, an epitope may include moieties of saccharides, phosphoryl groups, or sulfonyl groups on the antigen.

[0073] As used herein, the term "Percent (%) amino acid sequence identity" with respect to a sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence

identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer softwares such as EMBOSS MATCHER, EMBOSS WATER, EMBOSS STRETCHER, EMBOSS NEEDLE, EMBOSS LALIGN, BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. Alignment for purposes of determining percent amino acid sequence identity can for example be achieved using publicly available sequence comparison computer program ALIGN-2. The source code for the ALIGN-2 sequence comparison computer program is available with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program can be compiled for use on a UNIX operating system, such as a digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0074] As used herein, "elimination half-time" is used in its ordinary sense, as is described in Goodman and Gillman's The Pharmaceutical Basis of Therapeutics 21-25 (Alfred Goodman Gilman, Louis S. Goodman, and Alfred Gilman, eds., 6th ed. 1980). Briefly, the term is meant to encompass a quantitative measure of the time course of drug elimination. The elimination of most drugs is exponential (*i.e.*, follows first-order kinetics), since drug concentrations usually do not approach those required for saturation of the elimination process. The rate of an exponential process may be expressed by its rate constant, k, which expresses the fractional change per unit of time, or by its half-time, $t_{1/2}$ the time required for 50% completion of the process. The units of these two constants are time−1 and time, respectively. A first-order rate constant and the half-time of the reaction are simply related ($k \times t_{1/2}=0.693$) and may be interchanged accordingly. Since first-order elimination kinetics dictates that a constant fraction of drug is lost per unit time, a plot of the log of drug concentration versus time is linear at all times following the initial distribution phase (*i.e.*, after drug absorption and distribution are complete). The half-time for drug elimination can be accurately determined from such a graph.

[0075] As used herein, the term "binding affinity" refers to the affinity of the proteins described in the disclosure to their binding targets, and is expressed numerically using "Kd" values. If two or more proteins are indicated to have comparable binding affinities

towards their binding targets, then the Kd values for binding of the respective proteins towards their binding targets, are within ±2-fold of each other. If two or more proteins are indicated to have comparable binding affinities towards single binding target, then the Kd values for binding of the respective proteins towards said single binding target, are within ±2-fold of each other. If a protein is indicated to bind two or more targets with comparable binding affinities, then the Kd values for binding of said protein to the two or more targets are within ±2-fold of each other. In general, a higher Kd value corresponds to a weaker binding. In some embodiments, the "Kd" is measured by a radiolabeled antigen binding assay (RIA) or surface plasmon resonance assays using a BIAcore™-2000 or a BIAcore™-3000 (BIAcore, Inc., Piscataway, N.J.). In certain embodiments, an "on-rate" or "rate of association" or "association rate" or "kon" and an "off-rate" or "rate of dissociation" or "dissociation rate" or "koff" are also determined with the surface plasmon resonance technique using a BIAcore™-2000 or a BIAcore™-3000 (BIAcore, Inc., Piscataway, N.J.). In additional embodiments, the "Kd", "kon", and "koff" are measured using the OCTET® Systems (Pall Life Sciences). In an exemplary method for measuring binding affinity using the OCTET® Systems, the ligand, *e.g.*, biotinylated human or cynomolgus FLT3 in case of an immune cell engaging protein comprising a FLT3 binding single domain antibody, is immobilized on the OCTET® streptavidin capillary sensor tip surface which streptavidin tips are then activated according to manufacturer's instructions using about 20-50 µg/ml human or cynomolgus FLT3 protein. A solution of PBS/Casein is also introduced as a blocking agent. For association kinetic measurements, FLT3 binding protein variants are introduced at a concentration ranging from about 10 ng/mL to about 100 µg/mL, about 50 ng/mL to about 5 µg/mL, or about 2 ng/mL to about 20 µg/mL. In some embodiments, the FLT3 binding single domain proteins are used at a concentration ranging from about 2 ng/mL to about 20 µg/mL. Complete dissociation is observed in case of the negative control, assay buffer without the binding proteins. The kinetic parameters of the binding reactions are then determined using an appropriate tool, *e.g.*, ForteBio software.

[0076] As used herein, in some embodiments, "treatment" or "treating" or "treated" refers to therapeutic treatment wherein the object is to slow (lessen) an undesired physiological condition, disorder or disease, or to obtain beneficial or desired clinical results. For the purposes described herein, beneficial or desired clinical results include, but are not limited to, alleviation of symptoms; diminishment of the extent of the condition, disorder or disease; stabilization (*i.e.*, not worsening) of the state of the condition, disorder or disease; delay in onset or slowing of the progression of the

condition, disorder or disease; amelioration of the condition, disorder or disease state; and remission (whether partial or total), whether detectable or undetectable, or enhancement or improvement of the condition, disorder or disease. Treatment includes eliciting a clinically significant response without excessive levels of side effects. Treatment also includes prolonging survival as compared to expected survival if not receiving treatment. In other embodiments, "treatment" or "treating" or "treated" refers to prophylactic measures, wherein the object is to delay onset of or reduce severity of an undesired physiological condition, disorder or disease, such as, for example is a person who is predisposed to a disease (*e.g.*, an individual who carries a genetic marker for a disease such as breast cancer).

[0077] Generally, it should be noted that the term single domain antibody as used herein in its broadest sense is not limited to a specific biological source or to a specific method of preparation. Single domain antibodies are antibodies whose complementary determining regions are part of a single domain polypeptide. Examples include, but are not limited to, heavy chain antibodies, antibodies naturally devoid of light chains, single domain antibodies derived from conventional 4-chain antibodies, engineered antibodies and single domain scaffolds other than those derived from antibodies. Single domain antibodies may be any of the art, or any future single domain antibodies. Single domain antibodies may be derived from any species including, but not limited to mouse, human, camel, llama, goat, rabbit, bovine. For example, in some embodiments, the single domain antibodies of the disclosure are obtained: (1) by isolating the VHH domain of a naturally occurring heavy chain antibody; (2) by expression of a nucleotide sequence encoding a naturally occurring VHH domain; (3) by "humanization" of a naturally occurring VHH domain or by expression of a nucleic acid encoding a such humanized VHH domain; (4) by "camelization" of a naturally occurring VH domain from any animal species, and in particular from a species of mammal, such as from a human being, or by expression of a nucleic acid encoding such a camelized VH domain; (5) by "camelization" of a "domain antibody" or "Dab," or by expression of a nucleic acid encoding such a camelized VH domain; (6) by using synthetic or semi-synthetic techniques for preparing proteins, polypeptides or other amino acid sequences; (7) by preparing a nucleic acid encoding a single domain antibody using techniques for nucleic acid synthesis known in the field, followed by expression of the nucleic acid thus obtained; and/or (8) by any combination of one or more of the foregoing.

[0078] In some embodiments, an immune cell engaging protein as described herein comprises an antibody, *e.g.*, a single domain antibody targeting an antigen, *e.g.*, PSMA,

MSLN, BCMA, DLL3, EGFR, EpCAM, FLT3, comprising an amino acid sequence that corresponds to the amino acid sequence of a naturally occurring VHH domain, but that has been "humanized", *e.g.*, by replacing one or more amino acid residues in the amino acid sequence of said naturally occurring VHH sequence (and in particular in the framework sequences) by one or more of the amino acid residues that occur at the corresponding position(s) in a VH domain from a conventional 4-chain antibody from a human being (*e.g.*, as indicated above). This can be performed in a manner known in the field, which will be clear to the skilled person, for example on the basis of the further description herein. Again, it should be noted that such humanized single domain antibodies of the disclosure are obtained in any suitable manner known per se (*e.g.*, as indicated under points (1)-(8) above) and thus are not strictly limited to polypeptides that have been obtained using a polypeptide that comprises a naturally occurring VHH domain as a starting material. In some additional embodiments, a single domain antibody, as described herein, comprises a single domain antibody with an amino acid sequence that corresponds to the amino acid sequence of a naturally occurring VH domain, but that has been "camelized", i.e., by replacing one or more amino acid residues in the amino acid sequence of a naturally occurring VH domain from a conventional 4-chain antibody by one or more of the amino acid residues that occur at the corresponding position(s) in a VHH domain of a heavy chain antibody. Such "camelizing" substitutions are preferably inserted at amino acid positions that form and/or are present at the VH-VL interface, and/or at the so-called Camelidae hallmark residues (*see* for example WO 94/04678 and Davies and Riechmann (1994 and 1996)). Preferably, the VH sequence that is used as a starting material or starting point for generating or designing the camelized single domain is preferably a VH sequence from a mammal, more preferably the VH sequence of a human being, such as a VH3 sequence. However, it should be noted that such camelized anti-MSLN single domain antibodies of the disclosure, in certain embodiments, are obtained in any suitable manner known in the field (*i.e.*, as indicated under points (1)-(8) above) and thus are not strictly limited to polypeptides that have been obtained using a polypeptide that comprises a naturally occurring VH domain as a starting material. For example, as further described herein, both "humanization" and "camelization" is performed by providing a nucleotide sequence that encodes a naturally occurring VHH domain or VH domain, respectively, and then changing, one or more codons in said nucleotide sequence in such a way that the new nucleotide sequence encodes a "humanized" or "camelized" single domain antibody, respectively. This nucleic acid can then be expressed, so as to provide a desired

single domain antibody of the disclosure. Alternatively, in other embodiments, based on the amino acid sequence of a naturally occurring VHH domain or VH domain, respectively, the amino acid sequence of the desired humanized or camelized single domain antibody of the disclosure, respectively, are designed and then synthesized *de novo* using known techniques for peptide synthesis. In some embodiments, based on the amino acid sequence or nucleotide sequence of a naturally occurring VHH domain or VH domain, respectively, a nucleotide sequence encoding the desired humanized or camelized single domain antibody of the disclosure, respectively, is designed and then synthesized *de novo* using known techniques for nucleic acid synthesis, after which the nucleic acid thus obtained is expressed in using known expression techniques, so as to provide the desired single domain antibody of the disclosure.

[0079] The terms "patient" or "subject" refers to any single subject for which therapy is desired or that is participating in a clinical trial, epidemiological study or used as a control, including humans and mammalian veterinary patients such as cattle, horses, dogs, and cats.

[0080] The term "therapeutic index" is the ratio of the TD_{50} (or LD_{50}) to the ED_{50}, determined from quantal dose-response curves. ED_{50} is the efficacious dose of a drug in 50% of subjects. TD_{50} is the toxic dose of a drug in 50% of subjects for humans. LD_{50} is the lethal dose of a drug for 50% of the population for animals. Therapeutic index demonstrates a quantitative measurement of the relative safety of the drug. A higher therapeutic index is preferable to a lower one: a patient would have to take a much higher dose of such a drug to reach the toxic threshold than the dose taken to elicit the therapeutic effect.

[0081] The term "significantly cleaved" means that a molecule is cleaved for more than 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 99%.

Extended-Release Binding Protein

[0082] Described herein is a pharmaceutical composition comprising an extended-release binding protein which comprises an antigen binding protein/immune cell engaging protein, a masking peptide, and a cleavable linker, wherein the extended-release binding protein releases an active version of the extended-release binding protein after the cleavable linker is cleaved.

[0083] Without being bound by any theory, it is contemplated that the masking peptide, connected to the antigen binding protein/immune cell engaging protein *via* a cleavable linker, confers extended-release properties to the antigen binding protein/immune cell engaging protein.

The extended-release binding protein is converted to an active form upon gradual cleaving of the cleavable linker, which removes the masking effect of the masking peptide, and releases the active form. The gradual release of the active form from the masked form (intact form) allows maintenance of a steady concentration of the active form for a longer duration of time, compared to directly administering the non-masked form. The extended-release binding protein is contemplated to have a higher therapeutic index than a corresponding antigen binding protein without the masking peptide. **FIG. 1C** shows the predicted concentrations of the intact version and the active version in systemic circulation after multiple administration events. **FIG. 1D** shows the predicted concentration of the active version of a corresponding antigen binding protein without the masking peptide in systemic circulation after multiple administration events. The concentration of the extended-release binding protein's active version is relatively constant compared to the concentration of the active version for a corresponding antigen binding protein without the masking peptide.

[0084] Cytokine release syndrome (CRS) is the major dose limiting toxicity, it is hypothesized that there are two factors contributing to CRS: 1) instant exposure to a high concentration of the active drug, and 2) exposures of the active drug that greatly exceed Cmin. The extended-release concept addresses both issues by having a slow initial release of active drug and by minimizing the difference between Cmax and Cmin. It is expected that relatively constant concentrations of the active drug in the serum result in relatively constant drug exposures to the tissues. Therefore, administration of the extended-release binding protein results in a lower Cytokine release syndrome (CRS) level than the CRS observed when a corresponding antigen binding protein without the masking peptide is administered.

[0085] In some embodiments, the masking peptide is linked to the N-terminus or the C-terminus of the antigen binding protein/immune cell engaging protein, through a cleavable linker. Various exemplary configurations are provided in FIGs. 2A through 2L. In some embodiments, the masking peptide is linked to the N-terminus of the domain that specifically binds to HSA, wherein the domain that specifically binds to HSA is connected, *via* its C-terminus (*e.g.*, through a linker) to the target antigen binding domain or the T-cell engaging domain. In some embodiments, the masking peptide is linked to the N-terminus of the target antigen binding domain, wherein the target antigen binding domain is connected, *via* its C-terminus (*e.g.*, through a linker) to the domain that specifically binds to HSA or the T-cell engaging domain. In some embodiments, the masking peptide is linked to the C-terminus of the target antigen binding domain, wherein the target antigen binding domain is connected, *via* its N-terminus (*e.g.*, through

a linker) to the domain that specifically binds to HSA or the T-cell engaging domain. In some embodiments, the masking peptide is linked to the N-terminus of the T-cell engaging domain. In some embodiments, the masking peptide is linked to the C-terminus of the T-cell engaging domain. In some embodiments, the masking peptide is linked to the VH or VL domain of a T-cell engaging domain that is a single chain variable fragment (*e.g.*, an scFv that is specific for a human CD3, such as CD3ε). Alternative formats include, but are not limited to an extended-release binding protein comprising, from N-terminus to C-terminus:

a masking peptide-a cleavable linker-a target antigen binding domain-a serum albumin binding domain-a T-cell engaging domain;

a masking peptide-a cleavable linker-a target antigen binding domain-a T-cell engaging domain-a serum albumin binding domain;

a masking peptide-a cleavable linker-a T-cell engaging domain-a serum albumin binding domain-a target antigen binding domain;

a masking peptide-a cleavable linker-a T-cell engaging domain-a target antigen binding domain-a serum albumin binding domain;

a masking peptide-a cleavable linker-a serum albumin binding domain-a T-cell engaging domain-a target antigen binding domain;

a masking peptide-a cleavable linker-a serum albumin binding domain-a target antigen binding domain-a T-cell engaging domain;

a target antigen binding domain-a serum albumin binding domain-a T-cell engaging domain-a cleavable linker-a masking peptide;

a target antigen binding domain-a T-cell engaging domain-a serum albumin binding domain-a cleavable linker-a masking peptide;

a T-cell engaging domain-a serum albumin binding domain-a target antigen binding domain-a cleavable linker-a masking peptide;

a T-cell engaging domain-a target antigen binding domain-a serum albumin binding domain-a cleavable linker-a masking peptide;

a serum albumin binding domain-a T-cell engaging domain-a target antigen binding domain-a cleavable linker-a masking peptide;

a serum albumin binding domain-a target antigen binding domain-a T-cell engaging domain-a cleavable linker-a masking peptide.

[0086] The antigen binding protein/extended-release immune cell engaging protein of this disclosure, in some embodiments, comprises an amino acid sequence that is at least

about 60% to about 100% identical to the sequence of SEQ ID NO: 3600, 3824-3858 or 3882.

Immune Cell Engaging Proteins

[0087] Described herein, in some embodiments, is a pharmaceutical composition comprising an extended-release binding protein which comprises an immune cell engaging protein, a masking peptide, and a cleavable linker. In some embodiments, the immune cell engaging protein is a half-life extended protein. In some embodiments, the masking peptide is covalently linked to the N-terminus or the C-terminus of the half-life extended immune cell engaging protein through the cleavable linker. In some embodiments, the cleavable linker is significantly cleaved in systemic circulation. In some embodiments, the immune cell engaging protein is a bi-specific protein, a tri-specific protein or a multi-specific protein. In some embodiments, the immune cell engaging protein comprises a domain that binds to a bulk serum protein, *e.g.*, a serum albumin. In some embodiments, the serum albumin is human serum albumin (HSA).

[0088] In some embodiments, the extended-release binding protein has a higher therapeutic index than a corresponding half-life-extended immune cell engaging protein without the masking peptide. In some embodiments, the administration of the extended-release binding protein results in a lower Cmax/Cmin ratio of an active version of the extended-release binding protein in systemic circulation than the Cmax/Cmin ratio when a corresponding half-life extended immune cell engaging protein without the masking peptide is administered. In some embodiments, multiple administration of the extended-release binding protein results in a more gradual increase of the level of an active version of the extended-release binding protein in systemic circulation than when a corresponding half-life-extended immune cell engaging protein without the masking peptide is administered. In some embodiments, administration of the extended-release binding protein results in a lower Cytokine release syndrome (CRS) level than the CRS observed when a corresponding half-life extended immune cell engaging protein without the masking peptide is administered.

[0089] In some embodiments, the immune cell engaging protein comprises an immune cell engaging domain. In some embodiments “an immune cell engaging domain” as used herein refers to one or more binding specificities that bind and/or activate an immune cell, *e.g.*, a cell involved in an immune response. In some embodiments, the immune cell is selected from a natural killer (NK) cell, a B cell, a dendritic cell, a macrophage cell. The immune cell engaging domain, in some embodiments, is an antibody or an antigen binding fragment thereof, a receptor molecule (*e.g.*, a full length receptor, receptor

fragment, or fusion thereof (*e.g.*, a receptor-Fc fusion)), or a ligand molecule (*e.g.*, a full length ligand, ligand fragment, or fusion thereof (*e.g.*, a ligand-Fc fusion)) that binds to an immune cell antigen (*e.g.*, the NK cell antigen, the B cell antigen, the dendritic cell antigen, and/or the macrophage cell antigen). In some embodiments, the immune cell engaging domain specifically binds to a target immune cell, *e.g.*, binds preferentially to the target immune cell. For example, in some embodiments the immune cell engaging domain is an antibody or an antigen binding fragment thereof that binds to the immune cell antigen (*e.g.*, the NK cell antigen, the B cell antigen, the dendritic cell antigen, and/or the macrophage cell antigen) with a dissociation constant of less than about 10 nM.

[0090] In some embodiments, the immune cell engaging domain comprises an NK cell engaging domain, a T cell engaging domain, a B cell engaging domain, a dendritic cell engaging domain, a macrophage cell engaging domain, or a combination thereof. In some embodiments, the immune cell engaging domain comprises the T-cell engaging domain. In some embodiments, the T cell engaging domain binds a CD3 molecule. In some embodiments, the CD3 molecule is at least one of: a CD3γ molecule, a CD3δ molecule, or a CD3ε molecule.

[0091] In some embodiments, the immune cell engaging protein comprises an antigen binding domain. In some examples, the antigen binding domain includes antibodies, single chain antibodies, Fabs, Fv, T-cell receptor binding domains, ligand binding domains, receptor binding domains, domain antibodies, single domain antibodies, minibodies, nanobodies, peptibodies, or various other antibody mimics (such as affimers, affitins, alphabodies, atrimers, CTLA4-based molecules, adnectins, anticalins, Kunitz domain-based proteins, avimers, knottins, fynomers, darpins, affibodies, affilins, monobodies and armadillo repeat protein-based proteins).

[0092] In some embodiments, the antigen is a tumor antigen, In some embodiments, the antigen is selected from the group consisting of: CD19 (B-lymphocyte antigen CD19, B-Lymphocyte Surface Antigen B4, T-Cell Surface Antigen Leu-12, CVID3), PSMA (prostate specific membrane antigen**),** MSLN (mesothelin), BCMA (B-cell maturation antigen), DLL3 (Delta-like ligand 3), EGFR (epidermal growth factor receptor), FLT3 (FMS-like tyrosine kinase 3), CD20 (B-lymphocyte antigen CD20, MS4A1, B1, Bp35, CVID5, LEU-16, MS4A2, S7, membrane spanning 4-domains A1), CD22 (SIGLEC-2, SIGLEC2), CD25 (IL2RA, interleulin-2 receptor alpha chain), CD27 (S152, S152. LPFS2, T14, TNFRSF7, Tp55), CD30 (TNFRSF8), CD33 (Siglec-3, sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67), CD37 (GP52-40, TSPAN26), CD38

(cyclic ADP ribose hydrolase, ADPRC1, ADPRC 1), CD40 (Bp50, CDW40, TNFRSF5, p50), CD44 (HCAM, homing cell adhesion molecule), Pgp-1 (phagocytic glycoprotein-1), Hermes antigen, lymphocyte homing receptor, ECM-III, and HUTCH-1), CD48 (BLAST-1, B-lymphocyte activation marker, SLAMF2, signaling lymphocytic activation molecule 2), CD52 (CAMPATH-1 antigen), CD70, CD73 (NT5E, ecto-5'-nucleotidase), CD39 (ENTPD1, Ectonucleoside triphosphate diphosphohydrolase-1), CD74 (HLA class II histocompatibility antigen gamma chain, HLA-DR antigens-associated invariant chain), CD79b (immunoglobulin-associated beta), CD80 (B7-1), CD86 (B7-2), CD123 (IL3RA, interleukin-3 receptor), CD133 (PROM1), CD137 (TNFRSF9, tumor necrosis factor receptor superfamily member 9, 4-1BB, ILA, induced by lymphocyte activation), CD138 (SDC1), alpha fetoprotein (AFP), c-Met; c-Kit; CD371 (CLEC12A, C-type lectin domain family 12 member A, CLL1)); CD370 (CLEC9A, C-type lectin domain containing 9A); cadherin 3 (CDH3, p-cadherin, PCAD); carbonic anhydrase 6 (CA6); carbonic anhydrase 9 (CA9, CAIX); carcinoembryonic antigen related cell adhesion molecule 3 (CEACAM3); carcinoembryonic antigen related cell adhesion molecule 5 (CEACAM5); CD66c (CEACAM6, carcinoembryonic antigen related cell adhesion molecule 6); chorionic somatomammotropin hormone 1 (CSH1, CS1); coagulation factor III, tissue factor (F3, TF); collectin subfamily member 10 (COLEC10); delta like canonical Notch ligand 3 (DLL3); ectonucleotide pyrophosphatase/ phosphodiesterase 3 (ENPP3); ephrin A1 (EFNA1); epidermal growth factor receptor (EGFR); EGFR variant III (EGFRvIII); EPH receptor A2 (EPHA2); epithelial cell adhesion molecule (EpCAM); erb-b2 receptor tyrosine kinase 2 (ERBB2, HER2); fibroblast activation protein alpha (FAP); fibroblast growth factor receptor 2 (FGFR2); fibroblast growth factor receptor 3 (FGFR3); folate hydrolase 1 (FOLH1, PSMA); folate receptor 1 (FOLR1, FRa); GD2 ganglioside; glycoprotein NMB (GPNMB, osteoactivin); guanylate cyclase 2C (GUCY2C, GCC); human papillomavirus (HPV) E6; HPV E7; major histocompatibility complex (MHC) class I-presented neoantigens, major histocompatibility complex (MHC) class II-presented neoantigens, major histocompatibility complex, class I, E (HLA-E); major histocompatibility complex, class I, F (HLA-F); major histocompatibility complex, class I, G (HLA-G, MHC-G); integrin subunit beta 7 (ITGB7); leukocyte immunoglobulin like receptor B1 (LILRB1, ILT2); leukocyte immunoglobulin like receptor B2 (LILRB2, ILT4); LY6/PLAUR domain containing 3 (LYPD3, C4.4A); glypican 3 (GPC3); KRAS proto-oncogene, GTPase (KRAS); MAGE family member A1 (MAGEA1); MAGE family member A3 (MAGEA3); MAGE family member A4 (MAGEA4); MAGE family member A11 (MAGEA11); MAGE family

member C1 (MAGEC1); MAGE family member C2 (MAGEC2); MAGE family member D1 (MAGED1); MAGE family member D2 (MAGED2); mesothelin (MSLN); mucin 1 (MUC1) and splice variants thereof (*e.g.*, MUC1/C, D, and Z); mucin 16 (MUC16); necdin (NDN); nectin cell adhesion molecule 4 (NECTIN4); SLIT and NTRK like family member 6 (SLITRK6); promyelocytic leukemia (PML, TRIM19); protein tyrosine kinase 7 (inactive) (PTK7); CD352 (SLAMF6, SLAM family member 6); CD319 (SLAMF7, SLAM family member 7, 19A, CRACC, CS1); sialic acid binding Ig like lectin 7 (SIGLEC7); sialic acid binding Ig like lectin 9 (SIGLEC9); solute carrier family 34 (sodium phosphate), member 2 (SLC34A2); solute carrier family 39 member 6 (SLC39A6, LIV1); STEAP family member 1 (STEAP1); STEAP family member 2 (STEAP2); CD134 (TNFRSF4, TNF receptor superfamily member 4, OX40); CD137L (TNFSF9, TNF superfamily member 9, 4-1BB-L); CD261 (TNFRSF10A, TNF receptor superfamily member 10a, DR4, TRAILR1); CD262 (TNFRSF10B, TNF receptor superfamily member 10b, DR5, TRAILR2); CD267 (TNFRSF13B, TNF receptor superfamily member 13B, TACI, IGAD2); CD269 (TNFRSF17, TNF receptor superfamily member 17, BCMA,); CD357 (TNFRSF18, TNF receptor superfamily member 18 GITR); transferrin (TF); transforming growth factor beta 1 (TGFB1); trophoblast glycoprotein (TPBG, 5T4); trophinin (TRO, MAGED3); tumor associated calcium signal transducer 2 (TACSTD2, TROP2, EGP1); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ROR1, CD30, and Lewis Y antigen. In some embodiments, the immune cell engaging protein specifically binds to PSMA, MSLN, BCMA, DLL3, EGFR, FLT3, or EpCAM.

[0093] Described herein, in some embodiments, is an immune cell engaging protein that comprises a first domain (A), which is a T cell engaging domain and specifically binds to human CD3, a second domain (B) which specifically binds to human serum albumin (HSA), and a third domain (C) which specifically binds to a target antigen. In some embodiments, the immune cell engaging protein's domains are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(B)-(A)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, H_2N-(B)-(C)-(A)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(B)-L1-(A)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH, H_2N-(B)-L1-(C)-L2-(A)-COOH. In some embodiments, the linkers L1 and L2 are each independently selected from an amino acid sequence of SEQ ID Nos: 3190-3200.

[0094] The design of the immune cell engaging proteins described herein allows the binding domain to a target antigen, the third domain (C) described above, to be flexible in that the binding domain to a target antigen can be any type of binding domain, including but not limited to, domains from a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, or a humanized antibody. In some embodiments, the binding domain to a target antigen is a single chain variable fragments (scFv), single-domain antibody such as a heavy chain variable domain (VH), a light chain variable domain (VL), a variable domain (VHH) of a llama derived sdAb, or a variable domain (VHH) of camelid derived single domain antibody. In other embodiments, the binding domain to a target antigen is a non-Ig binding domain, *e.g.*, antibody mimetic, such as anticalins, affilins, affibody molecules, affimers, affitins, alphabodies, avimers, DARPins, fynomers, kunitz domain peptides, and monobodies. In further embodiments, the binding domain to a target antigen is a ligand or peptide that binds to or associates with the target antigen. In yet further embodiments, the binding domain to a target antigen is a knottin. In yet further embodiments, the binding domain to a target antigen is a small molecular entity.

[0095] In some embodiments, the target antigen binding domain is an antibody or an antibody variant. As used herein, the term "antibody variant" refers to variants and derivatives of an antibody described herein. In certain embodiments, amino acid sequence variants of the antibodies described herein are contemplated. For example, in certain embodiments amino acid sequence variants of antibodies described herein are contemplated to improve the binding affinity and/or other biological properties of the antibodies. Exemplary methods for preparing amino acid variants include, but are not limited to, 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.

[0096] 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. In certain embodiments, antibody variants having one or more amino acid substitutions are provided. Sites of interest for substitution mutagenesis include the CDRs and framework regions. Examples of such substitutions are described below. 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 T-cell mediated cytotoxicity (TDCC). Both

conservative and non-conservative amino acid substitutions are contemplated for preparing the antibody variants.

[0097] In another example of a substitution to create a variant antibody, one or more hypervariable region residues of a parent antibody are substituted. In general, variants are then selected based on improvements in desired properties compared to a parent antibody, for example, increased affinity, reduced affinity, reduced immunogenicity, or increased pH dependence of binding.

[0098] In one embodiment, a single domain antibody corresponds to the VHH domains of naturally occurring heavy chain antibodies directed against a target antigen. As further described herein, such VHH sequences can generally be generated or obtained by suitably immunizing a species of Llama with the target antigen, (i.e., so as to raise an immune response and/or heavy chain antibodies directed against the target antigen), by obtaining a suitable biological sample from said Llama (such as a blood sample, serum sample or sample of B-cells), and by generating VHH sequences directed against the target antigen, starting from said sample, using any suitable technique known in the field.

[0099] In another embodiment, such naturally occurring VHH domains against the target antigen, are obtained from naïve libraries of Camelid VHH sequences, for example by screening such a library using the target antigen, or at least one part, fragment, antigenic determinant or epitope thereof using one or more screening techniques known in the field. Such libraries and techniques are for example described in WO 99/37681, WO 01/90190, WO 03/025020 and WO 03/035694. Alternatively, improved synthetic or semi-synthetic libraries derived from naïve VHH libraries are used, such as VHH libraries obtained from naïve VHH libraries by techniques such as random mutagenesis and/or CDR shuffling, as for example described in WO 00/43507.

[00100] In a further embodiment, yet another technique for obtaining VHH sequences directed against a target antigen, involves suitably immunizing a transgenic mammal that is capable of expressing heavy chain antibodies (i.e., so as to raise an immune response and/or heavy chain antibodies directed against the target antigen), obtaining a suitable biological sample from said transgenic mammal (such as a blood sample, serum sample or sample of B-cells), and then generating VHH sequences directed against the target antigen, starting from said sample, using any suitable technique known in the field. For example, for this purpose, the heavy chain antibody-expressing rats or mice and the further methods and techniques described in WO 02/085945 and in WO 04/049794 can be used.

[00101] In some embodiments, a single domain antibody of the target antigen specific immune cell engaging protein comprises a single domain antibody with an amino acid sequence that corresponds to the amino acid sequence of a naturally occurring VHH domain, but that has been "humanized", *i.e.*, by replacing one or more amino acid residues in the amino acid sequence of said naturally occurring VHH sequence (and in particular in the framework sequences) by one or more of the amino acid residues that occur at the corresponding position(s) in a VH domain from a conventional 4-chain antibody from a human being (*e.g.*, as indicated above).

[00102] Other suitable methods and techniques for obtaining a target antigen binding single domain antibody of the disclosure and/or nucleic acids encoding the same, starting from naturally occurring VH sequences or VHH sequences for example comprises combining one or more parts of one or more naturally occurring VH sequences (such as one or more framework (FR) sequences and/or complementarity determining region (CDR) sequences), one or more parts of one or more naturally occurring VHH sequences (such as one or more FR sequences or CDR sequences), and/or one or more synthetic or semi-synthetic sequences, in a suitable manner, so as to provide a target antigen binding single domain antibody of the disclosure or a nucleotide sequence or nucleic acid encoding the same.

[00103] In some embodiments, the target antigen binding domain is an antibody comprising a heavy chain variable complementarity determining region CDR1, a heavy chain variable CDR2, a heavy chain variable CDR3, a light chain variable CDR1, a light chain variable CDR2, and a light chain variable CDR3. In some embodiments, examples of the target antigen binding domain include but are not limited to domains from a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, or antigen binding fragments such as single domain antibodies (sdAb), Fab, Fab′, F(ab)2, and Fv fragments, fragments comprised of one or more CDRs, single-chain antibodies (*e.g.*, single chain Fv fragments (scFv)), disulfide stabilized (dsFv) Fv fragments, heteroconjugate antibodies (*e.g.*, bispecific antibodies), pFv fragments, heavy chain monomers or dimers, light chain monomers or dimers, and dimers consisting of one heavy chain and one light chain. In some embodiments, the target antigen binding domain is a single domain antibody. In some embodiments, the single domain antibody comprises heavy chain variable complementarity determining regions (CDR), CDR1, CDR2, and CDR3.

[00104] In some embodiments, the immune cell engaging protein comprising the target antigen binding domain specifically binds to the target with equivalent or better affinity

compared to that of an immune cell engaging protein comprising a reference target antigen binding domain, and the target antigen binding domain in such embodiments comprises an affinity matured target antigen binding domain, and is derived from a parental molecule, comprising one or more amino acid mutations (*e.g.*, a stabilizing mutation, or a destabilizing mutation) with respect to the parental molecule. In some embodiments, the affinity matured target antigen binding molecule has superior stability with respect to selected destabilizing agents, as that of a reference parental molecule specific to the same antigen. In some embodiments, the affinity matured target antigen binding molecule is identified in a process comprising panning of one or more pre-candidate target antigen binding molecules derived from one or more parental molecule, expressed in a phage display library, against a target protein. The pre-candidate target antigen binding molecule comprises, in some embodiments, amino acid substitutions in the variable regions, CDRs, or framework residues, relative to a parental molecule.

[00105] As used herein, "Phage display" refers to a technique by which variant polypeptides are displayed as fusion proteins to at least a portion of a coat protein on the surface of phage, *e.g.*, filamentous phage, particles. A utility of phage display lies in the fact that large libraries of randomized protein variants can be rapidly and efficiently selected for those sequences that bind to a target molecule with high affinity. Display of peptide and protein libraries on phage has been used for screening millions of polypeptides for ones with specific binding properties. Polyvalent phage display methods have been used for displaying small random peptides and small proteins through fusions to either gene IΠ or gene VIII of filamentous phage. *See e.g.*, Wells and Lowman, Curr. Opin. Struct. Biol, 3:355-362 (1992), and references cited therein. In monovalent phage display, a protein or peptide library is fused to a gene III or a portion thereof, and expressed at low levels in the presence of wild type gene III protein so that phage particles display one copy or none of the fusion proteins. Avidity effects are reduced relative to polyvalent phage so that selection is on the basis of intrinsic ligand affinity, and phagemid vectors are used, which simplify DNA manipulations. *See e.g.*, Lowman and Wells, Methods: A companion to Methods in Enzymology, 3:205-0216 (1991).

[00106] In some embodiments, the panning comprises using varying binding times and concentrations to identify target antigen binding molecules with increased or decreased on-rates, from pre-candidate target antigen binding molecules. In some embodiments, the panning comprises using varying wash times to identify target antigen binding molecules with increased or decreased off-rates, from pre-candidate target antigen molecules. In some embodiments, the panning comprises using both varying binding times and varying wash times. In some embodiments, one or more stabilizing mutations are combined to increase the stability of the

affinity matured target antigen binding molecule, for example, by shuffling to create a second-stage combinatorial library from such mutants and conducting a second round of panning followed by a binding selection.

[00107] In some embodiments, the affinity matured target antigen binding molecule comprises an equivalent or better affinity to a target antigen protein (such as human target antigen protein) as that of a target antigen binding parental molecule, but that has reduced cross reactivity, or in some embodiments, increased cross reactivity, with selected substances, such as ligands, proteins, antigens, or the like, other than the target antigen epitope for which the target antigen binding parental molecule is specific, or is designed to be specific for. In regard to the latter, an affinity matured target antigen binding molecule, in some embodiments, is more successfully tested in animal models if the affinity matured target antigen binding molecule is reacted with both human target and the corresponding target of the animal model, *e.g.* mouse target or cynomolgus target. In some embodiments, the parental target antigen binding molecule binds to human target antigen with an affinity of about 500 nM or less, 400 nM or less, 300 nM or less, 200 nM or less, 100 nM or less, 50 nM or less, 10 nM or less, and to cynomolgus EpCAM with an affinity of about 500 nM or less, 400 nM or less, 300 nM or less, 200 nM or less, 100 nM or less, 50 nM or less, 15 nM or less, or 10 nM or less. In some embodiments, the affinity matured target antigen binding molecule, identified after one round of panning, binds to human target antigen with an affinity of about 5 nM or less, such as 1 nM or less, and to cynomolgus target antigen with an affinity of about 7.5 nM or less, such as 1 nM or less. In some embodiments, the affinity matured target antigen binding molecule, identified after two rounds of panning, binds to human target antigen with an affinity of about 2.5 nM or less, and to cynomolgus target antigen with an affinity of about 3.5 nM or less.

[00108] In some embodiments, the domains of the immune cell engaging protein are linked by one or more internal linkers. In certain embodiments, the internal linkers are "short," *i.e.*, consist of 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acid residues. Thus, in certain instances, the internal linkers consist of about 12 or less amino acid residues. In the case of 0 amino acid residues, the internal linker is a peptide bond. In certain embodiments, the internal linkers are "long," *i.e.*, consist of 15to 25 amino acid residues. In some embodiments, the internal linkers consist of about 3 to about 15, for example 8, 9 or 10 contiguous amino acid residues. Regarding the amino acid composition of the internal linkers, peptides are selected with properties that confer flexibility to the target antigen binding proteins, do not interfere with the binding domains as well as resist cleavage from proteases. For example, glycine and serine residues generally provide protease resistance. Examples of internal linkers suitable for linking the domains in the target antigen binding proteins include but are not limited to $(GS)_n$ (SEQ ID No.

3859), $(GGS)_n$ (SEQ ID No. 3860), $(GGGS)_n$ (SEQ ID No. 3861), $(GGSG)_n$ (SEQ ID No. 3862), $(GGSGG)_n$ (SEQ ID No. 3863), $(GGGGS)_n$ (SEQ ID No. 3864), $(GGGGG)_n$ (SEQ ID No. 3865), or $(GGG)_n$ (SEQ ID No. 3866), wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. In one embodiment, the linker is (GGGGSGGGGSGGGGSGGGGS)(SEQ ID No. 3867), (GGGGSGGGGSGGGGS) (SEQ ID No. 3868), LPETG (SEQ ID NO. 3869), (GGGGSGGGS) (SEQ ID No. 3871) or SGGG (SEQ ID NO. 3872).

[00109] In some embodiments, the immune cell engaging protein described herein comprise a polypeptide having a sequence described in SEQ ID NOs: 3218-3462 and subsequences thereof. In some embodiments, the immune cell engaging protein comprises a polypeptide having at least 70%-95% or more identity to a sequence described in SEQ ID NO: 3218-3462. In some embodiments, the immune cell engaging protein comprises a polypeptide having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence described in SEQ ID NO: 3218-3462. In some embodiments, the immune cell engaging protein has a sequence comprising at least a portion of a sequence described in SEQ ID NO: 3218-3462. In some embodiments, the immune cell engaging protein comprises a polypeptide comprising one or more of the sequences described in SEQ ID NO: 3218-3462.

[00110] In some embodiments, the immune cell engaging protein described herein comprise a polypeptide having a sequence described in SEQ ID NOs: 3255, 3340, 3376, and 3462 and subsequences thereof. In some embodiments, the immune cell engaging protein comprises a polypeptide having at least 70%-95% or more identity to a sequence described in SEQ ID NO: 3255, 3340, 3376, and 3462. In some embodiments, the immune cell engaging protein comprises a polypeptide having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence described in SEQ ID NO: 3255, 3340, 3376, and 3462. In some embodiments, the immune cell engaging protein has a sequence comprising at least a portion of a sequence described in SEQ ID NO: 3255, 3340, 3376, and 3462. In some embodiments, the immune cell engaging protein comprises a polypeptide comprising one or more of the sequences described in SEQ ID NO: 3255, 3340, 3376, and 3462.

CD19 Binding Domain

[00111] Described herein are immune cell engaging proteins that comprise a CD19 binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins

comprising a CD19 binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00112] The CD19 binding domain, in some embodiments, are specific for CD19 expressed on cell surface. The anti-CD19 antibodies disclosed herein, in some instances, show high binding affinity to CD19 (*e.g.*, cell-surface CD19), high stability, and/or bind to different CD19 epitopes compared to FMC63, which is an anti-CD19 scFv. CD19 is a 95 kDa transmembrane glycoprotein expressed primarily on B lineage cells and follicular dendritic cells. It is a member of the immunoglobulin super family. CD19 molecules from various species are well known in the art. For example, the amino acid sequence of human CD19 can be found under GenBank accession no. AAA69966. CD19 plays essential roles in B cell malignancies and autoimmunity. CD19 is reported to be expressed on the surface of cancer cells in 90% of acute lymphoblastic leukemia (ALL) patients, as well as on cancer cells of B-cell non- Hodgkin' s lymphoma (NHL) and chronic lymphocytic leukemia (CLL) patients. Therefore, CD19 has been considered as a promising target for immunotherapy of cancers of B cell lineage. *See, e.g.*, Stanciu-Herrera *et al.*, Leuk Res. 2008; 32:625-32; and Le Gall *et al.*, FEBS Lett. 1999; 453:164-8.

[00113] In some embodiments, the CD19 binding domain comprises a sequence that is at least about 70% to about 99% or more identical to a sequence selected from the group consisting of SEQ ID Nos.: 3771-3792. In some embodiments, the CD19 binding domain comprises a sequence that is at least about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID Nos.: 3771-3792. In some embodiments, the CD19 binding domain comprises a sequence selected from the group consisting of SED ID Nos.: 3771-3792.

CD20 Binding Domain

[00114] Described herein are immune cell engaging proteins that comprise a CD20 binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising a CD20 binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00115] CD20 molecule is a non-glycosylated phosphoprotein specifically labeled on the surface of human lymphocyte subgroup (B cell group). It consists of 297 amino acids with a molecular weight of 33-37 kDa, and is expressed on the surface of more than 95% of B cells. CD20 molecule exists in both normal B cells and malignant cells, and is

especially expressed in more than 90% of B-cell non-Hodgkin's lymphoma. The CD20 molecule has four transmembrane regions, and the amino terminus and the carboxy terminus are located on the inner side of the plasma membrane. Between the third transmembrane region and the fourth transmembrane region, there is a loop region composed of 43 amino acid residues, which constitutes the main epitope. The CD20 antigen molecule is relatively exposed and accessible. When CD20 is close to each other under the action of antibodies, the polymer formed by cross-linking or even super-crosslinking functions as a calcium ion channel, allowing extracellular calcium ions to flow into the cells; in addition, the tyrosine protein kinases of the Src family activate each other due to proximity. Signaling pathways are initiated and endogenous calcium stores are mobilized, both of which lead to an increase in intracellular calcium ion concentration and then affect the operation of cell cycle, regulate cell proliferation and differentiation and even lead to the occurrence of apoptosis. Although the actual role of CD20 in promoting the proliferation and differentiation of B cells is not clear, CD20 provides an important target for antibody-mediated therapy, which can be used for controlling the B cells involved in cancers and autoimmune diseases.

[00116] In some embodiments, the CD20 binding domain comprises a sequence that is at least about 70% to about 99% or more identical to a sequence selected from the group consisting of SEQ ID Nos.: 3793-3808 and 3880. In some embodiments, the CD20 binding domain comprises a sequence that is at least about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID Nos.: 3793-3808 and 3880. In some embodiments, the CD20 binding domain comprises a sequence of SED ID No.: 3793-3808 and 3880.

CD33 Binding Domain

[00117] Described herein are immune cell engaging proteins that comprise a CD33 binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising a CD33 binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00118] CD33 (also known as Siglec-3, SIGLEC3, gp67, p67) is a 67 kDa plasma membrane protein that binds to sialic acid and is a member of the sialic acid-binding Ig-related lectin (SIGLEC) family of proteins. Siglec proteins are thought to be involved in diverse biological processes such as hematopoiesis, neuronal development and immunity (Vinson et al, J. Biol. Chem. 271 :9267-9272 (1996)). Studies also suggest that Siglec

proteins mediate cell adhesion/cell signaling through recognition of sialyated cell surface glycans (Kelm et al, Glycoconj. J. 13:913-926 (1996); Kelm et al, Eur. J. Biochem. 255:663- 672 (1998); Vinson et al., J Biol. Chem. 271 :9267-9272 (1996)). The extracellular portion of CD33 contains two immunoglobulin domains (one IgV domain and one IgC2 domain). The IgV domain is distal to the membrane whereas the IgC2 domain is proximal to the membrane. The intracellular portion of CD33 contains immunoreceptor tyrosine-based inhibitory motifs (ITIMs). In the immune response, CD33 may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) that block signal transduction through dephosphorylation of signaling molecules.

[00119] CD33 is known to be expressed on myeloid cells. CD33 expression has also been reported on a number of malignant cells. Anti-CD33 agents are generally allocated in four groups: naked antibodies, antibody toxin conjugates, radionuclide conjugates, and bispecific antibodies. Although CD33 has been targeted for treatment of cancer, *e.g.*, acute myeloid leukemia, no effective CD33-targeted treatments are currently on the market. Existing anti-CD33 agents suffer from, inter alia, inferior tumor antigen binding avidity and short *in vivo* half-life.

[00120] In some embodiments, the CD33 binding domain comprises a sequence that is at least about 70% to about 99% or more identical to a sequence selected from the group consisting of SEQ ID Nos.: 3809-3823. In some embodiments, the CD33 binding domain comprises a sequence that is at least about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to a sequence selected from the group consisting of SEQ ID Nos.: 3809-3823. In some embodiments, the CD33 binding domain comprises a sequence selected from the group consisting of SEQ ID Nos.: 3809-3823.

Prostate Specific Membrane Antigen (PSMA) Binding Proteins

[00121] Described herein are immune cell engaging proteins that comprise a PSMA binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising a PSMA binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00122] PSMA is a 100 kD Type II membrane glycoprotein expressed in prostate tissues having sequence identity with the transferrin receptor with NAALADase activity. PSMA is expressed in increased amounts in prostate cancer, and elevated levels of PSMA are also detectable in the sera of these patients. PSMA expression increases with

disease progression, becoming highest in metastatic, hormone-refractory disease for which there is no present therapy.

[00123] In some embodiments, the PSMA binding domain comprises the following formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues, and wherein r1 comprises SEQ ID No. 462, SEQ ID No. 463, SEQ ID No. 464, or SEQ ID NOL 465, r2 comprises SEQ ID No. 466, SEQ ID NO. 467, SEQ ID No. 468, SEQ ID No. 469, SEQ ID No. 470, SEQ ID No. 471, SEQ ID No. 472, or SEQ ID NO: 473, and r3 comprises SEQ ID No. 474, or SEQ ID NO: 475.

[00124] In some embodiments, PSMA binding domains described herein comprise a polypeptide having a sequence described in SEQ ID NO: 462-489 and subsequences thereof. In some embodiments, the PSMA binding domain comprises a polypeptide having at least 70%-95% or more homology to a sequence described in SEQ ID NO: 462-489. In some embodiments, the PSMA binding domain comprises a polypeptide having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence described in SEQ ID NO: 462-489. In some embodiments, the PSMA binding domain has a sequence comprising at least a portion of a sequence described in SEQ ID NO: 462-489. In some embodiments, the HSA binding domain comprises a polypeptide comprising one or more of the sequences described in SEQ ID NO: 462-489.

[00125] In some embodiments, PSMA binding domains described herein comprise a single domain antibody with a CDR1 comprising SEQ ID NO: 462-465. In some embodiments, PSMA binding domains described herein comprise a single domain antibody with a CDR2 comprising SEQ ID NO: 466-473. In some embodiments, PSMA binding domains described herein comprise a single domain antibody with a CDR3 comprising SE ID NO: 474 and 475.

Mesothelin (MSLN) Binding Proteins

[00126] Described herein are immune cell engaging proteins that comprise an MSLN binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising an MSLN binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00127] MSLN is a GPI-linked membrane bound tumor antigen. MSLN is overexpressed ovarian, pancreatic, lung and triple-negative breast cancers and mesothelioma. Normal tissue expression of MSLN is restricted to single-cell, mesothelial

layers lining the pleural, pericardial, and peritoneal cavities. Overexpression of MSLN is associated with poor prognosis in lung adenocarcinoma and triple-negative breast cancer. MSLN has been used as cancer antigen for numerous modalities, including immunotoxins, vaccines, antibody drug conjugates and CAR-T cells. Early signs of clinical efficacy have validated MSLN as a target, but therapies with improved efficacy are needed to treat MSLN-expressing cancers.

[00128] Mesothelin is a glycoprotein present on the surface of cells of the mesothelial lining of the peritoneal, pleural and pericardial body cavities. The mesothelin gene (*MSLN*) encodes a 71 kD precursor protein that is processed to a 40 kD protein termed mesothelin, which is a glycosyl-phosphatidylinositol-anchored glycoprotein present on the cell surface (Chang, *et al*, Proc Natl Acad Sci USA (1996) 93:136-40). The mesothelin cDNA was cloned from a library prepared from the HPC-Y5 cell line (Kojima *et al*. (1995) J. Biol. Chem. 270:21984-21990). The cDNA also was cloned using the monoclonal antibody K1, which recognizes mesotheliomas (Chang and Pastan (1996) Proc. Natl. Acad. Sci. USA 93:136-40). Mesothelin is a differentiation antigen whose expression in normal human tissues is limited to mesothelial cells lining the body cavity, such as the pleura, pericardium and peritoneum. Mesothelin is also highly expressed in several different human cancers, including mesotheliomas, pancreatic adenocarcinomas, ovarian cancers, stomach and lung adenocarcinomas. (Hassan, *et al*., Eur J Cancer (2008) 44:46-53) (Ordonez, Am J Surg Pathol (2003) 27:1418-28; Ho, *et al*., Clin Cancer Res (2007) 13:1571-5). Mesothelin is overexpressed in a vast majority of primary pancreatic adenocarcinomas with rare and weak expression *see*n in benign pancreatic tissue. Argani P, *et al*. Clin Cancer Res. 2001; 7(12):3862-3868. Epithelial malignant pleural mesothelioma (MPM) universally expresses mesothelin while sarcomatoid MPM likely does not express mesothelin. Most serous epithelial ovarian carcinomas, and the related primary peritoneal carcinomas, express mesothelin.

[00129] Mesothelin can also be used a marker for diagnosis and prognosis of certain types of cancer because trace amounts of mesothelin can be detected in the blood of some patients with mesothelin-positive cancers (Cristaudo *et al*., Clin. Cancer Res. 13:5076-5081, 2007). It has been reported that mesothelin may be released into serum through deletion at its carboxyl terminus or by proteolytic cleavage from its membrane bound form (Hassan *et al*., Clin. Cancer Res. 10:3937-3942, 2004). An increase in the soluble form of mesothelin was detectable several years before malignant mesotheliomas occurred among workers exposed to asbestos (Creaney and Robinson, Hematol. Oncol. Clin. North Am. 19:1025-1040, 2005). Furthermore, patients with ovarian, pancreatic,

and lung cancers also have elevated soluble mesothelin in serum (Cristaudo *et al.*, Clin. Cancer Res. 13:5076-5081, 2007; Hassan *et al.*, Clin. Cancer Res. 12:447-453, 2006; Croso *et al.*, Cancer Detect. Prev. 30:180-187, 2006). Accordingly, mesothelin is an appropriate target for methods of disease prevention or treatment and there is a need for effective antibodies specific for mesothelin.

[00130] It has been shown that cell surface mature mesothelin comprises three distinct domains, namely Regions I (comprising residues 296–390), II (comprising residues 391–486), and III (comprising residue 487–598). (Tang *et al.*, A human single-domain antibody elicits potent antitumor activity by targeting an epitope in mesothelin close to the cancer cell surface, Mol. Can. Therapeutics, 12(4): 416-426, 2013). The first antibodies generated against mesothelin for therapeutic intervention were designed to interfere with the interaction between mesothelin and CA-125. Phage display identified the Fv SS, which was affinity optimized and used to generate a recombinant immunotoxin targeting mesothelin, SS1P. The MORAb-009 antibody amatuximab, which also uses SS1, recognizes a non-linear epitope in the amino terminal 64 amino acids of mesothelin, within region I. The SS1 Fv was also used to generate chimeric antigen receptor-engineered T cells. Recently, new anti-mesothelin antibodies have been reported that recognize other regions of the mesothelin protein. The present disclosure provides, in certain embodiments, MSLN targeting immune cell engaging proteins containing binding domains which specifically bind to MSLN on the surface of tumor target cells.

[00131] In some embodiments, the MSLN binding domain binds to a protein comprising the sequence of SEQ ID NO: 3204. In some embodiments, the MSLN binding domain binds to a protein comprising a truncated sequence compared to SEQ ID NO: 3204.

[00132] In some embodiments, the MSLN binding domains disclosed herein recognize full-length mesothelin. In certain instances, the MSLN binding domains disclosed herein recognize an epitope in region I (comprising amino acid residues 296-390 of SEQ ID NO: 3204), region II (comprising amino acid residue 391-486 of SEQ ID NO: 3204), or region III (comprising amino acid residues 487-598 of SEQ ID NO: 3204) of mesothelin. It is contemplated that the MSLN binding domains of the present disclosure may, in some embodiments, recognize and bind to epitopes that are located outside regions I, II, or III of mesothelin. In yet other embodiments are disclosed MSLN binding domains that recognize and bind to an epitope different than the MORAb-009 antibody.

[00133] In some embodiments, the MSLN binding domain is a polypeptide comprising an amino acid sequence that is comprised of four framework regions/sequences (f1-f4) interrupted by three complementarity determining regions/sequences, as represented by the formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues. The framework residues of the MSLN binding protein of the present disclosure comprise, for example, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, or 94 amino acid residues, and the complementarity determining regions comprise, for example, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 amino acid residues. In some embodiments, the MSLN binding domain comprises an amino acid sequence selected from SEQ ID NOs: 607-650, or a sequence comprising at least 75% to about 95% or more (*e.g.*, 96%, 97%, 98%, 99%, or more) identity to a sequence selected from the group consisting of SEQ ID NOs: 605-670.

[00134] In some embodiments, the CDR1 comprises the amino acid sequence as set forth in SEQ ID NO: 490 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in SEQ ID NO: 490. In some embodiments, the CDR2 comprises a sequence as set forth in SEQ ID NO: 3505 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in SEQ ID NO: 3505. In some embodiments, the CDR3 comprises a sequence as set forth in SEQ ID NO: 3506 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in SEQ ID NO: 3506.

[00135] In some embodiments, the CDR1 comprises the amino acid sequence as set forth in SEQ ID NO: 518 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in SEQ ID NO: 518. In some embodiments, the CDR2 comprises a sequence as set forth in SEQ ID NO: 3507 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in SEQ ID NO: 3507. In some embodiments, the CDR3 comprises a sequence as set forth in SEQ ID NO: 3508 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in SEQ ID NO: 3508.

[00136] In some embodiments, the CDR1 comprises the amino acid sequence as set forth in any one of SEQ ID Nos.: 490-528 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in any one of SEQ ID Nos.: 490-528. In some embodiments, the CDR2 comprises a sequence as set forth in any one of SEQ ID Nos.: 529-567 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in any one of SEQ ID Nos.: 529-567. In some

embodiments, the CDR3 comprises a sequence as set forth in any one of SEQ ID Nos.: 568-606 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in any one of SEQ ID Nos.: 568-606.

[00137] In various embodiments, the MSLN binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 607-650.

[00138] In various embodiments, a complementarity determining region of the MSLN binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 490, SEQ ID NO: 518, or any one of SEQ ID Nos.: 490-528.

[00139] In various embodiments, a complementarity determining region of the MSLN binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 3505, SEQ ID NO: 3507, or any one of SEQ ID Nos.: 529-567.

[0027] In various embodiments, a complementarity determining region of the MSLN binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID NO: 3506, SEQ ID NO: 3508, or any one of SEQ ID Nos.: 568-606.

[00140] In some embodiments, any of the foregoing MSLN binding domains (*e.g.*, anti-MSLN single domain antibodies of SEQ ID NOs: 607-650) are affinity peptide tagged for ease of purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as 6X-his (SEQ ID NO: 3503).

[00141] In certain embodiments, the MSLN binding domains of the present disclosure preferentially bind membrane bound mesothelin over soluble mesothelin. Membrane bound mesothelin refers to the presence of mesothelin in or on the cell membrane surface of a cell that expresses mesothelin. Soluble mesothelin refers to mesothelin that is no longer on in or on the cell membrane surface of a cell that expresses or expressed mesothelin. In certain instances, the soluble mesothelin is present in the blood and/or lymphatic circulation in a subject. In one embodiment, the MSLN binding domains bind membrane-bound mesothelin at least 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 100 fold, 500 fold, or 1000 fold greater than soluble mesothelin. In one embodiment, the MSLN targeting immune cell engaging proteins of the present disclosure preferentially bind membrane-bound mesothelin 30 fold greater than soluble mesothelin. Determining the preferential binding of an antigen binding protein to membrane bound MSLN over soluble MSLN can be readily determined using assays well known in the art.

B Cell Maturation Antigen (BCMA) Binding Proteins

[00142] Described herein are immune cell engaging proteins that comprise an BCMA binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising an BCMA binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00143] B cell maturation antigen (BCMA, TNFRSF17, CD269) is a transmembrane protein belonging to the tumor necrosis family receptor (TNFR) super family that is primarily expressed on terminally differentiated B cells. BCMA expression is restricted to the B cell lineage and mainly present on plasma cells and plasmablasts and to some extent on memory B cells, but virtually absent on peripheral and naive B cells. BCMA is also expressed on multiple myeloma (MM) cells, on leukemia cells and lymphoma cells.

[00144] BCMA was identified through molecular analysis of a t(4;16)(q26;p13) translocation found in a human intestinal T cell lymphoma and an in-frame sequence was mapped to the 16p13.1 chromosome band.

[00145] Human BCMA cDNA has an open reading frame of 552 bp that encodes a 184 amino acid polypeptide. The BCMA gene is organized into three exons that are separated by two introns, each flanked by GT donor and AG acceptor consensus splicing sites, and codes for a transcript of 1.2 kb. The structure of BCMA protein includes an integral transmembrane protein based on a central 24 amino acid hydrophobic region in an alpha-helix structure.

[00146] The murine BCMA gene is located on chromosome 16 syntenic to the human 16p13 region, and also includes three exons that are separated by two introns. The gene encodes a 185 amino acid protein. Murine BCMA mRNA is expressed as a 404 bp transcript at the highest levels in plasmacytoma cells (J558) and at modest levels in the A20 B cell lymphoma line. Murine BCMA mRNA transcripts have also been detected at low levels in T cell lymphoma (EL4, BW5147) and dendritic cell (CB1D6, D2SC1) lines in contrast to human cell lines of T cell and dendritic cell origin. The murine BCMA cDNA sequence has 69.3% nucleotide identity with the human BCMA cDNA sequence and slightly higher identity (73.7%) when comparing the coding regions between these two cDNA sequences. Mouse BCMA protein is 62% identical to human BCMA protein and, like human BCMA, contains a single hydrophobic region, which may be an internal transmembrane segment. The N-terminal 40 amino acid domain of both murine and human BCMA protein have six conserved cysteine residues, consistent with the formation of a cysteine repeat motif found in the extracellular domain of TNFRs. Similar to members of the TNFR superfamily, BCMA protein contains a conserved aromatic residue four to six residues C-terminal from the first cysteine.

[00147] BCMA is not expressed at the cell surface, but rather, is located on the Golgi apparatus. The amount of BCMA expression is proportional to the stage of cellular differentiation (highest in plasma cells).

[00148] BCMA is involved in B cell development and homeostasis due to its interaction with its ligands BAFF (B cell activating factor, also designated as TALL-1 or TNFSF13B) and APRIL (A proliferation inducing ligand). BCMA regulates different aspects of humoral immunity, B cell development and homeostasis along with its family members TACI (transmembrane activator and cyclophylin ligand interactor) and BAFF-R (B cell activation factor receptor, also known as tumor necrosis factor receptor superfamily member 13C). Expression of BCMA appears rather late in B cell differentiation and contributes to the long-term survival of plasmablasts and plasma cells in the bone marrow. BCMA also supports growth and survival of multiple myeloma (MM) cells. BCMA is mostly known for its functional activity in mediating the survival of plasma cells that maintain long-term humoral immunity.

[00149] The present disclosure provides, in certain embodiments, single domain proteins which specifically bind to BCMA on the surface of tumor target cells.

[00150] In some embodiments, the BCMA binding domain binds to a protein comprising the sequence of SEQ ID NO: 3201, 3202 or 3203. In some embodiments, the BCMA binding

domain binds to a protein comprising a truncated sequence compared to SEQ ID NO: 3201, 3202 or 3203.

[00151] In some embodiments, the BCMA binding protein of the present disclosure is a polypeptide comprising an amino acid sequence that is comprised of four framework regions/sequences (f1-f4) interrupted by three complementarity determining regions/sequences, as represented by the formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues. The r1 residues of the BCMA binding protein of the present disclosure comprise, for example, amino acid residues 26, 27, 28, 29, 30, 31, 32, 33 and 34; the r2 residues of the BCMA binding protein of the present disclosure comprise, for example, amino acid residues, for example, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59,60, 61, 62 and 63; and the r3 residues of the BCMA binding protein of the present disclosure comprise, for example, amino acid residues, for example, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107 and 108. In some embodiments, the BCMA binding protein comprises an amino acid sequence selected from SEQ ID NOs: 346-460, or a sequence comprising at least 75% to about 95% or more (*e.g.*, 96%, 97%, 98%, 99%, or more) identity to a sequence selected from the group consisting of SEQ ID NOs: 346-460.

[00152] In some embodiments, an exemplary CDR1 comprises the amino acid sequence as set forth in SEQ ID NO: 1-115. In some embodiments, another exemplary CDR2 comprises the amino acid sequence as set forth in SEQ ID NO: 116-230. In some embodiments, another exemplary CDR3 comprises the amino acid sequence as set forth in SEQ ID NO: 231-345.

[00153] In various embodiments, the BCMA binding protein of the present disclosure has a CDR1 that has an amino acid sequence that is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 1-115.

[00154] In various embodiments, the BCMA binding protein of the present disclosure has a CDR2 that has an amino acid sequence that is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 116-230.

[00155] In various embodiments, a complementarity determining region of the BCMA binding protein of the present disclosure has a CDR3 that has an amino acid sequence that is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 231-345.

[00156] In various embodiments, a BCMA binding protein of the present disclosure has an amino acid sequence that is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 346-460.

[00157] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 346. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 347. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 348. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 349. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 350. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 351. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 352. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 353. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 354. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 355. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 356. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 357. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 358. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 359.

[00158] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 360. In some embodiments, the BCMA binding protein

is a single domain antibody comprising the sequence of SEQ ID NO: 361. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 362. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 363. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 364. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 365. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 366. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 367. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 368. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 369.

[00159] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 370. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 371. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 372. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 373. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 374. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 375. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 376. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 377. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 378. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 379.

[00160] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 380. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 381. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 382. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 383. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 384. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 385. In some embodiments, the BCMA binding protein is a single

domain antibody comprising the sequence of SEQ ID NO: 386. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 387. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 388. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 389.

[00161] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 390. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 391. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 392. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 393. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 394. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 395. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 396. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 397. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 398. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 399.

[00162] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 400. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 401. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 402. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 403. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 404. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 405. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 406. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 407. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 408. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 409.

[00163] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 410. In some embodiments, the BCMA binding protein

is a single domain antibody comprising the sequence of SEQ ID NO: 411. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 412. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 413. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 414. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 415. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 416. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 417. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 418. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 419.

[00164] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 420. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 421. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 422. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 423. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 424. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 425. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 426. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 427. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 428. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 429.

[00165] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 430. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 431. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 432. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 433. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 434. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 435. In some embodiments, the BCMA binding protein is a single

domain antibody comprising the sequence of SEQ ID NO: 436. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 437. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 438. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 439.

[00166] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 440. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 441. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 442. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 443. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 444. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 445. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 446. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 447. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 448. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 449.

[00167] In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 450. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 451. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 452. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 453. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 454. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 455. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 456. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 457. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 458. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 459. In some embodiments, the BCMA binding protein is a single domain antibody comprising the sequence of SEQ ID NO: 460.

[00168] In some embodiments, any of the foregoing BCMA binding domains are affinity peptide tagged for ease of purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as a His tag or 6X-his (His-His-His-His-His-His; SEQ ID NO: 3503).

[00169] In certain embodiments, the BCMA binding domains of the present disclosure preferentially bind membrane bound BCMA over soluble BCMA. Membrane bound BCMA refers to the presence of BCMA in or on the cell membrane surface of a cell that expresses BCMA. Soluble BCMA refers to BCMA that is no longer on in or on the cell membrane surface of a cell that expresses or expressed BCMA. In certain instances, the soluble BCMA is present in the blood and/or lymphatic circulation in a subject. In one embodiment, the BCMA binding domains bind membrane-bound BCMA at least 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 100 fold, 500 fold, or 1000 fold greater than soluble BCMA. In one embodiment, the BCMA targeting immune cell engaging proteins of the present disclosure preferentially bind membrane-bound BCMA 30 fold greater than soluble BCMA. Determining the preferential binding of an antigen binding protein to membrane bound BCMA over soluble BCMA can be readily determined using assays well known in the art.

Delta-like Ligand 3 (DLL3) binding proteins

[00170] DLL3 (also known as Delta-like Ligand 3 or SCDO1) is a member of the Delta-like family of Notch DSL ligands. Representative DLL3 protein orthologs include, but are not limited to, human (Accession Nos. NP_058637 and NP_982353), chimpanzee (Accession No. XP_003316395), mouse (Accession No. NP_031892), and rat (Accession No. NP_446118). In humans, the DLL3 gene consists of 8 exons spanning 9.5 kbp located on chromosome 19q13. Alternate splicing within the last exon gives rise to two processed transcripts, one of 2389 bases (Accession No. NM_016941) and one of 2052 bases (Accession No. NM_203486). The former transcript encodes a 618 amino acid protein (Accession No. NP_058637), whereas the latter encodes a 587 amino acid protein (Accession No. NP_982353). These two protein isoforms of DLL3 share overall 100% identity across their extracellular domains and their transmembrane domains, differing only in that the longer isoform contains an extended cytoplasmic tail containing 32 additional residues at the carboxy terminus of the protein. The extracellular region of the DLL3 protein, comprises six EGF-like domains, the single DSL domain and the N-terminal domain. Generally, the EGF domains are recognized as occurring at about amino acid residues 216-249 (domain 1), 274-310 (domain 2), 312-351 (domain 3), 353-389 (domain 4), 391-427 (domain 5) and 429-465 (domain 6), with the DSL domain at about amino acid residues 176-215 and the N-terminal domain at about amino acid residues 27-175 of hDLL3. Each of the EGF-like domains, the DSL domain and the N-terminal domain comprise part of the DLL3

protein as defined by a distinct amino acid sequence. The EGF-like domains are termed, in some embodiments, as EGF1 to EGF6 with EGF1 being closest to the N-terminal portion of the protein. In general, DSL ligands are composed of a series of structural domains: a unique N-terminal domain, followed by a conserved DSL domain, multiple tandem epidermal growth factor (EGF)-like repeats, a transmembrane domain, and a cytoplasmic domain not highly conserved across ligands but one which contains multiple lysine residues that are potential sites for ubiquitination by unique E3 ubiquitin ligases. The DSL domain is a degenerate EGF-domain that is necessary but not sufficient for interactions with Notch receptors. Additionally, the first two EGF-like repeats of most DSL ligands contain a smaller protein sequence motif known as a DOS domain that co-operatively interacts with the DSL domain when activating Notch signaling.

[00171] In some embodiments, the disclosed DLL3 immune cell engaging proteins of this disclosure are generated, fabricated, engineered or selected so as to react with a selected domain, motif or epitope within a DLL3 protein. In some embodiments, the DLL3 targeting immune cell engaging protein binds to the DSL domain and, in some embodiments, binds to an epitope comprising G203, R205, P206 within the DSL domain.

[00172] The DLL3 binding domain of the DLL3 targeting immune cell engaging proteins of the present disclosure are, in some embodiments, engineered fabricated and/or selected to react with both isoform(s) of DLL3 or a single isoform of the protein or, conversely, comprise a pan-DLL binding domain that reacts or associates with at least one additional DLL family member in addition to DLL3. In some embodiments, the DLL3 binding domain, such as DLL3 binding domain are engineered, fabricated, and/or selected so that they react with domains (or epitopes therein) that are exhibited by DLL3 only or with domains that are at least somewhat conserved across multiple or all DLL family members.

[00173] In some embodiments the DLL3 binding domain associates or binds to a specific epitope, portion, motif or domain of DLL3. Both DLL3 isoforms incorporate an identical extracellular region comprising at least an N-terminal domain, a DSL (Delta/Serrate/lag-2) domain and six EGF-like domains (*i.e.*, EGF1-EGF6). Accordingly, in certain embodiments the DLL3 binding domain binds or associate with the N-terminal domain of DLL3 (amino acids 27-175 in the mature protein) while in other embodiments the DLL3 binding domain associates with the DSL domain (amino acids 176-215) or epitope therein. In other aspects of the present disclosure the DLL3 binding domain associates or bind to a specific epitope located in a particular EGF-like domain of DLL3. In some embodiments, the DLL3 binding domain associates or binds to an epitope located in EGF1 (amino acids 216-249), EGF2 (amino acids 274-310), EGF3 (amino acids 312-351), EGF4 (amino acids 353-389), EGF5 (amino acids

391.427) or EGF6 (amino acids 429-465). In some embodiments, each of the aforementioned domains comprises more than one epitope and/or more than one bin. In some embodiments the DLL3 binding domain binds, reacts or associates with the DSL domain or an epitope therein. In other embodiments the DLL3 binding domain binds, reacts or associates with a particular EGF-like domain or an epitope therein. In some embodiments the DLL3 binding domain binds, reacts or associates with the N-terminal domain or an epitope therein.

[00174] In some embodiments, the DLL3 binding proteins of this disclosure, such as the DLL3 binding domain of the immune cell engaging proteins of this disclosure binds to the full length DLL3 protein or to a fragment thereof, such as epitope containing fragments within the full length DLL3 protein, as described above. In some cases, the epitope containing fragment comprises antigenic or immunogenic fragments and derivatives thereof of the DLL3 protein. Epitope containing fragments, including antigenic or immunogenic fragments, are, in some embodiments, 12 amino acids or more, 20 amino acids or more, 50 or 100 amino acids or more. The DLL3 fragments, in some embodiments, comprises 95% or more of the length of the full protein, 90% or more, 75% or 50% or 25% or 10% or more of the length of the full protein. In some embodiments, the epitope-containing fragments of DLL3 including antigenic or immunogenic fragments are capable of eliciting a relevant immune response in a patient. Derivatives of DLL3 include, in some embodiments, variants on the sequence in which one or more (*e.g.,* 1-20 such as 15 amino acids, or up to 20% such as up to 10% or 5% or 1% by number of amino acids based on the total length of the protein) deletions, insertions or substitutions have been made to the DLL3 sequence provided in SEQ ID No. 3216 (UniProtKB Accession Q9NYJ7). In some embodiments, substitutions comprise conservative substitutions. Derivatives and variants of DLL3, in some examples, have essentially the same biological function as the DLL3 protein from which they are derived. For instance, derivatives and variants of DLL3 are, in some cases, comparably antigenic or immunogenic to the protein from which they are derived, have either the ligand-binding activity, or the active receptor-complex forming ability, or preferably both, of the protein from which they are derived, and have the same tissue distribution as DLL3.

[00175] In some embodiments, the DLL3 binding domain binds to a protein comprising the sequence of SEQ ID No. 3216 (UniProtKB Accession Q9NYJ7). In some embodiments, the DLL3 binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3216 (UniProtKB Accession Q9NYJ7). In some embodiments, the DLL3 binding domain binds to a protein comprising the sequence of SEQ ID No. 3509 or SEQ ID No. 3217 (which is the mature extracellular domain of a DLL3 protein). In some embodiments, the DLL3 binding domain binds to a protein comprising amino acids 47-492 of SEQ ID No. 3509. In some

embodiments, the DLL3 binding domain recognizes an epitope within amino acids 47-4492 of SEQ ID No. 3509.

[00176] In another example of a substitution to create a variant anti-DLL3 antibody, one or more hypervariable region residues of a parent antibody are substituted. In general, variants are then selected based on improvements in desired properties compared to a parent antibody, for example, increased affinity, reduced affinity, reduced immunogenicity, increased pH dependence of binding.

[00177] In some embodiments, the DLL3 binding domain is a polypeptide comprising an amino acid sequence that is comprised of four framework regions/sequences (f1-f4) interrupted by three complementarity determining regions/sequences, as represented by the formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues. The framework residues of the DLL3 binding protein of the present disclosure comprise, for example, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, or 94 amino acid residues, and the complementarity determining regions comprise, for example, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 amino acid residues. In some embodiments, the DLL3 binding domain comprises an amino acid sequence selected from SEQ ID Nos. 1308-1750. In some embodiments, CDR1 of the DLL3 binding domain comprises a sequence selected from SEQ ID Nos. 1751-2193, or one or more amino acid substitutions relative to a sequence selected from the group consisting of SEQ ID Nos. 1751-2193. In some embodiments, CDR2 comprises a sequence selected from the group consisting of SEQ ID Nos. 2194-2636, or one or more amino acid substitutions relative to a sequence selected from the group consisting of SEQ ID Nos. 2194-2636. In some embodiments, the CDR3 comprises a sequence selected from the group consisting of SEQ ID Nos. 2637-3080, or one or more substitutions relative to a sequence selected from SEQ ID Nos. 2637-3080.

[00178] In some embodiments, the CDR1 comprises an amino acid sequence selected from SEQ ID Nos. 1751-2193 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid selected from SEQ ID Nos. 1751-2193. In some embodiments, the CDR2 comprises an amino acid sequence selected from SEQ ID Nos. 2194-2636 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid sequence selected from SEQ ID Nos. 2194-2636. In some embodiments, the CDR3 comprises an amino acid sequence selected from SEQ ID Nos. 2637-3080 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in a sequence selected from SEQ ID Nos. 2637-3080.

[00179] In some embodiments, the CDR1 comprises an amino acid sequence selected from SEQ ID Nos. 1803-1836 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid selected from SEQ ID Nos. 1803-1836. In some embodiments, the CDR2 comprises an amino acid sequence selected from SEQ ID Nos. 2246-2279 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid sequence selected from SEQ ID Nos. 2246-2279. In some embodiments, the CDR3 comprises an amino acid sequence selected from SEQ ID Nos. 2689-2722 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in a sequence selected from SEQ ID Nos. 2689-2722.

[00180] In some embodiments, the CDR1 comprises an amino acid sequence selected from SEQ ID Nos. 1837-2117 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid selected from SEQ ID Nos. 1837-2117. In some embodiments, the CDR2 comprises an amino acid sequence selected from SEQ ID Nos. 2280-2560 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid sequence selected from SEQ ID Nos. 2280-2560. In some embodiments, the CDR3 comprises an amino acid sequence selected from SEQ ID Nos. 2723-3003 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in a sequence selected from SEQ ID Nos. 2723-3003.

[00181] In some embodiments, the CDR1 comprises an amino acid sequence selected from SEQ ID Nos. 2118-2193 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid selected from SEQ ID Nos. 2118-2193. In some embodiments, the CDR2 comprises an amino acid sequence selected from SEQ ID Nos. 2561-2636 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in an amino acid sequence selected from SEQ ID Nos. 2561-2636. In some embodiments, the CDR3 comprises an amino acid sequence selected from SEQ ID Nos. 3004-3080 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in a sequence selected from SEQ ID Nos. 3004-3080.

[00182] In various embodiments, the DLL3 binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID Nos. 1308-1750. In various embodiments, the DLL3 binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about

90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID Nos. 1360-1393.

[00183] In various embodiments, the DLL3 binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID Nos. 1394-1674.

[00184] In various embodiments, the DLL3 binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to SEQ ID No.1375, or a sequence derived from SEQ ID No. 1375.

[00185] In various embodiments, the DLL3 binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to SEQ ID No.1382, or a sequence derived from SEQ ID No.1382.

[00186] In certain embodiments, the DLL3 binding domains of the present disclosure preferentially bind membrane bound DLL3 over soluble DLL3. Membrane bound DLL3 refers to the presence of DLL3 in or on the cell membrane surface of a cell that expresses DLL3. Soluble DLL3 refers to DLL3 that is no longer on in or on the cell membrane surface of a cell that expresses or expressed DLL3. In certain instances, the soluble DLL3 is present in the blood and/or lymphatic circulation in a subject. In one embodiment, the DLL3 binding proteins bind membrane-bound DLL3 at least 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 100 fold, 500 fold, or 1000 fold greater than soluble DLL3. In one embodiment, the antigen binding proteins of the present disclosure preferentially bind membrane-bound DLL3 30 fold greater than soluble DLL3. Determining the preferential binding of an antigen binding protein to membrane bound DLL3 over soluble DLL3 can be readily determined using assays well known in the art.

[00187] In some embodiments, any of the foregoing DLL3 binding domains (*e.g.,* anti-DLL3 single domain antibodies of SEQ ID Nos. 1308-1750) are affinity peptide tagged for ease of

purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as 6X-his (SEQ ID No. 3503).

[00188] In some embodiments, any of the foregoing DLL3 binding domains (*e.g.*, anti-DLL3 single domain antibodies of SEQ ID Nos. 1308-1750) are affinity peptide tagged for ease of purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as 6X-his (SEQ ID No. 3503).

Epidermal growth factor receptor (EGFR) binding proteins

[00189] Described herein are immune cell engaging proteins that comprise an EGFR binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising an EGFR binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00190] Epidermal growth factor receptor (EGFR) has been causally implicated in human malignancy. Abnormal activity of the Her family of receptors is involved with breast cancer. EGFR, Her-3, and Her-4 are frequently expressed in ovarian granulosa cell tumors (Leibl, S. *et al.*, Gynecol Oncol 101:18-23 (2005). In particular, increased expression of EGFR has been observed in breast, bladder, lung, head, neck and stomach cancer as well as glioblastomas.

[00191] Increased EGFR receptor expression may be associated with increased production of a EGFR ligand, transforming growth factor alpha (TGF-α), by the same tumor cells resulting in receptor activation by an autocrine stimulatory pathway.

[00192] Cetuximab (Erbitux™), an anti-EGFR antibody, has been associated with potentially life-threatening infusion reactions (Thomas, M., Clin J Oncol Nurs. 9(3):332-8 (2005)). Gefitinib (Iressa™) and erlotinib (Tarceva™), both EGFR specific small molecule inhibitors, are associated with a risk of interstitial lung disease (Sandler A, Oncology 20(5 Suppl 2):35-40 (2006)). Individual patients may be predisposed to particular types of complications that affect the choice of drug treatment. There is a need for a greater choice of treatment options which allows physicians to select the therapeutic with the best side effect profile for an individual patient. The present disclosure provides novel polypeptides and protein therapeutics useful in methods of treatment, particularly for treatment of conditions associated with abnormal expression of EGFR.

[00193] Epidermal growth factor receptor (EGFR, also known as HER1 or ErbB1) is a member of the ErbB/HER family of type 1 receptor tyrosine kinases (RTKs). Other members of this family include ErbB2 (HER2 or Neu), ErbB3 (HER3) and ErbB4 (HER4). Known ligands for EGFR include epidermal growth factor (EGF) and transforming growth factor alpha (TGF-

alpha). Ligand binding to EGFR is known to induce tyrosine phosphorylation and receptor dimerization with other ErbB family members.

[00194] RTKs such as EGFR function to allow cells to respond to diverse external stimuli. However, aberrant activation and/or overexpression of EGFR is associated with the development and progression of several human cancers. Accordingly, EGFR is a target for anti-cancer therapies. Approved drugs targeting EGFR include small molecule inhibitors such as gefitinib (Iressa®) and erlotinib (Tarceva®), and anti-EGFR antibodies such as cetuximab (Erbitux®) and panitumumab (Vectibix®). Anti-EGFR antibodies are mentioned in, *e.g.*, U.S. Pat. No. 4,943,533, U.S. Pat. No. 5,844,093, U.S. Pat. No. 7,060,808, U.S. Pat. No. 7,247,301, U.S. Pat. No. 7,595,378, U.S. Pat. No. 7,723,484, and U.S. Pat. No. 7,939,072. There is still a need for having available further options for the treatment of diseases related to the overexpression of EGFR, including, but not limited to, renal cell carcinoma, pancreatic carcinoma, breast cancer, head and neck cancer, prostate cancer, malignant gliomas, osteosarcoma, colorectal cancer, gastric cancer (*e.g.*, gastric cancer with MET amplification), malignant mesothelioma, multiple myeloma, ovarian cancer, small cell lung cancer, non-small cell lung cancer (*e.g.*, EGFR-dependent non-small cell lung cancer), synovial sarcoma, thyroid cancer, or melanoma. The present disclosure provides, in certain embodiments, EGFR binding proteins, EGFR targeting immune cell engaging proteins containing EGFR binding domains which specifically bind to EGFR on the surface of tumor target cells.

[00195] In some embodiments, the EGFR binding domain of this disclosure binds to a protein comprising the sequence of SEQ ID No. 3205 (UniProt Accession No. Q504U8). In some embodiments, the EGFR binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3205. In some embodiments, the EGFR binding domain binds to a protein comprising the sequence of SEQ ID No. 3206 (UniProt Accession No. Q01279). In some embodiments, the EGFR binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3206. In some embodiments, the EGFR binding domain binds to a protein comprising the sequence of SEQ ID No. 3207 (UniProt Accession No. A0A2K5WK39). In some embodiments, the EGFR binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3207.

[00196] In some embodiments, the EGFR binding domains disclosed herein recognize full-length EGFR. In certain instances, the EGFR binding domains disclosed herein recognize an epitope within EGFR, such as, in some cases the EGFR targeting immune cell engaging proteins interact with one or more amino acids found within the extracellular domain of human EGFR (*e.g.*, within extracellular domain I, II, III, and/or IV). The epitope to which the antibodies bind may consist of a single contiguous sequence of 3 or more (*e.g.*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13,

14, 15, 16, 17, 18, 19, 20 or more) amino acids located within the extracellular domain of EGFR. Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) located within the extracellular domain of EGFR.

[00197] In some embodiments, the EGFR binding proteins of this disclosure binds to the full-length EGFR protein or to a fragment thereof, such as epitope containing fragments within the full length EGFR protein, as described above. In some cases, the epitope containing fragment comprises antigenic or immunogenic fragments and derivatives thereof of the EGFR protein. Epitope containing fragments, including antigenic or immunogenic fragments, are, in some embodiments, 12 amino acids or more, *e.g.*, 20 amino acids or more, 50 or 100 amino acids or more. The EGFR fragments, in some embodiments, comprises 95% or more of the length of the full protein, 90% or more, 75% or 50% or 25% or 10% or more of the length of the full protein. In some embodiments, the epitope-containing fragments of EGFR including antigenic or immunogenic fragments are capable of eliciting a relevant immune response in a patient. Derivatives of EGFR include, in some embodiments, variants on the sequence in which one or more (*e.g.*, 1-20 such as 15 amino acids, or up to 20% such as up to 10% or 5% or 1% by number of amino acids based on the total length of the protein) deletions, insertions or substitutions have been made to the EGFR sequence provided in SEQ ID No. 3205, 3206, or 3207.

[00198] In some embodiments, the EGFR binding domain is a polypeptide comprising an amino acid sequence that is comprised of four framework regions/sequences (f1-f4) interrupted by three complementarity determining regions/sequences, as represented by the formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues. The framework residues of the EGFR binding protein of the present disclosure comprise, for example, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, or 94 amino acid residues, and the complementarity determining regions comprise, for example, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 amino acid residues. In some embodiments, the EGFR binding domain comprises an amino acid sequence selected from SEQ ID Nos. 798-846.

[00199] In some embodiments, the EGFR binding domains described herein comprise a polypeptide having a sequence selected from SEQ ID Nos. 798-846, subsequences thereof, and variants thereof. In some embodiments, the EGFR binding protein comprises at least 70%-95% or more identity to a sequence selected from SEQ ID Nos. 798-846, subsequences thereof, and variants thereof. In some embodiments, the EGFR binding protein comprises at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence selected from SEQ ID Nos. 798-846, subsequences thereof, and variants thereof.

[00200] In some embodiments, the CDR1 comprises the amino acid sequence as set forth in any one of SEQ ID Nos. 651-699 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in any one of SEQ ID Nos. 651-699. In some embodiments, the CDR2 comprises a sequence as set forth in any one of SEQ ID Nos. 700-748 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in any one of SEQ ID Nos. 700-748. In some embodiments, the CDR3 comprises a sequence as set forth in any one of SEQ ID Nos. 148-196 or a variant having one, two, three, four, five, six, seven, eight, nine, or ten amino acid substitutions in any one of SEQ ID Nos. 749-797.

[00201] In various embodiments, the EGFR binding domain of the present disclosure is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID Nos. 798-846.

[00202] In various embodiments, a complementarity determining region of the EGFR binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence set forth in any one of SEQ ID Nos. 651-699.

[00203] In various embodiments, a complementarity determining region of the EGFR binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence set forth in any one of SEQ ID Nos. 700-748.

[0027] In various embodiments, a complementarity determining region of the EGFR binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence set forth in any one of SEQ ID Nos. 749-797.

[00204] In some embodiments, any of the foregoing EGFR binding domains (*e.g.*, anti-EGFR single domain antibodies of SEQ ID Nos. 798-846) are affinity peptide tagged for ease of

purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as 6X-his (SEQ ID No. 3503).

[00205] In certain embodiments, the EGFR binding domains of the present disclosure preferentially bind membrane bound EGFR over soluble EGFR Membrane bound EGFR refers to the presence of EGFR in or on the cell membrane surface of a cell that expresses EGFR. Soluble EGFR refers to EGFR that is no longer on in or on the cell membrane surface of a cell that expresses or expressed EGFR. In certain instances, the soluble EGFR is present in the blood and/or lymphatic circulation in a subject. In one embodiment, the EGFR binding domains bind membrane-bound EGFR at least 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 100 fold, 500 fold, or 1000 fold greater than soluble EGFR. In one embodiment, the EGFR targeting immune cell engaging proteins of the present disclosure preferentially bind membrane-bound EGFR 30 fold greater than soluble EGFR. Determining the preferential binding of an antigen binding protein to membrane bound EGFR over soluble EGFR can be readily determined using binding assays. It is contemplated that in some embodiments the EGFR binding protein is fairly small and no more than 25 kDa, no more than 20 kDa, no more than 15 kDa, or no more than 10 kDa in some embodiments. In certain instances, the EGFR binding protein is 5 kDa or less if it is a peptide or small molecule entity.

[00206] In other embodiments, the EGFR binding proteins described herein comprise small molecule entity (SME) binders for EGFR. SME binders are small molecules averaging about 500 to 2000 Da in size and are attached to the EGFR binding proteins by known methods, such as sortase ligation or conjugation. In these instances, the EGFR binding protein comprises a domain comprising a sortase recognition sequence, *e.g.*, LPETG (SEQ ID No. 3200). To attach a SME binder to EGFR binding protein comprising a sortase recognition sequence, the protein is incubated with a sortase and a SME binder whereby the sortase attaches the SME binder to the recognition sequence. In yet other embodiments, the EGFR binding proteins described herein comprise a knottin peptide for binding EGFR. Knottins are disufide-stabilized peptides with a cysteine knot scaffold and have average sizes about 3.5 kDa. Knottins have been contemplated for binding to certain tumor molecules such as EGFR. In further embodiments, the EGFR binding proteins described herein comprise a natural EGFR ligand.

[00207] In some embodiments, the EGFR binding protein comprises more than one domain and are of a single-polypeptide design with flexible linkage of the domains. This allows for facile production and manufacturing of the EGFR binding proteins as they can be encoded by single cDNA molecule to be easily incorporated into a vector. Further, in some embodiments where the EGFR binding proteins described herein are a monomeric single polypeptide chain, there are no chain pairing issues or a requirement for dimerization. It is contemplated that, in such

embodiments, the EGFR binding proteins described herein have a reduced tendency to aggregate.

[00208] In some cases, where the EGFR binding protein comprises more than one domain, the domains within the EGFR binding proteins are conjugated using an enzymatic site-specific conjugation method which involves the use of a mammalian or bacterial transglutaminase enzyme. Microbial transglutaminases (mTGs) are versatile tools in modern research and biotechnology. The availability of large quantities of relatively pure enzymes, ease of use, and lack of regulation by calcium and guanosine-5'-triphosphate (GTP) has propelled mTG to be the main cross-linking enzyme used in both the food industry and biotechnology. Currently, mTGs are used in many applications to attach proteins and peptides to small molecules, polymers, surfaces, DNA, as well as to other proteins. *See, e.g.*, Pavel Strp, Veracity of microbial transglutaminase, Bioconjugate Chem. 25, 5, 855-862).

[00209] In some examples are provided EGFR binding proteins comprising more than one domain, wherein one of the domains comprises an acceptor glutamine in a constant region, which can then be conjugated to another domain *via* a lysine-based linker (*e.g.*, any primary amine chain which is a substrate for TGase, *e.g.* comprising an alkylamine, oxoamine) wherein the conjugation occurs exclusively on one or more acceptor glutamine residues present in the targeting moiety outside of the antigen combining site (*e.g.*, outside a variable region, in a constant region). Conjugation thus does not occur on a glutamine, *e.g.* an at least partly surface exposed glutamine, within the variable region. The EGFR binding protein, in some examples, is formed by reacting one of the domains with a lysine-based linker in the presence of a TGase.

[00210] In some embodiments, where one or more domains within the EGFR binding proteins are directly joined, a hybrid vector is made where the DNA encoding the directly joined domains are themselves directly ligated to each other. In some embodiments, where linkers are used, a hybrid vector is made where the DNA encoding one domain is ligated to the DNA encoding one end of a linker moiety and the DNA encoding another domain is ligated to the other end of the linker moiety.

[00211] In some embodiments, the EGFR binding proteins as set forth above are fused to an Fc region from any species, including but not limited to, human immunoglobulin, such as human IgG1, a human IgG2, a human IgG3, human IgG4, to generate Fc-fusion proteins. In some embodiments, the Fc-fusion proteins of this disclosure have extended half-life compared to an otherwise identical EGFR binding protein. In some embodiments, the Fc-fusion EGFR binding proteins of this disclosure contain *inter alia* one or more additional amino acid residue substitutions, mutations and/or modifications, *e.g.*, in the Fc region, which result in a binding

protein with preferred characteristics including, but not limited to: altered pharmacokinetics, extended serum half-life.

[00212] In some embodiments, such Fc-fused EGFR binding proteins provide extended half-lives in a mammal, such as in a human, of greater than 5 days, greater than 10 days, greater than 15 days, greater than 20 days, greater than 25 days, greater than 30 days, greater than 35 days, greater than 40 days, greater than 45 days, greater than 2 months, greater than 3 months, greater than 4 months, or greater than 5 months. The increased half-life, in some cases, results in a higher serum titer which thus reduces the frequency of the administration of the EGFR binding proteins and/or reduces the concentration of the antibodies to be administered. Binding to human FcRn *in vivo* and serum half-life of human FcRn high affinity binding polypeptides is assayed, in some examples, in transgenic mice or transfected human cell lines expressing human FcRn, or in primates to which the polypeptides with a variant Fc region are administered.

[00213] The EGFR binding proteins, in some cases, are differentially modified during or after production, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications are carried out by techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH4, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

[00214] Various post-translational modifications of the EGFR binding proteins also encompassed by the disclosure include, for example, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends, attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. Moreover, the EGFR binding proteins are, in some cases, modified with a detectable label, such as an enzymatic, fluorescent, radioisotopic or affinity label to allow for detection and isolation of the modulator.

[00215] In some embodiments, the EGFR binding proteins of the disclosure are monovalent or multivalent bivalent, trivalent, etc.). As used herein, the term “valency” refers to the number of potential target binding sites associated with an antibody. Each target binding site specifically binds one target molecule or specific position or locus on a target molecule. When an antibody is monovalent, each binding site of the molecule will specifically bind to a single antigen position or epitope. When an antibody comprises more than one target binding site (multivalent), each target binding site may specifically bind the same or different molecules (*e.g.*, may bind to different ligands or different antigens, or different epitopes or positions on the same antigen).

FLT3 binding proteins

[00216] Described herein are immune cell engaging proteins that comprise an FLT3 binding domain as the target antigen binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising an FLT3 binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders.

[00217] FLT3, also known as fetal liver kinase 2 (FLK-2), stem cell tyrosine kinase 1 (STK-1) and CD135, is a member of the class III receptor tyrosine kinases. Normally, FLT3 is expressed on immature myeloid-lymphocytic precursor cells and dendritic cell precursors, but rarely on mature adult cells. FLT3 is overexpressed in approximately 90% of acute myeloid leukemia (AML), a majority of acute lymphocytic leukemia (ALL) and the blast-crisis phase of chronic myeloid leukemia (BC-CML). Stimulation by FLT3 ligand (FL) enhances the proliferation and survival of leukemia cells. Inhibition of FLT3 signaling leads to apoptosis in dendritic cells and inhibition of immune responses. The MAPK, PI3K and Stat5 pathways have been identified to be involved in the downstream signaling of activated FLT3 (*See e.g.*, Stirewalt D L and J P, Radich, J P. Nat Rev Cancer 3:650-665 (2003)).

[00218] Described herein are immune cell engaging proteins that comprise an FLT3 binding domain, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed proteins comprising an FLT3 binding domain of this disclosure, in the prevention, and/or treatment of diseases, conditions and disorders. In some embodiments, an FLT3 binding domain of this disclosure inhibits FL-induced phosphorylation of wild-type FLT3 and downstream kinases of MPK, PI3K, and STAT5 pathways in a disease such as leukemia. In some embodiments, an FLT3 binding domain of this disclosure has an improved ability to activate downstream immune effector functions such as antibody dependent cellular cytotoxicity (ADCC).

[00219] In some embodiments, the FLT3 binding domain binds to a human FLT3 protein comprising a sequence as set forth in SEQ ID No. 3215 (UniProt ID: P36888). In some embodiments, the FLT3 binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3215 (UniProt ID: P36888).

[00220] In some embodiments, the FLT3 binding domains disclosed herein recognize full-length FLT3 (*e.g.*, an FLT3 protein comprising the sequence of SEQ ID No. 3215 (UniProt ID: P36888). In certain instances, the FLT3 binding domains disclosed herein

recognize an epitope within FLT3, such as, in some cases the FLT3 binding proteins interact with one or more amino acids found within a domain of human FLT3. The epitope to which the antibodies bind may consist of a single contiguous sequence of 3 or more (*e.g.*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) amino acids located within a domain of FLT3 (*e.g.*, an FLT3 protein comprising the sequence of SEQ ID No. 3215 (UniProt ID: P36888). Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) located within a domain of FLT3 (*e.g.*, an FLT3 protein comprising the sequence of SEQ ID No. 3215 (UniProt ID: P36888).

[00221] In some embodiments, the FLT3 binding proteins of this disclosure binds to the full length of an FLT3 protein or to a fragment thereof, such as epitope containing fragments within the full length FLT3 protein, as described above. In some cases, the epitope containing fragment comprises antigenic or immunogenic fragments and derivatives thereof of the FLT3 protein. Epitope containing fragments, including antigenic or immunogenic fragments, are, in some embodiments, 12 amino acids or more, *e.g.*, 20 amino acids or more, 50 or 100 amino acids or more. The FLT3 fragments, in some embodiments, comprises 95% or more of the length of the full protein, 90% or more, 75% or 50% or 25% or 10% or more of the length of the full protein. In some embodiments, the epitope-containing fragments of FLT3 including antigenic or immunogenic fragments are capable of eliciting a relevant immune response in a patient. Derivatives of FLT3 include, in some embodiments, variants on the sequence in which one or more (*e.g.*, 1-20 such as 15 amino acids, or up to 20% such as up to 10% or 5% or 1% by number of amino acids based on the total length of the protein) deletions, insertions or substitutions have been made to the FLT3 sequence (*e.g.*, an FLT3 protein comprising the sequence of SEQ ID No. 3215 (UniProt ID: P36888).

[00222] In some embodiments, the affinity matured FLT3 binding molecule comprises an equivalent or better affinity to a FLT3 protein (such as human FLT3 protein) as that of a FLT3 binding parental molecule, but that has reduced cross reactivity, or in some embodiments, increased cross reactivity, with selected substances, such as ligands, proteins, antigens, or the like, other than the FLT3 epitope for which the FLT3 binding parental molecule is specific, or is designed to be specific for. In regard to the latter, an affinity matured FLT3 binding molecule, in some embodiments, is more successfully tested in animal models if the affinity matured FLT3 binding molecule is reacted with both human FLT3 and the corresponding target of the animal model, *e.g.* mouse FLT3 or cynomolgus FLT3.

[00223] In another example of a substitution to create a variant anti-FLT3 antibody or antigen binding fragments thereof, one or more hypervariable region residues of a parent antibody or antigen binding fragments thereof are substituted. In general, variants are then selected based on improvements in desired properties compared to a parent antibody, for example, increased affinity, reduced affinity, reduced immunogenicity, increased pH dependence of binding.

[00224] In some embodiments, the FLT3 binding domain is a polypeptide comprising an amino acid sequence that is comprised of four framework regions/sequences (f1-f4) interrupted by three complementarity determining regions/sequences, as represented by the formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues. The framework residues of the FLT3 binding protein of the present disclosure comprise, for example, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, or 94 amino acid residues, and the complementarity determining regions comprise, for example, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 amino acid residues.

[00225] In some embodiments, the binding proteins described herein comprise a polypeptide having a sequence selected from SEQ ID Nos. 1004-1079 and 3495-3496, subsequences thereof, and variants thereof. In some embodiments, the FLT3 binding protein comprises at least 75%-95% or more homology to a sequence selected from SEQ ID Nos. 1004-1079 and 3495-3496, subsequences thereof, and variants thereof. In some embodiments, the FLT3 binding protein comprises at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence selected from SEQ ID Nos. 1004-1079 and 3495-3496, subsequences thereof, and variants thereof. In some embodiments, the FLT3 binding protein comprises at least 60%-95% or more identity to a sequence selected from SEQ ID Nos. 1004-1079 and 3495-3496, subsequences thereof, and variants thereof. In some embodiments, the FLT3 binding protein comprises at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence selected from SEQ ID Nos. 1004-1079, subsequences thereof, and variants thereof.

[00226] In some embodiments, the CDR1 comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 1080-1155, and 3497-3498, or a sequence comprising one or more amino acid substitutions in a sequence selected from the group consisting of SEQ ID Nos. 1080-1155, and 3497-3498. In some embodiments, the CDR2 comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 1156-1231, and 3499-3500 or a sequence comprising one or more amino acid

substitutions in a sequence selected from the group consisting of SEQ ID Nos. 1156-1231, and 3499-3500. In some embodiments, the CDR3 comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 1232-1307, and 3501-3502 or a sequence comprising one or more amino acid substitutions in a sequence selected from the group consisting of SEQ ID Nos. 1232-1307, and 3501-3502. In some embodiments, the CDR1 comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 1150, 1152, 3497, and 3498, or a sequence comprising one or more amino acid substitutions in a sequence selected from the group consisting of SEQ ID Nos. 1150, 1152, 3497, and 3498. In some embodiments, the CDR2 comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 1226, 1228, 3499, and 3500, or a sequence comprising one or more amino acid substitutions in a sequence selected from the group consisting of SEQ ID Nos. 1226, 1228, 3499, and 3500. In some embodiments, the CDR3 comprises the amino acid sequence selected from the group consisting of SEQ ID Nos. 1302, 1304, 3501, and 3502 or a sequence comprising one or more amino acid substitutions in a sequence selected from the group consisting of SEQ ID Nos. 1293 or 1302.

[00227] In various embodiments, the FLT3 binding domain of the present disclosure is at least about about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID Nos. 1004-1079, and 3495-3496.

[00228] In various embodiments, a complementarity determining region of the FLT3 binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in any one of SEQ ID Nos. 1080-1155, and 3497-3498.

[00229] In various embodiments, a complementarity determining region of the FLT3 binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%,

about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID Nos. 1156-1231 and 3499-3500.

[00230] In various embodiments, a complementarity determining region of the FLT3 binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID Nos. 1232-1307 and 3501-3502.

[00231] In various embodiments, a complementarity determining region of the FLT3 binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in any one of SEQ ID Nos. 1074, 1076, 3495, and 3496 and wherein the FLT3 binding domain comprises a humanized FLT3 binding domain.

[00232] In some embodiments, any of the foregoing FLT3 binding domains (*e.g.*, anti-FLT3 single domain antibodies of SEQ ID Nos. 1004-1079) are affinity peptide tagged for ease of purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as 6X-his (SEQ ID No. 3503). In certain embodiments, the FLT3 binding domains of the present disclosure preferentially bind membrane bound FLT3 over soluble FLT3 Membrane bound FLT3 refers to the presence of FLT3 in or on the cell membrane surface of a cell that expresses FLT3. Soluble FLT3 refers to FLT3 that is no longer on in or on the cell membrane surface of a cell that expresses or expressed FLT3. In certain instances, the soluble FLT3 is present in the blood and/or lymphatic circulation in a subject. In one embodiment, the FLT3 binding domains bind membrane-bound FLT3 at least 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 100 fold, 500 fold, or 1000 fold greater than soluble FLT3. In one embodiment, the FLT3 binding proteins of the present disclosure preferentially bind membrane-bound FLT3 30 fold greater than soluble FLT3. Determining the preferential binding of an antigen binding protein to membrane bound FLT3 over soluble FLT3 can be readily determined using binding assays.

[00233] It is contemplated that in some embodiments the FLT3 binding protein is fairly small and no more than 25 kDa, no more than 20 kDa, no more than 15 kDa, or no more

than 10 kDa in some embodiments. In certain instances, the FLT3 binding protein is 5 kDa or less if it is a peptide or small molecule entity.

[00234] In other embodiments, the FLT3 binding proteins described herein comprise small molecule entity (SME) binders for FLT3. SME binders are small molecules averaging about 500 to 2000 Da in size and are attached to the FLT3 binding proteins by known methods, such as sortase ligation or conjugation. In these instances, the FLT3 binding protein comprises a domain comprising a sortase recognition sequence, *e.g.*, LPETG (SEQ ID No. 3200). To attach a SME binder to FLT3 binding protein comprising a sortase recognition sequence, the protein is incubated with a sortase and a SME binder whereby the sortase attaches the SME binder to the recognition sequence. In yet other embodiments, the FLT3 binding proteins described herein comprise a knottin peptide for binding FLT3. Knottins are disufide-stabilized peptides with a cysteine knot scaffold and have average sizes about 3.5 kDa. Knottins have been contemplated for binding to certain tumor molecules such as FLT3. In further embodiments, the FLT3 binding proteins described herein comprise a natural FLT3 ligand.

[00235] In some embodiments, the FLT3 binding protein comprises more than one domain and are of a single-polypeptide design with flexible linkage of the domains. This allows for facile production and manufacturing of the FLT3 binding proteins as they can be encoded by single cDNA molecule to be easily incorporated into a vector. Further, in some embodiments where the FLT3 binding proteins described herein are a monomeric single polypeptide chain, there are no chain pairing issues or a requirement for dimerization. It is contemplated that, in such embodiments, the FLT3 binding proteins described herein have a reduced tendency to aggregate.

[00236] In some cases, where the FLT3 binding protein comprises more than one domain, the domains within the FLT3 binding proteins are conjugated using an enzymatic site-specific conjugation method which involves the use of a mammalian or bacterial transglutaminase enzyme. Microbial transglutaminases (mTGs) are versatile tools in modern research and biotechnology. The availability of large quantities of relatively pure enzymes, ease of use, and lack of regulation by calcium and guanosine-5'-triphosphate (GTP) has propelled mTG to be the main cross-linking enzyme used in both the food industry and biotechnology. Currently, mTGs are used in many applications to attach proteins and peptides to small molecules, polymers, surfaces, DNA, as well as to other proteins. *See e.g.*, Pavel Strp, Veracity of microbial transglutaminase, Bioconjugate Chem. 25, 5, 855-862.

[00237] In some examples are provided FLT3 binding proteins comprising more than one domain, wherein one of the domains comprises an acceptor glutamine in a constant region, which can then be conjugated to another domain *via* a lysine-based linker (*e.g.*, any primary amine chain which is a substrate for TGase, *e.g.* comprising an alkylamine, oxoamine) wherein the conjugation occurs exclusively on one or more acceptor glutamine residues present in the targeting moiety outside of the antigen combining site (*e.g.*, outside a variable region, in a constant region). Conjugation thus does not occur on a glutamine, *e.g.* an at least partly surface exposed glutamine, within the variable region. The FLT3 binding protein, in some examples, is formed by reacting one of the domains with a lysine-based linker in the presence of a TGase.

[00238] In some embodiments, where one or more domains within the FLT3 binding proteins are directly joined, a hybrid vector is made where the DNA encoding the directly joined domains are themselves directly ligated to each other. In some embodiments, where linkers are used, a hybrid vector is made where the DNA encoding one domain is ligated to the DNA encoding one end of a linker moiety and the DNA encoding another domain is ligated to the other end of the linker moiety.

[00239] In certain embodiments, the FLT3 binding proteins according to the present disclosure may be incorporated into immune cell engaging proteins. In some embodiments, the immune cell engaging proteins comprise a CD3 binding domain, a half-life extension domain, and an FLT3 binding domain according to this disclosure. In some embodiments, the FLT3 binding trispecific protein comprises a trispecific antibody.

EpCAM binding proteins

[00240] Described herein are immune cell engaging proteins that bind EpCAM, pharmaceutical compositions thereof, as well as nucleic acids, recombinant expression vectors and host cells for making such proteins thereof. Also provided are methods of using the disclosed EpCAM binding proteins in the prevention, and/or treatment of diseases, conditions and disorders. In some embodiments, the EpCAM binding proteins are part of immune cell engaging proteins that comprise an EpCAM binding domain as described herein.

[00241] The epithelial cell adhesion molecule (EpCAM) is a membrane glycoprotein that is expressed in most normal human epithelia and overexpressed in most carcinomas. This molecule is responsible for cell-to-cell adhesion and additionally participates in signaling, cell migration, proliferation and differentiation. Therefore, EpCAM has been the target of immunotherapy in clinical trials of several solid tumors. It has been found to

play an important role in the detection and isolation of circulating tumor cells (CTCs). EpCAM has been shown in various studies to be beneficial in diagnosis and therapy of various carcinomas. Furthermore, in many cases, tumor cells were observed to express EpCAM to a much higher degree than their parental epithelium or less aggressive forms of said cancers. For example, EpCAM expression was shown to be significantly higher on neoplastic tissue and in adenocarcinoma than on normal prostate epithelium ($n=76$; $p<0.0001$), suggesting that increased EpCAM expression represents an early event in the development of prostate cancer. *See* Poczatek, J Urol., 1999, 162, 1462-1644. In addition, in the majority of both squamous and adenocarcinomas of the cervix a strong EpCAM expression has been shown to correlate with an increased proliferation and the disappearance of markers for terminal differentiation. *See* Litvinov, Am. J. Pathol. 1996, 148, 865-75. One example is breast cancer where overexpression of EpCAM on tumor cells is a predictor of survival. *See* Gastl, Lancet. 2000, 356, 1981-1982. Furthermore, EpCAM has been described as a marker for the detection of disseminated tumor cells in patients suffering from squamous cell carcinoma of the head, neck and lung. *See* Chaubal, Anticancer Res 1999, 19, 2237-2242, Piyathilake, Hum Pathol. 2000, 31, 482-487. Normal squamous epithelium, as found in epidermis, oral cavity, epiglottis, pharynx, larynx and esophagus did not significantly express EpCAM. *See* Quak, Hybridoma, 1990, 9, 377-387.

[00242] EpCAM is contemplated to serve to adhere epithelial cells in an oriented and highly ordered fashion. *See* Litvinov, J Cell Biol. 1997, 139, 1337-1348. Upon malignant transformation of epithelial cells the rapidly growing tumor cells are believed to abandon the high cellular order of epithelia. Consequently, the surface distribution of EpCAM is contemplated to become less restricted and the molecule better exposed on tumor cells. Due to their epithelial cell origin, tumor cells from most carcinomas are expected to express EpCAM on their surface.

[00243] EpCAM, is a 40-kDa membrane-integrated glycoprotein of 314 amino acids with specific expression in certain epithelia and on many human carcinomas. *See, e.g.*, in Balzar, J. Mol. Med. 1999, 77, 699-712). EpCAM was discovered and subsequently cloned through its recognition by the murine monoclonal antibody 17-1A/edrecolomab. *See* Goettlinger, Int J Cancer. 1986; 38, 47-53 and Simon, Proc. Natl. Acad. Sci. USA. 1990; 87, 2755-2759. Monoclonal antibody 17-1A was generated by immunization of mice with human colon carcinoma cells. *See* Koprowski, Somatic Cell Genet. 1979, 5, 957-971. The EGF-like repeats of EpCAM were shown to mediate lateral and reciprocal interactions in homophilic cell adhesion. *See, e.g.*, Balzar, Mol. Cell. Biol. 2001, 21,

2570-2580) and, for that reason, is predominantly located between epithelial cells (Litvinov, J Cell Biol. 1997, 139, 1337-1348, Balzar, J Mol Med. 1999, 77, 699-712 and Trebak, J Biol Chem. 2001, 276, 2299-2309).

[00244] EpCAM is also known by the following alternate names: Epithelial Cell Adhesion Molecule, Tumor-Associated Calcium Signal Transducer, Major Gastrointestinal Tumor-Associated Protein GA733-2, Adenocarcinoma-Associated Antigen, Cell Surface Glycoprotein Trop-1, Epithelial Glycoprotein 314, TACSTD1, EGP314, MIC18, TROP1, M4S1, KSA, Membrane Component Chromosome 4 Surface marker (35 kD glycoprotein), Antigen identified by monoclonal antibody AUA-1, human epithelial glycoprotein-2, epithelial cell surface antigen, epithelial glycoprotein, KS 1/4Antigen, CD326 Antigen, GA722-2, HEGP314, HNPCC8, Ep-CAM, DIAR5, EGP-2, EGP40, KS ¼, MK-1, M1S2, ESA, and EGP. Exemplary protein sequences for EpCAM is provided in UniProtkB ID Nos. P16422 and B5MCA4. In some embodiments, the EpCAM binding proteins of this disclosure binds to an EpCAM sequence provided in UniProtkB ID Nos. P16422 (SEQ ID No.478) or B5MCA4 (SEQ ID No. 475).

[00245] In some embodiments, the EpCAM binding domain binds to an extracellular domain of the mature EpCAM protein. The human extracellular domain sequence is provided in SEQ ID No. 3212; the cynomolgus extracellular domain sequence is provided in SEQ ID No. 3213; and the mouse extracellular domain sequence is provided in SEQ ID No. 3214.

[00246] In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3208. In some embodiments, the EPCAM binding domain binds to a protein comprising the sequence of SEQ ID No. 3208. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3209. In some embodiments, the EpCAM binding domain binds to a protein comprising the sequence of SEQ ID No. 3209. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3210. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3210. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 478. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3211. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3212. In some embodiments, the EpCAM binding domain binds to a protein comprising a

truncated sequence compared to SEQ ID No. 3212. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3213. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3213. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3214. In some embodiments, the EpCAM binding domain binds to a protein comprising a truncated sequence compared to SEQ ID No. 3214.

[00247] In some embodiments, the EpCAM binding domains disclosed herein recognize full-length EpCAM. In certain instances, the EpCAM binding domains disclosed herein recognize an epitope within EpCAM, such as, in some cases the EpCAM binding proteins interact with one or more amino acids found within a domain of human EpCAM. The epitope to which the antibodies bind may consist of a single contiguous sequence of 3 or more (*e.g.*, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more) amino acids located within a domain of EpCAM. Alternatively, the epitope may consist of a plurality of non-contiguous amino acids (or amino acid sequences) located within a domain of EpCAM.

[00248] In some embodiments, the EpCAM binding proteins of this disclosure binds to the full length EpCAM protein or to a fragment thereof, such as epitope containing fragments within the full length EpCAM protein, as described above. In some cases, the epitope containing fragment comprises antigenic or immunogenic fragments and derivatives thereof of the EpCAM protein. Epitope containing fragments, including antigenic or immunogenic fragments, are, in some embodiments, 12 amino acids or more, *e.g.*, 20 amino acids or more, 50 or 100 amino acids or more. The EpCAM fragments, in some embodiments, comprises 95% or more of the length of the full protein, 90% or more, 75% or 50% or 25% or 10% or more of the length of the full protein. In some embodiments, the epitope-containing fragments of EpCAM including antigenic or immunogenic fragments are capable of eliciting a relevant immune response in a patient. Derivatives of EpCAM include, in some embodiments, variants on the sequence in which one or more (*e.g.*, 1-20 such as 15 amino acids, or up to 20% such as up to 10% or 5% or 1% by number of amino acids based on the total length of the protein) deletions, insertions or substitutions have been made to the EpCAM sequence provided in SEQ ID Nos. 3208-3214.

[00249] In another example of a substitution to create a variant anti-EpCAM antibody or antigen binding fragments thereof, one or more hypervariable region residues of a parent antibody are substituted. In general, variants are then selected based on

improvements in desired properties compared to a parent antibody or antigen binding fragments thereof, for example, increased affinity, reduced affinity, reduced immunogenicity, increased pH dependence of binding.

[00250] In some embodiments, the EpCAM binding domain is a polypeptide comprising an amino acid sequence that is comprised of four framework regions/sequences (f1-f4) interrupted by three complementarity determining regions/sequences, as represented by the formula: f1-r1-f2-r2-f3-r3-f4, wherein r1, r2, and r3 are complementarity determining regions CDR1, CDR2, and CDR3, respectively, and f1, f2, f3, and f4 are framework residues. The framework residues of the EpCAM binding protein of the present disclosure comprise, for example, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, or 94 amino acid residues, and the complementarity determining regions comprise, for example, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, or 36 amino acid residues. In some embodiments, the EpCAM binding domain comprises an amino acid sequence selected from SEQ ID NOs: 961-1003.

[00251] In some embodiments, the EpCAM binding protein comprises at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or more identity to a sequence selected from SEQ ID Nos. 961-1003, subsequences thereof, and variants thereof. In some embodiments, the EpCAM binding protein comprises at least 70%-95% or more identity to a sequence selected from SEQ ID Nos. 961-1003, subsequences thereof, and variants thereof.

[00252] In some embodiments, the CDR1 comprises the amino acid sequence as set forth in any one of SEQ ID Nos. 847-884 or a sequence comprising one or more substitutions compared to a sequence selected from the group consisting of SEQ ID Nos. 847-884. In some embodiments, the CDR2 comprises a sequence as set forth in any one of SEQ ID Nos.885-922 or a sequence comprising one or more substitutions compared to a sequence selected from the group consisting of SEQ ID Nos. 885-922. In some embodiments, the CDR3 comprises a sequence as set forth in any one of SEQ ID Nos. 923-960 a sequence comprising one or more substitutions compared to a sequence selected from the group consisting of SEQ ID Nos. 923-960.

[00253] In various embodiments, a complementarity determining region of the EpCAM binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%,

about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID Nos. 847-884.

[00254] In various embodiments, a complementarity determining region of the EpCAM binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID Nos. 885-922.

[0027] In various embodiments, a complementarity determining region of the EpCAM binding domain of the present disclosure is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to the amino acid sequence set forth in SEQ ID Nos. 923-960.

[00255] In some embodiments, any of the foregoing EpCAM binding domains (*e.g.*, anti-EpCAM single domain antibodies of SEQ ID Nos. 961-1003) are affinity peptide tagged for ease of purification. In some embodiments, the affinity peptide tag is six consecutive histidine residues, also referred to as 6X-his (SEQ ID No. 3503).

[00256] In certain embodiments, the EpCAM binding domains of the present disclosure preferentially bind membrane bound EpCAM over soluble EpCAM Membrane bound EpCAM refers to the presence of EpCAM in or on the cell membrane surface of a cell that expresses EpCAM. Soluble EpCAM refers to EpCAM that is no longer on in or on the cell membrane surface of a cell that expresses or expressed EpCAM. In certain instances, the soluble EpCAM is present in the blood and/or lymphatic circulation in a subject. In one embodiment, the EpCAM binding domains bind membrane-bound EpCAM at least 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 100 fold, 500 fold, or 1000 fold greater than soluble EpCAM. In one embodiment, the EpCAM binding proteins of the present disclosure preferentially bind membrane-bound EpCAM 30 fold greater than soluble EpCAM. Determining the preferential binding of an antigen binding protein to membrane bound EpCAM over soluble EpCAM can be readily determined using binding assays.

[00257] It is contemplated that in some embodiments the EpCAM binding protein is fairly small and no more than 25 kDa, no more than 20 kDa, no more than 15 kDa, or no

more than 10 kDa in some embodiments. In certain instances, the EpCAM binding protein is 5 kDa or less if it is a peptide or small molecule entity.

[00258] In other embodiments, the EpCAM binding proteins described herein comprise small molecule entity (SME) binders for EpCAM. SME binders are small molecules averaging about 500 to 2000 Da in size and are attached to the EpCAM binding proteins by known methods, such as sortase ligation or conjugation. In these instances, the EpCAM binding protein comprises a domain comprising a sortase recognition sequence, *e.g.*, LPETG (SEQ ID No. 3200). To attach a SME binder to EpCAM binding protein comprising a sortase recognition sequence, the protein is incubated with a sortase and a SME binder whereby the sortase attaches the SME binder to the recognition sequence. In yet other embodiments, the EpCAM binding proteins described herein comprise a knottin peptide for binding EpCAM. Knottins are disufide-stabilized peptides with a cysteine knot scaffold and have average sizes about 3.5 kDa. Knottins have been contemplated for binding to certain tumor molecules such as EpCAM. In further embodiments, the EPCAM binding proteins described herein comprise a natural EpCAM ligand.

[00259] In some embodiments, the EpCAM binding protein comprises more than one domain and are of a single-polypeptide design with flexible linkage of the domains. This allows for facile production and manufacturing of the EpCAM binding proteins as they can be encoded by single cDNA molecule to be easily incorporated into a vector. Further, in some embodiments where the EpCAM binding proteins described herein are a monomeric single polypeptide chain, there are no chain pairing issues or a requirement for dimerization. It is contemplated that, in such embodiments, the EpCAM binding proteins described herein have a reduced tendency to aggregate.

[00260] In the EpCAM binding proteins comprising more than one domain, the domains are linked by one or more internal linker. In certain embodiments, the internal linkers are "short," *i.e.*, consist of 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acid residues. Thus, in certain instances, the internal linkers consist of about 12 or less amino acid residues. In the case of 0 amino acid residues, the internal linker is a peptide bond. In certain embodiments, the internal linkers are "long," *i.e.*, consist of 15, 20 or 25 amino acid residues. In some embodiments, the internal linkers consist of about 3 to about 15, for example 8, 9 or 10 contiguous amino acid residues. Regarding the amino acid composition of the internal linkers, peptides are selected with properties that confer flexibility to the EpCAM binding proteins, do not interfere with the binding domains as well as resist cleavage from proteases. For example, glycine and serine residues

generally provide protease resistance. Examples of internal linkers suitable for linking the domains in the EpCAM binding proteins include but are not limited to $(GS)_n$ (SEQ ID No. 3859), $(GGS)_n$ (SEQ ID No. 3860), $(GGGS)_n$ (SEQ ID No. 3861), $(GGSG)_n$ (SEQ ID No. 3862), $(GGSGG)_n$ (SEQ ID No. 3863), $(GGGGS)_n$ (SEQ ID No. 3864), $(GGGGG)_n$ (SEQ ID No. 3865), or $(GGG)_n$ (SEQ ID No. 3866), wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. In one embodiment, the linker is (GGGGSGGGGSGGGGSGGGGS)(SEQ ID No. 3867), (GGGGSGGGGSGGGGS) (SEQ ID No. 3868), LPETG (SEQ ID NO. 3869), (GGGGSGGGS) (SEQ ID No. 3871) or SGGG (SEQ ID NO. 3872).

[00261] In some cases, where the EpCAM binding protein comprises more than one domain, the domains within the EpCAM binding proteins are conjugated using an enzymatic site-specific conjugation method which involves the use of a mammalian or bacterial transglutaminase enzyme. Microbial transglutaminases (mTGs) are versatile tools in modern research and biotechnology. The availability of large quantities of relatively pure enzymes, ease of use, and lack of regulation by calcium and guanosine-5'-triphosphate (GTP) has propelled mTG to be the main cross-linking enzyme used in both the food industry and biotechnology. Currently, mTGs are used in many applications to attach proteins and peptides to small molecules, polymers, surfaces, DNA, as well as to other proteins. *See, e.g.*, Pavel Strp, Veracity of microbial transglutaminase, Bioconjugate Chem. 25, 5, 855-862.

[00262] In some examples are provided EpCAM binding proteins comprising more than one domain, wherein one of the domains comprises an acceptor glutamine in a constant region, which can then be conjugated to another domain *via* a lysine-based linker (*e.g.*, any primary amine chain which is a substrate for TGase, *e.g.* comprising an alkylamine, oxoamine) wherein the conjugation occurs exclusively on one or more acceptor glutamine residues present in the targeting moiety outside of the antigen combining site (*e.g.*, outside a variable region, in a constant region). Conjugation thus does not occur on a glutamine, *e.g.* an at least partly surface exposed glutamine, within the variable region. The EpCAM binding protein, in some examples, is formed by reacting one of the domains with a lysine-based linker in the presence of a TGase.

[00263] In some embodiments, where one or more domains within the EpCAM binding proteins are directly joined, a hybrid vector is made where the DNA encoding the directly joined domains are themselves directly ligated to each other. In some embodiments, where linkers are used, a hybrid vector is made where the DNA encoding

one domain is ligated to the DNA encoding one end of a linker moiety and the DNA encoding another domain is ligated to the other end of the linker moiety.

[00264] In certain embodiments, the EpCAM binding proteins according to the present disclosure may be incorporated into immune cell engaging proteins. In some embodiments, the immune cell engaging proteins comprise a CD3 binding domain, a half-life extension domain, and an EpCAM binding domain according to this disclosure. In some embodiments, the immune cell engaging protein comprises a trispecific antibody.

CD3 Binding Domain

[00265] The immune cell engaging protein described herein comprises an immune cell engaging domain. In some embodiments, the immune cell engaging domain comprises a natural killer (NK) cell engaging domain, a T cell engaging domain, a B cell engaging domain, a dendritic cell engaging domain, a macrophage cell engaging domain, or a combination thereof. In some embodiments, the immune cell engaging protein comprises a T-cell engaging domain. In some embodiments, the T cell engaging domain is a CD3 binding domain.

[00266] The specificity of the response of T cells is mediated by the recognition of antigen (displayed in context of a major histocompatibility complex, MHC) by the T cell receptor complex. As part of the T cell receptor complex, CD3 is a protein complex that includes a CD3γ (gamma) chain, a CD3δ (delta) chain, and two CD3ε (epsilon) chains which are present on the cell surface. CD3 associates with the α (alpha) and β (beta) chains of the T cell receptor (TCR) as well as and CD3 ζ (zeta) altogether to comprise the T cell receptor complex. Clustering of CD3 on T cells, such as by immobilized anti-CD3 antibodies leads to T cell activation similar to the engagement of the T cell receptor but independent of its clone-typical specificity.

[00267] In one aspect, the single chain variable fragment CD3 binding proteins described herein comprise a domain which specifically binds to CD3. In one aspect, the single chain variable fragment CD3 binding proteins described herein comprise a domain which specifically binds to human CD3. In one aspect, the single chain variable fragment CD3 binding proteins described herein comprise a domain which specifically binds to cynomolgus CD3. In one aspect, the single chain variable fragment CD3 binding proteins described herein comprise a domain which binds to human CD3 and cynomolgus CD3. In some embodiments, the single chain variable fragment CD3 binding proteins described herein comprise a domain which specifically binds to CD3γ. In some embodiments, the single chain variable fragment CD3 binding proteins

described herein comprise a domain which specifically binds to CD3δ. In some embodiments, the single chain variable fragment CD3 binding proteins described herein comprise a domain which specifically binds to CD3ε.

[00268] In another aspect is provided an immune cell engaging protein comprising a single chain variable fragment CD3 binding protein according to the present disclosure. In some embodiments, the immune cell engaging protein comprising a single chain variable fragment CD3 binding protein according to the present disclosure specifically binds to the T cell receptor (TCR). In certain instances, the immune cell engaging protein comprising a single chain variable fragment CD3 binding protein according to the present disclosure binds the α chain of the TCR. In certain instances, the immune cell engaging protein comprising a single chain variable fragment CD3 binding protein according to the present disclosure binds the β chain of the TCR.

[00269] In certain embodiments, the CD3 binding domain of the immune cell engaging protein described herein exhibit not only potent CD3 binding affinities with human CD3, but show also excellent crossreactivity with the respective cynomolgus monkey CD3 proteins. In some instances, the CD3 binding domain of the immune cell engaging protein binding proteins are cross-reactive with CD3 from cynomolgus monkey. In certain instances, the Kd for binding human CD3 (hKd) is about the same as the Kd for binding cynomolgus CD3 (cKd). In certain instances, the ratio between hKd and cKd (hKd:cKd) is between about 20:1 to about 1:2.

[00270] In some embodiments, the CD3 binding domain of immune cell engaging protein can be any domain that binds to CD3 including but not limited to domains from a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody. In some instances, it is beneficial for the CD3 binding domain to be derived from the same species in which the immune cell engaging protein will ultimately be used. For example, for use in humans, it may be beneficial for the CD3 binding domain to comprise human or humanized residues from the antigen binding domain of an antibody or antibody fragment.

[00271] Thus, in one aspect, the antigen-binding domain comprises a humanized or human antibody or an antibody fragment, or a murine antibody or antibody fragment. In one embodiment, the humanized or human anti-CD3 binding domain comprises one or more (*e.g.*, all three) light chain complementary determining region 1 (LC CDR1), light chain complementary determining region 2 (LC CDR2), and light chain complementary determining region 3 (LC CDR3) of a humanized or human anti- CD3 binding domain described herein, and/or one or more (*e.g.*, all three) heavy chain complementary

determining region 1 (HC CDR1), heavy chain complementary determining region 2 (CDR2), and heavy chain complementary determining region 3 (CDR3) of a humanized or human anti-CD3 binding domain described herein, *e.g.*, a humanized or human anti-CD3 binding domain comprising one or more, *e.g.*, all three, LC CDRs and one or more, *e.g.*, all three, HC CDRs.

[00272] In some embodiments, the humanized or human anti-CD3 binding domain comprises a humanized or human light chain variable region specific to CD3 where the light chain variable region specific to CD3 comprises human or non-human light chain CDRs in a human light chain framework region. In certain instances, the light chain framework region is a λ (lambda) light chain framework. In other instances, the light chain framework region is a κ (kappa) light chain framework.

[00273] In some embodiments, the humanized or human anti-CD3 binding domain comprises a humanized or human heavy chain variable region specific to CD3 where the heavy chain variable region specific to CD3 comprises human or non-human heavy chain CDRs in a human heavy chain framework region.

[00274] In certain instances, the complementary determining regions of the heavy chain and/or the light chain are derived from known anti-CD3 antibodies, such as, for example, muromonab-CD3 (OKT3), otelixizumab (TRX4), teplizumab (MGA031), visilizumab (Nuvion), SP34, TR-66 or X35-3, VIT3, BMA030 (BW264/56), CLB-T3/3, CRIS7, YTH12.5, F111-409, CLB-T3.4.2, TR-66, WT32, SPv-T3b, 11D8, XIII-141, XIII-46, XIII-87, 12F6, T3/RW2-8C8, T3/RW2-4B6, OKT3D, M-T301, SMC2, F101.01, UCHT-1 and WT-31.

[00275] In one embodiment, the anti-CD3 binding domain is a single chain variable fragment (scFv) comprising a light chain and a heavy chain of an amino acid sequence provided herein. As used herein, "single chain variable fragment" or "scFv" refers to an antibody fragment comprising a variable region of a light chain and at least one antibody fragment comprising a variable region of a heavy chain, wherein the light and heavy chain variable regions are contiguously linked via a short flexible polypeptide linker, and capable of being expressed as a single polypeptide chain, and wherein the scFv retains the specificity of the intact antibody from which it is derived. In an embodiment, the anti-CD3 binding domain comprises: a light chain variable region comprising an amino acid sequence having at least one, two or three modifications (*e.g.*, substitutions) but not more than 30, 20 or 10 modifications (*e.g.*, substitutions) of an amino acid sequence of a light chain variable region provided herein, or a sequence with 95-99% identity with an amino acid sequence provided herein; and/or a heavy chain variable region comprising

an amino acid sequence having at least one, two or three modifications (*e.g.*, substitutions) but not more than 30, 20 or 10 modifications (*e.g.*, substitutions) of an amino acid sequence of a heavy chain variable region provided herein, or a sequence with 95-99% identity to an amino acid sequence provided herein. In one embodiment, the humanized or human anti-CD3 binding domain is a scFv, and a light chain variable region comprising an amino acid sequence described herein, is attached to a heavy chain variable region comprising an amino acid sequence described herein, via a scFv linker. The light chain variable region and heavy chain variable region of a scFv can be, *e.g.*, in any of the following configurations: light chain variable region- scFv linker-heavy chain variable region or heavy chain variable region- scFv linker-light chain variable region.

[00276] In some instances, scFvs which bind to CD3 are prepared according to known methods. For example, scFv molecules can be produced by linking VH and VL regions together using flexible polypeptide linkers. The scFv molecules comprise a scFv linker (*e.g.*, a Ser-Gly linker) with an optimized length and/or amino acid composition. Accordingly, in some embodiments, the length of the scFv linker is such that the VH or VL domain can associate intermolecularly with the other variable domain to form the CD3 binding site. In certain embodiments, such scFv linkers are "short", i.e. consist of 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acid residues. Thus, in certain instances, the scFv linkers consist of about 12 or less amino acid residues. In the case of 0 amino acid residues, the scFv linker is a peptide bond. In some embodiments, these scFv linkers consist of about 3 to about 15, for example 8, 10 or 15 contiguous amino acid residues. Regarding the amino acid composition of the scFv linkers, peptides are selected that confer flexibility, do not interfere with the variable domains as well as allow inter-chain folding to bring the two variable domains together to form a functional CD3 binding site. For example, scFv linkers comprising glycine and serine residues generally provide protease resistance. In some embodiments, linkers in a scFv comprise glycine and serine residues. The amino acid sequence of the scFv linkers can be optimized, for example, by phage-display methods to improve the CD3 binding and production yield of the scFv. Examples of peptide scFv linkers suitable for linking a variable light chain domain and a variable heavy chain domain in a scFv include but are not limited to $(GS)_n$ (SEQ ID No. 3859), $(GGS)_n$ (SEQ ID No. 3860), $(GGGS)_n$ (SEQ ID No. 3861), $(GGSG)_n$ (SEQ ID No. 3862), $(GGSGG)_n$ (SEQ ID No. 3863), $(GGGGS)_n$ (SEQ ID No. 3864), $(GGGGG)_n$ (SEQ ID No. 3865), or $(GGG)_n$ (SEQ ID No. 3866), wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. In one embodiment, the linker is (GGGGSGGGGSGGGGSGGGGS)(SEQ ID No. 3867), (GGGGSGGGGSGGGGS) (SEQ ID No. 3868), LPETG (SEQ ID NO. 3869), (GGGGSGGGS) (SEQ ID No. 3871) or SGGG (SEQ

ID NO. 3872). Variation in the linker length may retain or enhance activity, giving rise to superior efficacy in activity studies.

[00277] In some embodiments, CD3 binding domain of an immune cell engaging protein has an affinity to CD3 on CD3 expressing cells with a K_d of 1000 nM or less, 500 nM or less, 200 nM or less, 100 nM or less, 80 nM or less, 50 nM or less, 20 nM or less, 10 nM or less, 5 nM or less, 1 nM or less, or 0.5 nM or less. In some embodiments, the CD3 binding domain of a single chain variable fragment CD3 binding protein has an affinity to CD3ε, γ, or δ with a K_d of 1000 nM or less, 500 nM or less, 200 nM or less, 100 nM or less, 80 nM or less, 50 nM or less, 20 nM or less, 10 nM or less, 5 nM or less, 1 nM or less, or 0.5 nM or less. In further embodiments, CD3 binding domain of a single chain variable fragment CD3 binding protein has low affinity to CD3, i.e., about 100 nM or greater.

[00278] In certain embodiments, the single chain variable fragment CD3 binding proteins described herein bind to human CD3 with a human Kd (hKd) and to cynomolgus CD3 with a cyno Kd (cKd). In some embodiments, hKd and cKd are between about between about 1 nM to about 2 nM, about 3 nM to about 5 nM, about 6 nM to about 10 nM, about 11 nM to about 20 nM, about 25 nM to about 40 nM,about 40 nM to about 60 nM, about 70 nM to about 90 nM, about 100 nM to about 120 nM, about 125 nM to about 140 nM, about 145 nM to about 160 nM, about 170 nM and to about 200 nM, about 210 nM to about 250 nM, about 260 nM to about 300 nM.

[00279] In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about the same as the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 1.1 fold to about 1.5 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 1.5 fold to about 2 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 2.5 fold to about 3 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 3 fold to about 5 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 6 fold to about 15 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO.

3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 15 fold to about 20 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 20 fold to about 50 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 55 fold to about 70 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 75 fold to about 100 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167. In some embodiments, the hKd and cKd of the single chain variable fragment CD3 binding proteins is about 120 fold to about 200 fold the Kd of a CD3 binding protein having the sequence as set forth is SEQ ID NO. 3167.

[00280] In some embodiments, the ratio between the hKd and cKd (hKd: cKd) ranges from about 20:1 to about 1:2. The affinity to bind to CD3 can be determined, for example, by the ability of the single chain variable fragment CD3 binding protein itself or its CD3 binding domain to bind to CD3 coated on an assay plate; displayed on a microbial cell surface; in solution; etc. The binding activity of the single chain variable fragment CD3 binding protein itself or its CD3 binding domain of the present disclosure to CD3 can be assayed by immobilizing the ligand (*e.g.*, CD3) or the single chain variable fragment CD3 binding protein itself or its CD3 binding domain, to a bead, substrate, cell, etc. Agents can be added in an appropriate buffer and the binding partners incubated for a period of time at a given temperature. After washes to remove unbound material, the bound protein can be released with, for example, SDS, buffers with a high or low pH, and the like and analyzed, for example, by Surface Plasmon Resonance (SPR).

[00281] In some embodiments, the single chain variable fragment CD3 binding protein has an amino acid sequence selected from SEQ ID NOs. 3153-3169. In various embodiments, the single chain variable fragment CD3 binding protein comprises an amino acid sequence that is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 3153-3169.

Single domain Serum albumin binding protein

[00282] The immune cell engaging protein described herein is a half-life extended protein. In some embodiments, the immune cell engaging protein comprises a domain binds to serum albumin. In some embodiments, the serum albumin is human serum albumin (HSA).

[00283] Serum albumin is produced by the liver, occurs dissolved in blood plasma and is the most abundant blood protein in mammals. Albumin is essential for maintaining the oncotic pressure needed for proper distribution of body fluids between blood vessels and body tissues; without albumin, the high pressure in the blood vessels would force more fluids out into the tissues. It also acts as a plasma carrier by non-specifically binding several hydrophobic steroid hormones and as a transport protein for hemin and fatty acids. Human serum albumin (HSA) (molecular mass ~67 kDa) is the most abundant protein in plasma, present at about 50 mg/ml (600 μM), and has a half-life of around 20 days in humans. HSA serves to maintain plasma pH, contributes to colloidal blood pressure, functions as carrier of many metabolites and fatty acids, and serves as a major drug transport protein in plasma. In some embodiments, the single domain serum albumin binding proteins bind to HSA. In some embodiments, the single domain serum albumin binding proteins bind to serum albumin protein from cynomolgus monkeys. In some embodiments, the single domain serum albumin binding proteins bind to HSA and serum albumin protein from cynomolgus monkeys. In some embodiments, the single domain serum albumin binding proteins also bind to mouse serum albumin protein. In some embodiments, the binding affinity towards mouse serum albumin is about 1.5- fold to about 20-fold weaker than that towards human or cynomolgus serum albumin.

[00284] Noncovalent association with albumin extends the elimination half-time of short-lived proteins. For example, a recombinant fusion of an albumin binding domain to a Fab fragment resulted in a decrease in *in vivo* clearance by 25- and 58-fold and a half-life extension of 26- and 37-fold when administered intravenously to mice and rabbits respectively as compared to the administration of the Fab fragment alone. In another example, when insulin is acylated with fatty acids to promote association with albumin, a protracted effect was observed when injected subcutaneously in rabbits or pigs. Together, these studies demonstrate a linkage between albumin binding and prolonged action/serum half-life.

[00285] In some embodiments, the single-domain serum albumin binding proteins described herein is a single domain antibody such as a heavy chain variable domain (VH), a variable domain (VHH) of camelid derived sdAb, peptide, ligand or small

molecule entity specific for serum albumin. In some embodiments, the single-domain serum albumin binding proteins described herein is a single domain antibody such as a heavy chain variable domain (VH), a variable domain (VHH) of camelid derived sdAb, peptide, ligand or small molecule entity specific for HSA. In some embodiments, the serum albumin binding domain of a single domain serum albumin binding protein described herein is any domain that binds to serum albumin including but not limited to domains from a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody. In certain embodiments, the serum albumin binding domain is a single-domain antibody. In other embodiments, the serum albumin binding domain is a peptide. In further embodiments, the serum albumin binding domain is a small molecule. It is contemplated that the single domain serum albumin binding protein is fairly small and no more than 25 kD, no more than 20 kD, no more than 15 kD, or no more than 10 kD in some embodiments. In certain instances, the single domain serum albumin binding protein binding is 5 kD or less if it is a peptide or small molecule entity.

[00286] In some embodiments, the single domain serum albumin binding protein described herein is a half-life extension domain which provides for altered pharmacodynamics and pharmacokinetics of the single domain serum albumin binding protein itself. As above, the half-life extension domain extends the elimination half-time. The half-life extension domain also alters pharmacodynamic properties including alteration of tissue distribution, penetration, and diffusion of the single domain serum albumin binding protein. In some embodiments, the half-life extension domain provides for improved tissue (including tumor) targeting, tissue distribution, tissue penetration, diffusion within the tissue, and enhanced efficacy as compared with a protein without a half-life extension domain. In one embodiment, therapeutic methods effectively and efficiently utilize a reduced amount of the single domain serum albumin binding protein, resulting in reduced side effects, such as reduced non-tumor cell cytotoxicity.

[00287] Further, the binding affinity of the single domain serum albumin binding protein towards its binding target can be selected so as to target a specific elimination half-time in a particular single domain serum albumin binding protein. Thus, in some embodiments, the single domain serum albumin binding protein has a high binding affinity towards its binding target. In other embodiments, the single domain serum albumin binding protein has a medium binding affinity towards its binding target. In yet other embodiments, the single domain serum albumin binding protein has a low or marginal binding affinity towards its binding target. Exemplary binding affinities include

K_D of 10 nM or less (high), between 10 nM and 100 nM (medium), and greater than 100 nM (low). As above, binding affinities of the single domain serum albumin binding proteins towards binding targets are determined by known methods such as Surface Plasmon Resonance (SPR).

[00288] In some embodiments, the single domain serum albumin binding protein has an amino acid sequence selected from SEQ ID NOs: 3185-3193. In various embodiments, the single chain variable fragment CD3 binding protein comprises an amino acid sequence that is at least about 75%, about 76%, about 77%, about 78%, about 79%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identical to an amino acid sequence selected from SEQ ID NOs: 3185-3193.

[00289] In some embodiments, the single domain serum albumin binding protein has an elimination half-time of at least 1 hour, at least 2 hours, at least 4 hours, at least 6 hours, at least 12 hours, at least 20 hours, at least 25 hours, at least 30 hours, at least 35 hours, at least 40 hours, at least 45 hours, at least 50 hours, or at least 100 hours.

Immune cell engaging protein modifications

[00290] The immune cell engaging protein described herein, including antigen binding domains and immune cell engaging domains encompass derivatives or analogs in which (i) an amino acid is substituted with an amino acid residue that is not one encoded by the genetic code, (ii) the mature polypeptide is fused with another compound such as polyethylene glycol, or (iii) additional amino acids are fused to the protein, such as a leader or secretory sequence or a sequence for purification of the protein.

[00291] Typical modifications include, but are not limited to, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

[00292] Modifications are made anywhere in the immune cell engaging protein described herein, including the peptide backbone, the amino acid side-chains, and the

amino or carboxyl termini. Certain common peptide modifications that are useful for modification of the FLT3 binding proteins include glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation, blockage of the amino or carboxyl group in a polypeptide, or both, by a covalent modification, and ADP-ribosylation.

[00293] In some embodiments, derivatives of the immune cell engaging protein as described herein comprise immunoreactive modulator derivatives and antigen binding molecules comprising one or more modifications.

[00294] In some embodiments, the immune cell engaging protein of the disclosure are monovalent or multivalent bivalent, trivalent, etc.). As used herein, the term "valency" refers to the number of potential target binding sites associated with an antibody. Each target binding site specifically binds one target molecule or specific position or locus on a target molecule. When an antibody is monovalent, each binding site of the molecule will specifically bind to a single antigen position or epitope. When an antibody comprises more than one target binding site (multivalent), each target binding site may specifically bind the same or different molecules (*e.g.*, may bind to different ligands or different antigens, or different epitopes or positions on the same antigen).

[00295] In some embodiments, the immune cell engaging protein as set forth above are fused to an Fc region from any species, including but not limited to, human immunoglobulin, such as human IgG1, a human IgG2, a human IgG3, human IgG4, to generate Fc-fusion FLT3 binding proteins. In some embodiments, the Fc-fusion immune cell engaging protein of this disclosure have extended half-life compared to an otherwise identical immune cell engaging protein. In some embodiments, the Fc-fusion immune cell engaging protein of this disclosure contain *inter alia* one or more additional amino acid residue substitutions, mutations and/or modifications, *e.g.*, in the Fc region. which result in a binding protein with preferred characteristics including, but not limited to: altered pharmacokinetics, extended serum half-life.

[00296] In some embodiments, such Fc-fused immune cell engaging protein provide extended half-lives in a mammal, such as in a human, of greater than 5 days, greater than 10 days, greater than 15 days, greater than 20 days, greater than 25 days, greater than 30 days, greater than 35 days, greater than 40 days, greater than 45 days, greater than 2 months, greater than 3 months, greater than 4 months, or greater than 5 months. The increased half-life, in some cases, results in a higher serum titer which thus reduces the frequency of the administration of the immune cell engaging protein and/or reduces the concentration of the antibodies to be administered. Binding to human FcRn *in vivo* and

serum half-life of human FcRn high affinity binding polypeptides is assayed, in some examples, in transgenic mice or transfected human cell lines expressing human FcRn, or in primates to which the polypeptides with a variant Fc region are administered.

[00297] The immune cell engaging protein, in some cases, are differentially modified during or after production, *e.g.*, by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications are carried out by techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH4, acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

[00298] Various post-translational modifications of the immune cell engaging protein also encompassed by the disclosure include, for example, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends, attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. Moreover, the FLT3 binding proteins are, in some cases, modified with a detectable label, such as an enzymatic, fluorescent, radioisotopic or affinity label to allow for detection and isolation of the modulator.

Peptide Mask

[00299] The extended-release binding protein described herein, in some embodiments, comprises a masking peptide. When bound to the antigen binding domain(s) of the immune cell engaging protein, the masking peptide, in some embodiments, blocks, occludes, inhibits (*e.g.*, decreases) or otherwise prevents (*e.g.*, masks) the activity or binding of the antigen binding domain(s) to the target(s). In some embodiments, the masking peptide interferes with the binding of the antigen binding domain to a target antigen. In some embodiments, the immune cell engaging protein comprises a CD3 binding domain and the masking peptide is specific for the CD3 binding domain and interferes with binding of the CD3 binding domain to its target.

[00300] The masking peptide, in certain instances, is covalently linked to the N-terminus or C-terminus of immune cell engaging protein, for example, through a cleavable linker. In some embodiments, the masking peptide comprises a sequence selected from the group consisting of SEQ ID NOs: 3663-3682, or a sequence comprising one or more amino acid substitutions relative to a sequence selected from the group consisting of SEQ ID NOs: 3663-3682.

[00301] In some embodiments, the masking peptide is a peptide that is 5 amino acids in length, 6 amino acids in length, 7 amino acids in length, 8 amino acids in length, 9 amino acids in length, 10 amino acids in length, 11 amino acids in length, 12 amino acids in length, 13 amino acids in length, 14 amino acids in length, or longer. In some embodiments, the masking peptide is at least 3 amino acids in length. In some embodiments, the masking peptide is 3 to 12 amino acids, 4 to 15 amino acids, 5 to 20 amino acids, or 6 to 25 amino acids, in length. In some embodiments, the masking peptide is 6 amino acids in length. In some embodiments, the masking peptide is a linear peptide or a cyclic peptide. In some embodiments, the cyclized peptide is formed by a di-sulfide bond connecting two cysteine amino acid residues. In some embodiments, the cysteine amino acid residues are terminal cysteines, located at or near the N-terminus and/or the C-terminus of the masking peptide. In some embodiments, the di-sulfide bond connects an N- terminal cysteine with a C-terminal cysteine.

[00302] In some embodiments, the masking peptide comprises a sequence selected from the group consisting of SEQ ID NOs: 3663-3682, or a sequence comprising one or more amino acid substitutions (*e.g.*, two or three amino acid substitutions) relative to a sequence selected from the group consisting of SEQ ID NOs: 3663-3682.

Cleavable Linker

[00303] As described above, in some embodiments, the masking peptide and the half-life extended immune cell engaging protein are connected through a cleavable linker. The cleavable linker, in some embodiments, facilitates release of an active immune cell engaging protein in a cell. Examples of cleavable linker include but are not limited to: an acid-labile linker, a peptidase- sensitive linker, a photolabile linker, a dimethyl linker or disulfide-containing linker (*see, e.g.*, Chari *et al.*, Cancer Res. 52:127-131 (1992); U.S. Patent No. 5,208,020). The cleavable linker, in some embodiments, comprises a sequence that is recognized by a protease. Examples of proteases include, but are not limited to: ABHD12, ADAM12, ABHD12B, ABHD13, ABHD17A, ADAM 19, ADAM20, ADAM21, ADAM28, ADAM30, ADAM33, ADAM8, ABHD17A, ADAMDEC1, AD AMTS 1, AD AMTS 10, AD AMTS 12, AD AMTS 13, AD AMTS 14, AD AMTS 15, AD AMTS 16, AD AMTS 17, AD AMTS 18, AD AMTS 19, ADAMTS2, ADAMTS20, AD AMTS 3, AD AMTS 4, ABHD17B, AD AMTS 5, AD AMTS 6, ADAMTS 7, ADAMTS 8, ADAMTS 9, ADAMTSL1, ADAMTSL2, ADAMTSL3, ABHD17C, ADAMTSL5, ASTL, BMP1, CELA1, CELA2A, CELA2B, CELA3A, CELA3B, ADAM 10, ADAM 15, ADAM 17, ADAM9, ADAMTS4, CTSE, CTSF, ADAMTSL4, CMA1, CTRB 1, CTRC, CTSO, CTR1, CTSA, CTSW, CTSB,

CTSC, CTSD, ESP1, CTSG, CTSH, GZMA, GZMB, GZMH, CTSK, GZMM, CTSL, CTSS, CTSV, CTSZ, HTRA4, KLK10, KLK11, KLK13, KLK14, KLK2, KLK4, DPP4, KLK6, KLK7, KLKB 1, ECE1, ECE2, ECEL1, MASP2, MEP1A, MEP1B, ELANE, FAP, GZMA, MMP11, GZMK, HGFAC, HPN, HTRA1, MMP11, MMP 16, MMP17, MMP 19, HTRA2, MMP20, MMP21, HTRA3, HTRA4, KEL, MMP23B, MMP24, MMP25, MMP26, MMP27, MMP28, KLK5, MMP3, MMP7, MMP8, MMP9, LGMN, LNPEP, MASP1, PAPPA, PAPPA2, PCSK1, NAPSA, PCSK5, PCSK6, MME, MMP1, MMP10, PLAT, PLAU, PLG, PRSS 1, PRSS 12, PRSS2, PRSS21, PRSS3, PRSS33, PRSS4, PRSS55, PRSS57, MMP 12, PRSS8, PRSS9, PRTN3, MMP13, MMP14, ST14, TMPRSS10, TMPRSS11A, TMPRSS11D, TMPRSS11E, TMPRSS11F, TMPRSS12, TMPRSS13, MMP15, TMPRSS15, MMP2, TMPRSS2, TMPRSS3, TMPRSS4, TMPRSS5, TMPRSS6, TMPRSS7, TMPRSS9, NRDC, OVCH1, PAMR1, PCSK3, PHEX, TINAG, TPSAB1, TPSD1, and TPSGE In some embodiments, the cleavable peptide is cleaved by one or more enzyme selected from the group consisting of: ADAM 17, HTRA1, PRSS1, FAP, GZMK, NAPSA, MMP1, MMP2, MMP9, MMP10, MMP7, MMP12, MMP28, AD AMTS 9, HGFAC, and HTRA3.

Exemplary protease recognition sequences are provided **Table 1**:

SEQ ID No.	Description	Sequence
3716	protease cleavage site	VANLA
3717	protease cleavage site	PLGL
3718	protease cleavage site	PQAS
3719	protease cleavage site	PKPQA
3720	protease cleavage site	PTGLE
3721	protease cleavage site	PENFF
3722	protease cleavage site	AATLK
3723	protease cleavage site	PQDLL
3724	protease cleavage site	PAGL
3725	protease cleavage site	VLGL
3726	protease cleavage site	RLQLKL
3727	protease cleavage site	RTRYED
3728	protease cleavage site	KPLGL
3729	Protease: MMP7	KRALGLPG
3730	Protease: MMP7	(DE)8RPLALWRS(DR)8
3731	Protease: MMP9	PR(S/T)(L/I)(S/T)
3732	Protease: MMP9	LEATA
3733	Protease: MMP11	GGAANLVRGG
3734	Protease: MMP14	SGRIGFLRTA
3735	Protease: MMP	PLGLAG
3736	Protease: MMP	PLGLAX
3737	Protease: MMP	PLGC(me)AG
3738	Protease: MMP	ESPAYYTA

SEQ ID No.	Description	Sequence
3739	Protease: MMP	RLQLKL
3740	Protease: MMP	RLQLKAC
3741	Protease: MMP2, MMP9, MMP14	EP(Cit)G(Hof)YL
3742	Protease: Urokinase plasminogen activator (uPA)	SGRSA
3743	Protease: Urokinase plasminogen activator (uPA)	DAFK
3744	Protease: Urokinase plasminogen activator (uPA)	GGGRR
3745	Protease: Lysosomal Enzyme	GFLG
3746	Protease: Lysosomal Enzyme	ALAL
3747	Protease: Lysosomal Enzyme	FK
3748	Protease: Cathepsin B	NLL
3749	Protease: Cathepsin D	PIC(Et)FF
3750	Protease: Cathepsin K	GGPRGLPG
3751	Protease: Prostate Specific Antigen	HSSKLQ
3752	Protease: Prostate Specific Antigen	HSSKLQL
3753	Protease: Prostate Specific Antigen	HSSKLQEDA
3754	Protease: Herpes Simplex Virus Protease	LVLASSSFGY
3755	Protease: HIV Protease	GVSQNYPIVG
3756	Protease: CMV Protease	GVVQASCRLA
3757	Protease: Thrombin	F(Pip)RS
3758	Protease: Thrombin	DPRSFL
3759	Protease: Thrombin	PPRSFL
3760	Protease: Caspase-3	DEVD
3761	Protease: Caspase-3	DEVDP
3762	Protease: Caspase-3	KGSGDVEG
3763	Protease: Interleukin 1β converting enzyme	GWEHDG
3764	Protease: Enterokinase	EDDDDKA
3765	Protease: FAP	KQEQNPGST
3766	Protease: Kallikrein 2	GKAFRR
3767	Protease: Plasmin	DAFK
3768	Protease: Plasmin	DVLK
3769	Protease: Plasmin	DAFK
3770	Protease: TOP	ALLLALL

[00304] In some embodiments, a linker as described herein comprises a sequence selected from the sequences provided in **Table 2.** In some embodiments, a linker as described herein further comprises sequences flanked on the N-terminal and/or C-terminal. In some embodiments, the flanked sequences may be (but are not limited to) the following: GGGG, GGGS, GGGT, GGGGG, GGGGS, and/or GGGGT.

Table 2. Selected linker sequences

SEQ ID NO:	Description	Sequence
3683	non-cleavable	SGGGGSGGVV
3684	non-cleavable	SGGGGSGGGGSGGGGS
3685	non-cleavable	SGGGGSGGGGSGGGGGS
3686	non-cleavable	SGGGGSGGGS
3687	non-cleavable	GGGGSGGGGSGGGGSGGG
3688	L001	KPLGLQARVV
3689	L040	PQASTGRSGG
3690	L041	PQGSTGRAAG
3691	L042	PPASSGRAGG
3692	L043	PQGSTARSAG
3693	L045	PIPVQGRAH
3694	L054	VANLASTGRA
3695	L055	PLGLSTGRA
3696	L056	PQASTGRA
3697	L057	PKPQASTGRA
3698	L058	PTGLESTGRA
3699	L059	PENFFSTGRA
3700	L060	AATLKSTGRA
3701	L061	PQDLLSTGRA
3702	L062	PAGLSTGRA
3703	L063	VLGLSTGRA
3704	L064	VANLASTGA
3705	L065	PLGLSTGA
3706	L066	PQASTGA
3707	L067	PKPQASTGA
3708	L068	PTGLESTGA
3709	L069	PENFFSTGA
3710	L070	AATLKSTGA
3711	L071	PQDLLSTGA
3712	L072	PAGLSTGA
3713	L073	VLGLSTGA
3714	L075	RTRYEDGGS
3715	L076	PQASTGGSG
3878	L085	KPLGLQAGVV

Polynucleotides Encoding the Extended-Release Binding Protein

[00305] Also provided, in some embodiments, are polynucleotide molecules encoding the extended-release binding protein described herein. In some embodiments, the polynucleotide molecules are provided as a DNA construct. In other embodiments, the polynucleotide molecules are provided as a messenger RNA transcript.

[00306] The polynucleotide molecules are constructed by known methods such as by combining the genes encoding the immune cell engaging protein or gene encoding various domains of the immune cell engaging protein comprising more than one domain. In some embodiments, the gene encoding the domains are either separated by peptide linkers or, in other embodiments, directly linked by a peptide bond, into a single genetic construct operably linked to a suitable promoter, and optionally a suitable transcription terminator, and expressing it in bacteria or other appropriate expression system such as, for example CHO cells. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. The promoter is selected such that it drives the expression of the polynucleotide in the respective host cell.

[00307] In some embodiments, the polynucleotide coding for an extended-release binding protein as described herein is inserted into a vector, preferably an expression vector, which represents a further embodiment. This recombinant vector can be constructed according to known methods. Vectors of particular interest include plasmids, phagemids, phage derivatives, virii (*e.g.*, retroviruses, adenoviruses, adeno-associated viruses, herpes viruses, lentiviruses, and the like), and cosmids.

[00308] A variety of expression vector/host systems may be utilized to contain and express the polynucleotide encoding the polypeptide of the described immune cell engaging protein. Examples of expression vectors for expression in *E.coli* are pSKK (Le Gall *et al.*, J Immunol Methods. (2004) 285(1):111-27) or pcDNA5 (Invitrogen) for expression in mammalian cells.

[00309] Thus, the extended-release binding protein as described herein, in some embodiments, are produced by introducing a vector encoding the protein as described above into a host cell and culturing said host cell under conditions whereby the protein domains are expressed, may be isolated and, optionally, further purified.

Protein with Masking Peptide

[00310] Described herein is a pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker. Without being bound by any theory, it is contemplated that the protein with the masking peptide described herein is able to reduce target-mediated drug disposition when administered to a subejct by gradually releasing the active form of the binding moiety when it is in systemic circulation.

[00311] In some aspects, the cleavable linker is significantly cleaved in systemic circulation. In some aspects, the half-life of the protein described herein in systemic

circulation is longer than a comparable protein without the masking peptide. In some aspects, a comparable protein without the masking peptide has a nonlinear pharmacokinetics (PK) across a dose range evaluated, and the protein described herein has an improved linearity of PK across the dose range evaluated compared to the comparable protein. In some aspects, the molar amount of the protein's binding moiety bound to the target when administered to the subject is lower compared to the molar amount of a binding moiety of a comparable protein without the masking peptide when administered to the subject at a same dose level. In some aspects, the binding rate between the protein's binding moiety and the target when administered to the subject is lower compared to the binding rate between a binding moiety of a comparable protein without the masking peptide and the target. Fig. 30 provides examplary consturcts of the protein with masking peptide described herein.

Targets

[00312] The binding moiety of the protein with masking peptide descrined herein may bind to various targets. A non-exhaustive list of the targets is ICOS (inducible T cell co-stimulator, CD278), OX40 (CD134, TNFRSF4, tumor necrosis factor receptor superfamily member 4), CD40 (TNFRSF5, tumor necrosis factor receptor superfamily member 5), DR5 (death receptor 5, TRAIL receptor 2), GITR (glucocorticoid-induced TNFR-related protein, TNFRSF18, tumor necrosis factor receptor superfamily member 18), and 4-1BB (CD137, TNFRSF9, tumor necrosis factor receptor superfamily member 9).

[00313] In some embodiments, the target may be ICOS. ICOS is a T-cell specific, CD28-superfamily costimulatory molecule and immune checkpoint protein. ICOS is normally expressed on certain activated T cells and plays a key role in the proliferation and activation of T cells.

[00314] In some embodiments, the target may be OX40. OX40 is a cell surface glycoprotein and member of the tumor necrosis factor receptor superfamily (TNFRSF). OX40 is expressed on T lymphocytes and plays an essential role in T-cell activation. Co-stimulation of activated T cells with agonistic monoclonal antibodies (mAb) against the tumor necrosis factor receptor superfamily member OX40 offers a novel immunotherapeutic approach to cancer. OX40 engagement may co-stimulate effector T cells and deplete regulatory T cells, resulting in enhanced tumor immunity.

[00315] In some embodiments, the target may be CD40. CD40 is a stimulatory receptor and a member of the tumor necrosis factor (TNF) receptor superfamily. CD40 is expressed on various immune cells, such as macrophages, dendritic cells and various

tumor cell types, such as many B-cell malignancies, and some solid tumors. CD40 plays a key role in the activation of the immune system, mediats both indirect tumor cell killing through the activation of the immune system and direct tumor cell apoptosis. CD40 is highly expressed on most B-lineage hematologic malignancies including multiple myeloma, non-Hodgkin lymphoma, chronic lymphocytic leukemia, Hodgkin disease and acute lymphoblastic leukemia.

[00316] In some embodiments, the target may be DR5. DR5, also known as TRAIL receptor 2 (TRAILR2) and tumor necrosis factor receptor superfamily member 10B (TNFRSF10B), is a cell surface receptor of the TNF-receptor superfamily that binds TRAIL and mediates apoptosis. DR5 contains an intracellular death domain. DR5 can be activated by tumor necrosis factor-related apoptosis inducing ligand (TNFSF10/TRAIL/APO-2L), and transduces apoptosis signal. TRAIL, a member of the TNF superfamily of cytokines, plays a key role in the induction of apoptosis through TRAIL-mediated death receptor pathways.

[00317] In some embodiments, the target may be GITR (glucocorticoid-induced tumor necrosis factor receptor; tumor necrosis factor superfamily, member 18; TNFRSF18). GITR is a TNF receptor superfamily costimulatory molecule expressed primarily by regulatory T cells (Treg), effector T cells, and natural killer cells that inhibits the suppressive activity of Tregs. Agonistic antibodies or GITR ligand binding to GITR in concert with T cell receptor (TCR) stimulation causes activation of the MAPK/ERK pathway and NFkB, resulting in augmentation of T cell proliferation and proinflammatory cytokine production and enhanced anti-tumor effector function, as well as resistance of CD4+ and CD8+ T cells to Treg suppression. In tumor models, signaling through GITR has been shown to inhibit Treg proliferation, induce Treg depletion, and cause tumor regression.

[00318] In some embodiments, the target may be 4-1BB. 4-1BB is a member of the tumor necrosis factor (TNF)/nerve growth factor (NGF) family of receptors and is expressed by activated T- and B-lymphocytes and monocytes. 4-1BB's ligand has been found to play an important role in the regulation of immune responses.

Antibodies

[00319] The protein with the masking peptide described herein may include an antibody. A non-exhaustive list of the antibody is GSK3359609 (GSK609, feladilimab), PF-8600 (PF-04518600, ivuxolimab), JNJ-64457107 (JNJ-107, JNJ 7107, ADC-1013, mitazalimab), CP-870,893, SGN-40 (huS2C6, Dacetuzumab), MEDI3039, ABBV-621

(eftozanermin alfa, APG880), MEDI1873 (efgivanermin alfa), AMG 228, PF-05082566 (Utomilumab, uto), and urelumab (BMS-663513).

[00320] In some embodiments, the antibody may be GSK3359609 (GSK609, feladilimab). GSK3359609 is an agonistic antibody for the inducible T-cell co-stimulator (ICOS; CD278), with potential immune checkpoint inhibitory and antineoplastic activities. Upon administration, GSK3359609 targets and binds to ICOS expressed on tumor infiltrating CD4-positive T cells. This stimulates ICOS-positive T-cell proliferation, enhances cytotoxic T-lymphocyte (CTL) survival and increases CTL-mediated immune responses against tumor cells.

[00321] In some embodiments, the antibody may be PF-8600 (PF-04518600, ivuxolimab). PF-8600 is a fully human agonist IgG2 mAb that targets the co-stimulatory receptor OX40 (CD134; TNFRSF4), with potential immunostimulatory activity. Upon administration, PF-8600 selectively binds to and activates OX40; which induces proliferation of memory and effector T lymphocytes. In the presence of tumor-associated antigens (TAAs), this may promote a T-cell-mediated immune response against TAA-expressing tumor cells.

[00322] In some embodiments, the antibody may be JNJ-64457107 (JNJ-107, JNJ 7107, ADC-1013, mitazalimab). JNJ-64457107 is a human immunoglobulin (Ig) G1 monoclonal antibody directed against the cell surface receptor CD40 with potential immunostimulatory and antineoplastic activities. Upon intratumoral administration, JNJ-64457107 binds to CD40 on antigen-presenting dendritic cells, which leads to the activation and proliferation of effector and memory T cells, and enhances the immune response against tumor cells. In addition, this agent binds to the CD40 antigen present on the surfaces of tumor cells, which induces antibody-dependent cytotoxicity (ADCC). This eventually inhibits the proliferation of CD40-expressing tumor cells.

[00323] In some embodiments, the antibody may be CP-870,893. CP-870,893 is a fully human monoclonal antibody (mAb) agonist of the cell surface receptor CD40 with potential immunostimulatory and antineoplastic activities. Similar to the CD40 ligand (CD40L or CD154), CP-870,893 binds to CD40 on a variety of immune cell types, triggering the cellular proliferation and activation of antigen-presenting cells (APCs), activating B cells and T cells, and enhancing the immune response; in addition, this agent may activate CD40 present on the surfaces of some solid tumor cells, resulting in apoptosis and decreased tumor growth.

[00324] In some embodiments, the antibody may be SGN-40 (huS2C6, Dacetuzumab). SGN-40 is a humanized monoclonal antibody directed against the CD40 receptor with

potential antineoplastic activity. SGN-40 specifically binds to and inhibits the CD40 receptor, thereby inducing apoptosis and inhibiting cellular proliferation via antibody-dependent cellular cytotoxicity (ADCC) in cells that overexpress this receptor.

[00325] In some embodiments, the antibody may be MEDI3039. MEDI3039 is a highly potent multivalent DR5 agonist. MEDI3039 is a modified protein derived from the third fibronectin type III domain of the glycoprotein tenascin C, which possesses a rgion similar to the variable region characteristic of antibodies. An optimized multivalent DR5 agonist was highly potent in triggering cell death in multiple TRAIL-sensitive cell lines, was one to two orders of magnitude more potent than TRAIL, and showed promising results in multiple cancer cells (colon, lung, leukemia, liver cancers) and *in vivo* colon cancer models.

[00326] In some embodiments, the antibody may be ABBV-621 (eftozanermin alfa, APG880). ABBV-621 is a fusion protein composed of a tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor agonist consisting of six receptor binding domains (RBDs) of TRAIL fused to the Fc-domain of a human immunoglobulin G1 (IgG1) antibody, with potential pro-apoptotic and antineoplastic activities. Upon administration, ABBV-621 binds to TRAIL-receptors, pro-apoptotic death receptors (DRs) TRAIL-R1 (death receptor 4; DR4) and TRAIL-R2 (death receptor 5; DR5), expressed on tumor cells, thereby inducing tumor cell apoptosis. ABBV-621 is designed to maximize receptor clustering for optimal efficacy.

[00327] In some embodiments, the antibody may be MEDI1873 (efgivanermin alfa). MEDI1873 is a homogenous hexameric agonist fusion protein composed of the extracellular domain (ECD) of the T-cell costimulatory receptor human GITR ligand (GITRL) and an immunoglobulin (Ig) G1 Fc domain, with potential immunomodulating and antineoplastic activities. Upon administration, MEDI1873 binds to and activates GITR found on multiple types of T cells, thereby inducing both the activation and proliferation of tumor antigen-specific T-effector cells. This abrogates the suppression of T-effector cells which is induced by inappropriately activated T-regulatory cells (Tregs), suppresses Tregs and decreases Treg tumor infiltration, and activates the immune system to help eradicate tumor cells.

[00328] In some embodiments, the antibody may be AMG 228. AMG 228 is an agonistic human IgG1 monoclonal antibody that binds to human GITR similar to MEDI1873.

[00329] In some embodiments, the antibody may be PF-05082566 (Utomilumab, uto). PF-05082566 is a humanized agonist IgG2 monoclonal antibodies for the tumor necrosis

factor superfamily receptors 4-1BB. PF-05082566's binding to human 4-1BB results in NF-κB activation and downstream cytokine production in cell lines and primary lymphocytes. PF-05082566 can induce human leukocyte proliferation and has demonstrated significant antitumor activity as a single agent in human peripheral blood lymphocyte (PBL) SCID xenograft tumor models.

[00330] In some embodiments, the antibody may be urelumab. Urelumab is a humanized agonistic monoclonal antibody targeting the 4-1BB receptor with potential immunostimulatory and antineoplastic activities. Urelumab specifically binds to and activates 4-1BB-expressing immune cells, stimulating an immune response, in particular a cytotoxic T cell response, against tumor cells.

Methods of Treatment

[00331] Also provided herein, in some embodiments, are methods and uses for stimulating the immune system of an individual in need thereof comprising administration of an extended-release binding protein and the protein with masking peptide as described herein. In some instances, administration induces and/or sustains cytotoxicity towards a cell expressing a target antigen. In some instances, the cell expressing a target antigen is a cancer or tumor cell, a virally infected cell, a bacterially infected cell, an autoreactive T or B cell, damaged red blood cells, arterial plaques, or fibrotic tissue. In some embodiments, the target antigen is an immune checkpoint protein.

[00332] Also provided herein are methods and uses for a treatment of a disease, disorder or condition associated with a target antigen comprising administering to an individual in need thereof an extended-release binding protein and the protein with masking peptide as described herein. Diseases, disorders or conditions associated with a target antigen include, but are not limited to, viral infection, bacterial infection, auto-immune disease, transplant rejection, atherosclerosis, or fibrosis. In other embodiments, the disease, disorder or condition associated with a target antigen is a proliferative disease, a tumorous disease, an inflammatory disease, an immunological disorder, an autoimmune disease, an infectious disease, a viral disease, an allergic reaction, a parasitic reaction, a graft-versus-host disease or a host-versus-graft disease. In one embodiment, the disease, disorder or condition associated with a target antigen is cancer. In one embodiment, the cancer is a hematological cancer. In one embodiment, the cancer is a melanoma. In one embodiment, the cancer is lung cancer. In one embodiment, the cancer is ovarian cancer. In one embodiment, the cancer is prostate cancer. In one embodiment, the cancer is pancreatic cancer. In one embodiment, the cancer is mesothelioma. In one embodiment, the cancer is neuroendocrine cancers. In one embodiment, the cancer is multiple myeloma. In one embodiment, the cancer is breast cancer.

[00333] As used herein, in some embodiments, "treatment" or "treating" or "treated" refers to therapeutic treatment wherein the object is to slow (lessen) an undesired physiological condition, disorder or disease, or to obtain beneficial or desired clinical results. For the purposes described herein, beneficial or desired clinical results include, but are not limited to, alleviation of symptoms; diminishment of the extent of the condition, disorder or disease; stabilization (*i.e.*, not worsening) of the state of the condition, disorder or disease; delay in onset or slowing of the progression of the condition, disorder or disease; amelioration of the condition, disorder or disease state; and remission (whether partial or total), whether detectable or undetectable, or enhancement or improvement of the condition, disorder or disease. Treatment includes eliciting a clinically significant response without excessive levels of side effects. Treatment also includes prolonging survival as compared to expected survival if not receiving treatment. In other embodiments, "treatment" or "treating" or "treated" refers to prophylactic measures, wherein the object is to delay onset of or reduce severity of an undesired physiological condition, disorder or disease, such as, for example is a person who is predisposed to a disease (*e.g.*, an individual who carries a genetic marker for a disease such as breast cancer).

[00334] In some embodiments of the methods described herein, the extended-release binding proteins and the protein with masking peptide described herein are administered in combination with an agent for treatment of the particular disease, disorder or condition. Agents include but are not limited to, therapies involving antibodies, small molecules (*e.g.*, chemotherapeutics), hormones (steroidal, peptide, and the like), radiotherapies (γ-rays, X-rays, and/or the directed delivery of radioisotopes, microwaves, UV radiation and the like), gene therapies (*e.g.*, antisense, retroviral therapy and the like) and other immunotherapies. In some embodiments, the extended-release binding proteins described herein are administered in combination with anti-diarrheal agents, anti-emetic agents, analgesics, opioids and/or non-steroidal anti-inflammatory agents. In some embodiments, the conditionally active binding proteins described herein is administered before, during, or after surgery.

[00335] Administration of the extended-release binding protein and the protein with masking peptide described herein can be effected by different ways, *e.g.* by intravenous, intraperitoneal, subcutaneous, intramuscular, topical or intradermal administration. In some embodiments, the route of administration depends on the kind of therapy and the kind of compound contained in the pharmaceutical composition. In some embodiments, the extended-release binding protein is injected or injectable.

EXAMPLES

[00336] The examples below further illustrate the described embodiments without limiting the scope of the disclosure.

Example 1: Exemplary constructs of an extended-release binding protein

[00337] An exemplary construct of an extended-release binding protein is shown in **Fig. 1**. TriTAC-XR is a tri-specific binding protein with anti-target, anti-albumin and anti-CD3 binding capabilities. The intact form of the extended-release binding protein (**Fig. 1A**) comprises a CD3 mask linked to the binding protein with a cleavable linker. When the cleavable linker is gradually cleaved in the subject, it releases the active version of the extended-release binding protein (**Fig. 1B**). **FIG. 1C** shows the predicted concentrations of the intact version and the active version in systemic circulation after multiple administration events. **FIG. 1D** shows the predicted concentration of the active version of a corresponding antigen binding protein without the masking peptide in systemic circulation after multiple administration events.

[00338] Additional extended-release binding protein constructs are shown in **Figs. 2A-L** with various configurations of the anti-target, anti-albumin and anti-CD3 binding domains. **Figs. 2A-C and Figs. 2G-I** illustrate the intact versions and **Figs. 2D-F and Figs. 2J-L** illustrate the active versions after cleavage of the linker.

Example 2: Production and purification of the extended-release binding proteins used in the present study

[00339] Protein Production: Sequences of exemplary TriTAC-XR molecules were cloned into mammalian expression vector pcDNA3.4 (Invitrogen) preceded by a leader sequence and followed by a 6x histidine tag. Expi293F cells (Life Technologies A14527) were maintained in suspension in between 0.2 to 8 x 10^6 cells/ml in Expi293 media. Purified plasmid DNA was transfected into Expi293 cells in accordance with Expi293 Expression System Kit (Life Technologies, A14635) protocols, and maintained for 4-6 days post transfection. The amount of the exemplary TriTAC-XR proteins in conditioned media was quantitated using an Octet RED96 instrument with Protein A tips (ForteBio /Sartorius) using a control trispecific protein for a standard curve.

[00340] Protein Purification: Conditioned media from either host cell was filtered and partially purified by affinity and desalting chromatography. TriTAC-XR proteins were subsequently polished by ion exchange and upon fraction pooling formulated in a neutral buffer containing excipients. Final purity was assessed by SDS-PAGE and analytical SEC using an Acquity BEH SEC 200 1.7u 4.6 x 150 mm column (Waters Corporation) resolved in an aqueous/organic mobile phase with excipients at neutral pH on a 1290 LC system and peaks integrated with Chemstation CDS software (Agilent).

Example 3: PSMA targeting extended-release binding proteins induced T cell-dependent cellular cytotoxicity assay

[00341] The binding proteins used in this study are summarized in **Table 3**. Stub:T:A:C is a PSMA binding protein without the masking domain. As described herein, stub refers to the residual linker remaining on the active drug fragment after protease cleavage. Peptide:NCLV is a PSMA binding protein with a peptide mask and non-cleavable linker. Peptide:L001 is a PSMA targeting extended-release binding protein with a peptide mask and linker L001, which is a cleavable linker. Ion exchange chromatography profiles (**Fig. 3**) demonstrate the purity of the PSMA targeting proteins and also show that there is little or no active drug present (stub:T:A:C) in the purified peptide:L001 protein.

Table 3. PSMA Binding Proteins and EC_{50} values

Protein	SEQ ID NO	EC_{50} (pM)	Fold over stub:T:A:C
stub:T:A:C	3609	5	1
peptide:NCLV	3601	6256	1249
peptide:L001	3600	81	16

[00342] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 3** were incubated in multi-well plates, with purified resting human T cells (effector cell) and MDAPCa2b cancer cells at 10:1 effector: target cell ratio for 48 h at 37°C in the presence of 15 mg/ml human serum albumin (HSA). The MDAPCa2b cells had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Fig. 4** demonstrates slow activation of peptide masked PSMA targeting extended-release binding proteins in TDCC assay. The EC_{50} values are provided in **Table 3**. The efficiency of masking is quantitated by the fold increase in EC_{50} of peptide:NCLV (SEQ ID NO: 3601) or peptide:L001 (SEQ ID NO: 3600) over stub:T:A:C (SEQ ID NO: 3609) (**Table 3**).

Example 4: PSMA targeting extended-release binding proteins with different peptide mask sequences induced T cell-dependent cellular cytotoxicity assay

[00343] The binding proteins with various masking peptides used in this study are summarized in **Table 4**. The configuration of the anti-target, anti-albumin and anti-CD3 binding domains are according to **Fig. 2A** (SEQ ID Nos: 3601 to 3608) and **Fig. 2D** (SEQ ID NO. 3609) except SEQ ID NO. 3610, which is a ProTriTAC molecule. Description a ProTriTAC molecule's structure can be found in WO2019222283A1, which is incorporated herein by reference.

Table 4. PSMA Binding Proteins and EC_{50} values

SEQ ID NO	Protein	EC_{50} (M)	Fold increase in EC_{50} over SEQ ID NO 3609
3601	QDGNEE:NCLV:αPSMA:αALB:αCD3	1E-09	720
3602	LDGNEE:NCLV:αPSMA:αALB:αCD3	7E-12	5
3603	PDGNEE:NCLV:αPSMA:αALB:αCD3	7E-12	5
3604	DDGNEE:NCLV:αPSMA:αALB:αCD3	3E-12	2
3605	EDGNEE:NCLV:αPSMA:αALB:αCD3	8E-12	5
3606	QEGNEE:NCLV:αPSMA:αALB:αCD3	2E-10	160
3607	QDANEE:NCLV:αPSMA:αALB:αCD3	2E-10	130
3608	QDSNEE:NCLV:αPSMA:αALB:αCD3	1E-11	8
3609	stub:αPSMA:αALB:αCD3	1E-12	1
3610	αALB-MASK027::NCLV:αPSMA:αALB:αCD3	2E-10	170

[00344] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 4** were incubated in multi-well plates, with purified resting human T cells (effector cell) and LNCaP cancer cells at 10:1 effector: target cell ratio for 48-72 h at 37°C. Human serum albumin is present. The cancer target cell lines had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Fig. 5** demonstrates the masking effects of various peptide masks. The EC_{50} values are provided in **Table 4**. The efficiency of masking is quantitated by the fold increase in EC_{50} of SEQ ID Nos 3601 to 3608 and 3610 over SEQ ID NO 3609 (**Table 4**). The results show that masking sequences QDGNEE, QDANEE and QEGNEE provide the most efficient masking effect.

Example 5: MSLN targeting extended-release binding proteins with different peptide mask sequences induced T cell-dependent cellular cytotoxicity assay

[00345] The binding proteins with various masking peptides used in this study are summarized in **Table 5**. The configuration of the anti-target, anti-albumin and anti-CD3 binding domains are according to **Fig. 2A** (SEQ ID NOS. 3659 to 3661) or **Fig 2D** (SEQ ID NO. 3662).

Table 5. MSLN Binding Proteins and EC_{50} values

SEQ ID NO	Protein	EC_{50} BSA (M)	EC_{50} HSA (M)	with BSA fold increase in EC_{50} over SEQ ID NO 3662	with HSA fold increase in EC_{50} over SEQ ID NO 3662
3659	QEGNEE:NCLV:αMSLN:αALB:αCD3	2E-11	9E-11	15	25
3660	QDANEE:NCLV:αMSLN:αALB:αCD3	1E-11	1E-10	14	26
3661	QDGNEE:NCLV:αMSLN:αALB:αCD3	1E-09	2E-09	1124	525
3662	stub:αMSLN:αALB:αCD3	1E-12	4E-12	1	1

[00346] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 5** were incubated, in multi-well plates, with purified resting human T cells (effector cell) and OVCAR8 cancer cells at 10:1 effector: target cell ratio for 48 h at 37°C. Bovine serum albumin (BSA) or HSA were present at 15 mg/ml. The cancer target cell lines had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Figs. 6A-B** demonstrates the masking effects of various peptide masks. The EC_{50} values are provided in **Table 5**. The efficiency of masking is quantitated by the fold increase in EC_{50} of SEQ ID Nos: 3659 to 3661 over SEQ ID NO 3663 (**Table 5**).

Example 6: CD19 targeting extended-release binding proteins with different domain configurations induced T cell-dependent cellular cytotoxicity assay

[00347] The binding proteins used in this study are summarized in **Table 6**. The configuration of the anti-target, anti-albumin and anti-CD3 binding domains are according to **Fig. 2A-C** and **Fig. 2G-I** (SEQ ID Nos: 3627 to 3631) and **Fig. 2D-F** and **Fig. 2J-L** (SEQ ID Nos: 3632 to 3636). SEQ ID Nos: 3627 to 3631 contain a masking domain and a non-cleavable linker. SEQ ID Nos: 3632 to 3636 are genetically engineered to encode the product after protease cleavage if the molecules had been made with a cleavable linker (stub:Active molecules).

Table 6. CD19 Binding Proteins and EC_{50} values

NCLV SEQ ID NO	stub:Active SEQ ID NO	Protein Name	NCLV EC50 (M)	stub:Active EC50 (M)	NCLV / stub:Active
3626	3632	αCD19 A:C:T	1E-09	8E-11	17
3627	3633	αCD19 A:T:C	3E-10	3E-11	9
3628	3634	αCD19 C:A:T	>1E-8	4E-11	>270
3629	3635	αCD19 C:T:A	>1E-8	1E-10	>80
3630	3611	αCD19 T:A:C	>1E-8	2E-11	>420
3631	3636	αCD19 T:C:A	>1E-8	1E-11	>870

[00348] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 6** were incubated, in multi-well plates, with purified resting human T cells (effector cell) and Raji cancer cells at 10:1 effector: target cell ratio for 72 h at 37°C. HSA was present. The cancer target cell lines had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Fig. 7** demonstrates the TDCC assay results of various CD19 targeting proteins. The EC_{50} values are provided in **Table 6**. The efficiency of masking is quantitated by the fold increase in EC_{50} of the NCLV protein over the stub:Active protein (**Table 6**). Results shows that T:A:C and T:C:A configurations have low double digit picomolar

stub: active EC_{50} and no activity when masked with a NCLV linker, while A:C:T and A:T:C configurations have poor masking effects.

Example 7: FLT3 targeting extended-release binding proteins with different domain configurations induced T cell-dependent cellular cytotoxicity assay

[00349] The binding proteins used in this study are summarized in **Table 7**. The configuration of the anti-target, anti-albumin and anti-CD3 binding domains are according to **Fig. 2A-C** and **Fig. 2G-I** (SEQ ID Nos: 3648 to 3653) and **Fig. 2D-F** and **Fig. 2J-L** (SEQ ID Nos: 3654 to 3658). SEQ ID Nos: 3648 to 3653 contain a masking domain and a non-cleavable linker. SEQ ID Nos: 3654 to 3658 are genetically engineered to encode the product after protease cleavage if the molecules had been made with a cleavable linker (stub:Active molecules). The FLT3 binder used in this study is 19C (SEQ ID NO: 1076).

Table 7. FLT3 Binding Proteins and EC_{50} values

NCLV SEQ ID NO	stub:Active SEQ ID NO	Protein Name	NCLV EC50 (M)	stub:Active EC50 (M)	NCLV / stub Active
3648	3654	αFLT3-H19C A:C:T	>1E-8	2E-09	>7
3649	3655	αFLT3-H19C A:T:C	~1E-8	8E-10	~13
3650	3656	αFLT3-H19C C:A:T	>1E-8	2E-10	>50
3651	3657	αFLT3-H19C C:T:A	>1E-8	5E-10	>20
3652	3613	αFLT3-H19C T:A:C	>1E-8	5E-11	>210
3653	3658	αFLT3-H19C T:C:A	>1E-8	3E-10	>30

[00350] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 7** were incubated, in multi-well plates, with purified resting human T cells (effector cell) and MOLM13 cancer cells at 10:1 effector: target cell ratio for 48-72 h at 37°C. HSA was present. The cancer target cell lines had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Fig. 8** demonstrates the TDCC assay results of various FLT3 targeting proteins. The EC_{50} values are provided in **Table 7**. The efficiency of masking is quantitated by the fold increase in EC_{50} of the NCLV protein over the stub:Active protein (**Table 7**). Results shows that TAC configuration has ~50 picomolar EC_{50} in the stub:Active form and no activity when masked with a NCLV linker, while A:C:T and A:T:C configurations have poor masking effects.

Example 8: FLT3 targeting extended-release binding proteins with different domain configurations induced T cell-dependent cellular cytotoxicity assay

[00351] The binding proteins used in this study are summarized in **Table 8**. The configuration of the anti-target, anti-albumin and anti-CD3 binding domains are according to **Fig. 2A-C** and **Fig. 2G-I** (SEQ ID NOS 3637 to 3642) and **Fig. 2D-F** and **Fig. 2J-L** (SEQ ID NOS 3643 to

3647). SEQ ID NOS. 3637 to 3642 contain a masking domain and a non-cleavable linker. SEQ ID NOS 3643 to 3647 are genetically engineered to encode the product after protease cleavage if the molecules had been made with a cleavable linker (stub:Active molecules). The FLT3 binder used in this study is 107 (SEQ ID NO: 1074).

Table 8. FLT3 Binding Proteins and EC_{50} values

NCLV SEQ ID NO	stub:Active SEQ ID NO	Protein Name	NCLV EC50 (M)	stub:Active EC50 (M)	NCLV / stub Active
3637	3643; did not express	αFLT3-H107 A:C:T	4E-10	Not Tested	N/A
3638	3644	αFLT3-H107 A:T:C	3.6E-10	5E-12	70
3639	3645	αFLT3-H107 C:A:T	>1E-8	7E-12	>1500
3640	3646	αFLT3-H107 C:T:A	>1E-8	5E-12	>2000
3641	3612	αFLT3-H107 T:A:C	>1E-8	8E-12	>1200
3642	3647	αFLT3-H107 T:C:A	>1E-8	7E-12	>1500

[00352] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 8** were incubated, in multi-well plates, with purified resting human T cells (effector cell) and MOLM13 cancer cells at 10:1 effector: target cell ratio for 48 h at 37°C. HSA was present. The cancer target cell lines had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Fig. 9** demonstrates the TDCC assay results of various FLT3 targeting proteins. The EC_{50} values are provided in **Table 8**. The efficiency of masking is quantitated by the fold increase in EC_{50} of the NCLV protein over the stub:Active protein (**Table 8**). Results shows that 4 configurations (C:A:T, C:T:A, T:A:C and T:C:A) have single digit picomolar Active EC_{50} in the active form and no activity when masked with a NCLV linker, while the A:T:C configuration has poor masking. The stub_A:C:T configuration did not express, so masking efficiency in the A:C:T configuration could not be assessed.

Example 9: CD33 targeting extended-release binding proteins with different domain configurations induced T cell-dependent cellular cytotoxicity assay

[00353] The binding proteins used in this study are summarized in **Table 9**. The configuration of the anti-target, anti-albumin and anti-CD3 binding domains are according to **Fig. 2A-C** and **Fig. 2G-I** (SEQ ID NOS 3614 to 3619) and **Fig. 2D-F** and **Fig. 2J-L** (SEQ ID NOS 3620 to 3625). SEQ ID NOS. 3614 to 3619 contain a masking domain and a non-cleavable linker. SEQ ID NOS 3620 to 3625 are genetically engineered to encode the product after protease cleavage if the molecules had been made with a cleavable linker (stub:Active molecules).

Table 9. CD33 Binding Proteins and EC_{50} values

NCLV SEQ ID NO	stub:Active SEQ ID NO	Protein Name	NCLV EC50 (M)	stub:Active EC50 (M)	NCLV / stub:Active
3614	3620	αCD33 A:C:T	2E-10	2E-11	13
3615	3621	αCD33 A:T:C	1E-10	4E-12	64
3616	3622	αCD33 C:A:T	>1E-7	4E-11	>2500
3617	3623	αCD33 C:T:A	>1E-7	2E-11	>4200
3618	3624	αCD33 T:A:C	>1E-7	8E-11	>1300
3619	3625	αCD33 T:C:A	>1E-7	7E-12	>15000

[00354] TDCC Assay: For functional potency in a T cell-dependent cellular cytotoxicity assays, soluble test molecules shown in **Table 9** were incubated, in multi-well plates, with purified resting human T cells (effector cell) and MOLM13 cancer cells at 10:1 effector: target cell ratio for 48 h at 37°C. HSA was present. The cancer target cell lines had been stably transduced with a luciferase reporter gene to allow specific T cell-mediated cell killing measurement by Steady-Glo (Promega). Results shown in **Fig. 10** demonstrates the TDCC assay results of various CD33 targeting proteins. The EC_{50} values are provided in **Table 9**. The efficiency of masking is quantitated by the fold increase in EC_{50} of the NCLV protein over the stub:Active protein (**Table 9**). Results shows that 4 configurations (C:A:T, C:T:A, T:A:C and T:C:A) have single digit picomolar Active EC_{50} in the active form and no activity when masked with a NCLV linker, while A:C:T and A:T:C configurations have poor masking effects.

Example 10: TDCC activity of the protease activated extended-release binding proteins

[00355] CD19-targeting extending-release binding proteins in the T:A:C or T:C:A (**Fig. 2A and B**) configurations were expressed and purified. For each configuration, four different versions of protein were produced. The first versions (SEQ ID Nos: 3842 and 3843) contained a protease cleavage site, L001 (SEQ ID NO: 3688), between the masking domain (SEQ ID NO: 3663) and the CD19 targeting domain. The second versions were identical to the first version except that the protein was treated with the ST14 protease. The third versions (SEQ ID Nos: 3630 and 3631) contained a non-cleavage linker (SEQ ID NO: 3687) between the masking domain and the targeting domain. The fourth versions (SEQ ID Nos: 3611 and 3636) were engineered with the amino acid sequence VVGGGG (SEQ ID No: 3879), referred to as "stub", on the N-terminus of the target binding domain to product of an extended-binding release protein after protease cleavage (**Fig. 2D and E**). These proteins were tested in a Raji TDCC assay as described in **Example 6** and the Raji cell viability data versus the concentration of CD19 protein added is plotted in **Fig. 11**. As expected, the CD19 binding proteins activated with protease or the stub CD19 proteins potently and effectively directed the T cells to kill the Raji cells. CD19 binding proteins with a non-cleavage linker were unable to direct T cells to kill the

Raji cells. CD19 proteins with a cleavable linker but not treated with protease were able to partially direct T cells to kill the Raji cells. It is hypothesized that during this 72 hour assay that these proteins became partially activated because of proteases produced by the T cells and/or Raji cells.

[00356] FLT3-targeting extending-release binding proteins in the T:A:C (**Fig. 2A**) configuration were expressed and purified. Four different versions of proteins were produced. The first version (SEQ ID NO: 3854) contained a protease cleavage linker L001 (SEQ ID NO: 3688) (and flanking sequence at the N-terminal and C-terminal of L001), between the masking domain (SEQ ID NO. 3633) and the FLT3 targeting domain. The second version was identical to the first version except that the protein was treated with the ST14 protease. The third version (SEQ ID NO: 3652) contained a non-cleavage linker (SEQ ID NO. 3687) between the masking domain and the targeting domain. The fourth version (SEQ ID NO: 3613) was engineered with the amino acid sequence VVGGGG (SEQ ID. 3879), referred to as "stub", on the N-terminus of the target binding domain to product of an extended-binding release protein after protease cleavage (**FIG. 2D**). These proteins were tested in a MOLM13 TDCC assay as described in **Example 6** and the MOLM13 cell viability data versus the concentration of FLT3 protein added is plotted in **Fig. 12**. As expected, the FLT3 binding protein activated with protease or the stub FLT3 protein potently and effectively directed the T cells to kill the MOLM13 cells. FLT3 binding protein with a non-cleavage linker was unable to direct T cells to kill the MOLM13 cells. FLT3 protein with a cleavable linker but not treated with protease were able to direct T cells to kill the MOLM13 cells but with less potency than the stub or protease activated proteins. It is hypothesized that during this 72 hour assay that these proteins became partially activated because of proteases produced by the T cells and/or MOLM13 cells.

Example 11: Binding of TriTAC-XR Prodrug and Activated Drug to Human CD3ε by ELISA

[00357] Exemplary TriTAC-XR with a non-cleavable (NCLV) linker (SEQ ID NO: 3630), a cleavable linker (SEQ ID NO: 3876), or an stub:Active control (SEQ ID NO: 3611) were assessed for binding to recombinant human CD3ε using ELISA. The results are shown in **Fig. 13A**. The mask reduced the binding to human CD3ε by more than 100-fold.

Example 12: Binding of TriTAC-XR Prodrug and Activated Drug to Human T cells by Flow Cytometry

[00358] Exemplary TriTAC-XR with a non-cleavable (NCLV) linker (SEQ ID NO: 3630), a cleavable linker (SEQ ID NO: 3876), or an stub:Active control (SEQ ID NO: 3611) were assessed for binding to human T cells using flow cytometry. The results are shown in **Fig. 13B**. The mask reduced the binding to human T cells by more than 100-fold.

Example 13: Phamacokinetics and Pharmacodynamics of FLT3 TriTAC-XR in Cynomolgus Monkeys

[00359] FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) or FLT3 TriTAC-XR-L085 (SEQ ID NO: 3874) was administered via single i.v. bolus injection to cynomolgus monkeys. FLT3 TriTAC-XR-L001 was administered at 300 and 1000 μg/kg and FLT3 TriTAC-XR-L085 was administered at 1000 μg/kg with two test subjects per dose group. FLT3 TriTAC binds to cynomolgus FLT3, CD3, and albumin with affinities of 2.7 nM, 3.3 nM and 4.4 nM, respectively, as determined using biolayer interferometry. FLT3 TriTAC-XR molecules have similar affinity to FLT3 and albumin as TriTAC, but reduced binding to CD3 due to the presence of a peptide mask, *see* examples 11 and 12.

[00360] The total amount of intact and active FLT3 TriTAC-XR (L001, SEQ ID NO: 3873, and L085, SEQ ID NO: 3874) present in serum samples was measured using an electrochemiluminescent ELISA assay using labeled antibodies recognizing non-overlapping epitopes on the anti-ALB domain of the TriTAC-XR molecule as capture and detection reagents. The amount of activated FLT3 TriTAC-XR present in serum samples was measured using an electrochemiluminescent ELISA assay using labeled antibodies recognizing the anti-ALB domain and the anti-CD3 domain of the TriTAC-XR molecule as capture and detection reagents. The antibody recognizing the anti-CD3 domain is blocked by the mask in the intact prodrug, resulting in 400x preferential detection of active drug. The amount of intact prodrug was calculated by subtracting the active drug concentration from the total drug concentration. The measured and calculated serum concentrations versus time are plotted in **Figs. 14A-14C**. The active form of the drug formed slowly after dosing, reaching a maximum concentration approximately 72 to 144 hours after dosing.

[00361] To determine if the FLT3 TriTAC-XR directed cynomolgus T cells to kill endogenous cynomolgus FLT3-expressing cells, soluble FLT3L in serum and FLT3 RNA in bone marrow were measured in samples collected from the pharmacokinetic study described above. Depletion of FLT3-expressing cells should result in an increase in soluble FLT3L (Brauchle et al. Mol Cancer Ther 2020;19:1875–88). An electrochemiluminescent ELISA specific for Non-Human Primate FLT3L (Meso Scale Discovery) was used to measure the levels of FLT3L in serum samples collected at different time points (**Fig. 15**). For all dose groups, the soluble FLT3L increased for the first 336 to 504 hours before declining back to baseline by 672 to 1176 hours.

[00362] If FLT3 expressing cells are depleted from bone marrow, then FLT3 transcripts should be depleted from RNA purified from bone marrow. RNA was purified from bone marrow using kits (Qiagen), cDNA was prepared by a reverse transcriptase reaction, and qPCR was used to measure the amount of FLT3 present using a standard curve qPCR method. FNTA was used as a

house keeping gene for the qPCR reactions. Plotted in **Fig. 16** are FTL3 RNA levels normalized to FNTA for bone marrow samples isolated from animals treated with TriTAC-XR. Compared to samples collected prior to dosing, FLT3 RNA is greatly reduced at all time points measured. The combined FLT3L (**Fig. 15**) and FLT3 RNA (**Fig. 16**) data indicate that the FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) and FLT3 TriTAC-XR-L085 (SEQ ID NO: 3874) reduced FLT3 expressing cells in cynomolgus monkeys.

Example 14: Phamacokinetics of FLT3 TriTAC in Cynomolgus Monkeys

[00363] FLT3 TriTAC (SEQ ID NO: 3875) was administered via single i.v. bolus injection to cynomolgus monkeys at 1mg/kg. Serum concentrations of the TriTAC were measured for 15 days at the indicated timepoints (**Fig. 17**). To compare the FLT3 TriTAC with TriTAC-XR-L001, the first 15 days of FLT3 TriTAC-XR data from **Example 13** were plotted in Fig. 18. The results show that TriTAC-XR resulted in a slow build-up of active drug, and a reduced Cmax/Cmin ratio for the active drug (**Fig. 17**) compared to the TriTAC. Plotted in **Fig. 18** are FTL3 RNA levels normalized to FNTA for bone marrow samples isolated from animals treated with TriTAC or TriTAC-XR (from Example 13). The FLT3 transcription levels in animals dosed i.v. with 1000 μg/kg FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) were compared to the FLT3 transcription levels in animals dosed i.v. with a constitutively active FLT3 TriTAC (SEQ ID NO: 3875). Compared to samples collected prior to dosing, FLT3 RNA is greatly reduced at all time points measured. The FLT3 RNA (**Fig. 18**) data indicate that the FLT3 TriTAC-XR-L001 (SEQ ID NO: 3873) and the constitutively active FLT3 TriTAC (SEQ ID NO: 3875) reduced FLT3 expressing cells in cynomolgus monkeys.

Example 15: Safety and efficacy of FLT3 TriTAC-XR in Cynomolgus Monkeys

[00364] To assess the safety improvement of TriTAC-XR, cytokines were measured at multiple timepoints between 2 and 48 hours after dosing. Cytokines levels were quantified using electrochemiluminescent ELISAs specific for Non-Human Primate IL-2 and IL-6 (Meso Scale Discovery). The peak cytokine levels in animals dosed i.v. with 300 and 1000 μg/kg FLT3 TriTAC-XR (FLT3 TriTAC-XR-L001, SEQ ID NO: 3873) were compared to the peak cytokine levels in animals dosed i.v. with a constitutively active FLT3 TriTAC (SEQ ID NO 3875) at 10, 100, and 1000 μg/kg and are shown in **Fig. 21** (IL-2 in **Fig. 21A**, IL-6 in **Fig. 21B**). Significant cytokines were generated from the constitutively active TriTAC at 100-fold lower doses than the TriTAC-XR-L001.

[00365] To assess the efficacy of TriTAC-XR, soluble FLT3L in serum were measured in samples collected from the safety study described above. Depletion of FLT3-expressing cells should result in an increase in soluble FLT3L (Brauchle et al. Mol Cancer Ther 2020;19:1875–88). An electrochemiluminescent ELISA specific for Non-Human Primate FLT3L (Meso Scale

Discovery) was used to measure the levels of FLT3L in serum samples collected at the indicated timepoints after dosing (**Fig. 22**). The soluble FLT3L levels in animals dosed i.v. with 300 and 1000 μg/kg FLT3 TriTAC-XR (FLT3 TriTAC-XR-L001, SEQ ID NO: 3873) were compared to the soluble FLT3L levels in animals dosed i.v. with a constitutively active FLT3 TriTAC (SEQ ID NO: 3875) at 10, 100, and 1000 μg/kg and are shown in **Fig. 22**. FLT3L was significantly elevated after administration of 100 and 1000 μg/kg TriTAC and 300 and 1000 μg/kg TriTAC-XR. (**Fig. 22**).

Example 16: Efficacy of FLT3 TriTAC-XR in Mouse

[00366] All animal experiments were conducted according to the protocol approved by Institutional Animal Care and Use Committee of Harpoon Therapeutics (protocol number HAR-001-2019). Animals were purchased from The Jackson Laboratory then housed in a pathogen free animal facility located at Harpoon Therapeutics in accordance with IACUC guidelines. All studies were performed in NSG™ (NOD-*scid* IL2Rgamma^{null}) female mice 8 weeks of age with $n = 5$ mice per group.

[00367] EoL-1 human eosinophilic leukemia cells (2×10^6) were implanted intravenously in NSG™ mice on Day 0, followed by intraperitoneally implanted activated and expanded human T cells (2×10^7) on Day 2. On Day 4, mice were administered a repeat intraperitoneal dose (q.d. x 10) of non-targeting GFP TriTAC (SEQ ID NO: 3877) or FLT3 targeting TriTAC-XR (SEQ ID NO: 3873). Clinical observations were recorded and body weight was monitored at least three times weekly. Survival analysis of EoL-1 disseminated mouse model demonstrated FLT3 TriTAC-XR extends survival (**Fig. 23**). Statistical significance was determined using Survival Curve Comparisons Log-rank (Mantel-Cox) and Gehan-Breslow-Wilcoxon tests, all groups compared to control non-targeting GFP TriTAC (**, $P<0.01$, **Fig. 23**).

Example 17: Phamacokinetics of CD19 TriTAC-XR in Cynomolgus Monkeys

[00368] CD19 TriTAC-XR (CD19 TriTAC-XR-L001, SEQ ID NO: 3842) or a constitutively active CD19 TriTAC (SEQ ID NO: 3611) was administered via single i.v. bolus injection to cynomolgus monkeys at 0.3 mg/kg. Serum concentrations of each drug were measured for 168 hours at the indicated timepoints (**Fig. 24**). For TriTAC-XR, two assays were used to quantify the Intact Prodrug and the Activated drug. After administration, the Intact Prodrug of TriTAC-XR is slowly cleaved, generating Active drug. The results show that TriTAC-XR resulted in a slow build-up of active drug, (**Fig. 24**) compared to the TriTAC.

Example 18: Safety and efficacy of CD19 TriTAC-XR in Cynomolgus Monkeys

[00369] To assess the safety improvement of TriTAC-XR, cytokines were measured at multiple timepoints after dosing. Cytokines levels were quantified using electrochemiluminescent ELISAs specific for Non-Human Primate IL2 and IL6 (Meso Scale Discovery). The peak

cytokine levels in animals dosed i.v. with 300 μg/kg CD19 TriTAC-XR (CD19 TriTAC-XR-L001, SEQ ID NO: 3842) were compared to the peak cytokine levels in animals dosed i.v. with 300 μg/kg of a constitutively active CD19 TriTAC (SEQ ID NO: 3611) are shown in **Fig. 25** (IL-2 in **Fig. 25A**, IL-6 in **Fig. 25B**). Significant cytokines were generated from the constitutively active TriTAC. **Fig. 26** shows that target cell (B cell) depletion is comparable between CD19 TriTAC and CD19 TriTAC-XR.

Example 19: Phamacokinetics of CD20 TriTAC-XR in Cynomolgus Monkeys

[00370] CD20 TriTAC-XR (CD20 TriTAC-XR-L001, SEQ ID NO: 3882) or a constitutively active CD20 TriTAC (SEQ ID NO: 3881) was administered via single i.v. bolus injection to cynomolgus monkeys at 0.03 mg/kg. Serum concentrations of each drug were measured for 120 hours at the indicated timepoints (**Fig. 27**). For TriTAC-XR, two assays were used to quantify the Intact Prodrug and the Activated drug. After administration, the Intact Prodrug of TriTAC-XR is slowly cleaved, generating Active drug. The results show that TriTAC-XR resulted in a slow build-up of active drug, (**Fig. 27**) compared to the TriTAC.

Example 20: Safety and efficacy of CD20 TriTAC-XR in Cynomolgus Monkeys

[00371] To assess the safety improvement of TriTAC-XR, cytokines were measured at multiple timepoints after dosing. Cytokines levels were quantified using electrochemiluminescent ELISAs specific for Non-Human Primate IL2 and IL6 (Meso Scale Discovery). The peak cytokine levels in animals dosed i.v. with 30 μg/kg CD20 TriTAC-XR (CD20 TriTAC-XR-L001, SEQ ID NO: 3882) were compared to the peak cytokine levels in animals dosed i.v. with a constitutively active CD20 TriTAC (SEQ ID NO: 3881) are shown in **Fig. 28** (IL-2 in **Fig. 28A**, IL-6 in **Fig. 28B**). Significant cytokines were generated from the constitutively active TriTAC. **Fig. 29** shows that target cell (B cell) depletion is comparable between CD20 TriTAC and CD20 TriTAC-XR.

Example 21. Predicted and empirical PK profiles

[00372] Based on the observation above, weekly repeat dosing of (1) intravenous administered TriTAC, (2) subcutaneous administered TriTAC, (3) and intravenous administered TriTAC-XR was modeled from single dose cynomolgus monkey pharmacokinetics data (**Fig. 19**). In vivo activated TriTAC-XR is predicted to have a lower Cmax, but similar Cmin to intravenous administered or subcutaneous administered TriTAC (**Fig. 19**). Repeated dosing of CD20 TriTAC-XR in cyno monkeys show a PK profile similar to the predicted PK profile where concentration of TriTAC-XR active drug in circulation ("apparent half-life") is near constant due to continual conversion of prodrug to active drug (**Fig. 20**).

[00373] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are

provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

[00374] Sequence listing tables

Table 10. BCMA binding protein sequences

SEQ ID NO:	Description	Sequence	Notes
1	01A01	TDIFSISPMG	CDR1
2	01A02	TNIFSSSPMG	CDR1
3	01A03	TNIFSISPGG	CDR1
4	01A04	TNIFMISPMG	CDR1
5	01A05	TNIFSSSPMG	CDR1
6	01A06	TNIFSIRPMG	CDR1
7	01A07	TNISSISPMG	CDR1
8	01A08	TNIFSSSPMG	CDR1
9	01A09	TNIFSITPMG	CDR1
10	01B01	TNIPSISPMG	CDR1
11	01B02	TNITSISPMG	CDR1
12	01B03	TNIFSKSPMG	CDR1
13	01B04	TNDFSISPMG	CDR1
14	01B05	TNITSISPMG	CDR1
15	01B06	TNIFSISPMG	CDR1
16	01B07	TNIFSRSPMG	CDR1
17	01B08	TNIESISPMG	CDR1
18	01B09	SNIFSISPMG	CDR1
19	01B12	TNIFSTSPMG	CDR1
20	01C01	TNIVSISPMG	CDR1
21	01C02	TNIESISPMG	CDR1
22	01C04	TNIPSISPMG	CDR1
23	01C05	TNIFSSSPMG	CDR1
24	01C06	TNIFSISPMG	CDR1
25	01C07	TNIFSIYPMG	CDR1
26	01C08	TNIFSNSPMG	CDR1
27	01C10	TNISSISPMG	CDR1
28	01D02	TNIVSISPMG	CDR1
29	01D03	TNIFSNSPMG	CDR1
30	01D04	TNITSISPMG	CDR1
31	01D05	TNIFSDSPMG	CDR1
32	01D06	TNIFSRSPMG	CDR1
33	01D07	TNIFSASPMG	CDR1
34	01D10	TNIFSASPMG	CDR1
35	01E03	TNITSISPMG	CDR1
36	01E04	TNIASISPMG	CDR1

37	01E05	TNIFSRSPMG	CDR1
38	01E06	TNIFSLSPMG	CDR1
39	01E07	TNIPSISPMG	CDR1
40	01E08	TNIFSQSPMG	CDR1
41	01E010	TNIESISPMG	CDR1
42	01F02	TNIFSHSPMG	CDR1
43	01F03	TNIFSESPMG	CDR1
44	01F04	TNIDSISPMG	CDR1
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46	01F07	TNIFSTSPMG	CDR1
47	01F08	TNITSVSPMG	CDR1
48	01F09	TNISSISPMG	CDR1
49	01F10	SNIFSISPMG	CDR1
50	01F12	TNIFRISPMG	CDR1
51	01G01	TNIVSISPMG	CDR1
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54	01G08	TNIQSISPMG	CDR1
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56	01G10	TNEFSISPMG	CDR1
57	01G11	TNIPSISPMG	CDR1
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60	01H05	TNIFSITPMG	CDR1
61	01H06	TSDFSISPMG	CDR1
62	01H08	TNIMSISPMG	CDR1
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64	01H10	TNIPSISPMG	CDR1
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66	02A04	TNIFSQSPMG	CDR1
67	02A05	TNIASISPMG	CDR1
68	02A07	TNIFSKSPMG	CDR1
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71	02B01	TNIFSNSPMG	CDR1
72	02B04	TNIFSTSPMG	CDR1
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75	02B07	TNIFSSSPMG	CDR1
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79	02C03	TNIASISPMG	CDR1
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81	02C06	TNIFSTSPMG	CDR1
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83	02D09	TNVVSISPMG	CDR1
84	02D11	TNEFSISPMG	CDR1

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87	02E06	TNIFSDSPMG	CDR1
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89	02F02	TNIFSKSPMG	CDR1
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92	02F05	TNIFSVSPMG	CDR1
93	02F06	TNIFSITPMG	CDR1
94	02F07	TNIESISPMG	CDR1
95	02F11	TNIFSTSPMG	CDR1
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342	01F01-M34G	VPWGDYHPGNVY	CDR3
343	02G02-M34Y	VPWGDYHPGNVY	CDR3
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345	253BH10 CDR3	VPWGDYHPRNVY	CDR3
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372	01E05	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGKY HPRNVYWGQGTQVTVSS	
373	01F02	EVQLVESGGGLVQPGRSLTLSCAASTNIFSHSPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
374	02C06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
375	02F11	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVQWGQGTQVTVSS	

376	01E06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSLSPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVYWGQGTQVTVSS	
377	01A03	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPGG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVYWGQGTQVTVSS	
378	02A11	EVQLVESGGGLVQPGRSLTLSCAASTNHFSISPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRVVYWGQGTQVTVSS	
379	01D07	EVQLVESGGGLVQPGRSLTLSCAASTNIFSASPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVNWGQGTQVTVSS	
380	01D10	EVQLVESGGGLVQPGRSLTLSCAASTNIFSASPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
381	01A07	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
382	02F12	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
383	02B05	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPYG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
384	01E04	EVQLVESGGGLVQPGRSLTLSCAASTNIASISPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
385	02A05	EVQLVESGGGLVQPGRSLTLSCAASTNIASISPMG WYRQAPGKQRELVAAIHGKSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
386	02C03	EVQLVESGGGLVQPGRSLTLSCAASTNIASISPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
387	01E03	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
388	01H09	EVQLVESGGGLVQPGRSLTLSCAASTNIMSISPMG WYRQAPGKQRELVAAIHGNSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	

389	02G05	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMG WYRQAPGKQRELVAAIHGNSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
390	01C01	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMG WYRQAPGKQRELVAAIHGHSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
391	01D02	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMG WYRQAPGKQRELVAAIHGKSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
392	02D09	EVQLVESGGGLVQPGRSLTLSCAASTNVVSISPMG WYRQAPGKQRELVAAIHGKSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPNNVYWGQGTQVTVSS	
393	02C01	EVQLVESGGGLVQPGRSLTLSCAASTNIISISPMG WYRQAPGKQRELVAAIHGASTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
394	02G02	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMG WYRQAPGKQRELVAAIHGASTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
395	01B05	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMG WYRQAPGKQRELVAAIHGFETLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
396	01G08	EVQLVESGGGLVQPGRSLTLSCAASTNIQSISPMG WYRQAPGKQRELVAAIHGFETLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
397	01H06	EVQLVESGGGLVQPGRSLTLSCAASTSDFSISPMG WYRQAPGKQRELVAAIHGFETLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
398	01F04	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMG WYRQAPGKQRELVAAIHGFQTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
399	01H08	EVQLVESGGGLVQPGRSLTLSCAASTNIMSISPMG WYRQAPGKQRELVAAIHGFSTVYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
400	02F07	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMG WYRQAPGKQRELVAAIHGFSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
401	01C05	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMG WYRQAPGKQRELVAAIHGFKTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTARYYCNKVPWGDY HPGNVYWGQGTQVTVSS	

402	02F04	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMG WYRQAPGKQRELVAAIHGFSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
403	02B06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSNSPMG WYRQAPGKQRELVAAIHGFSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
404	01F07	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMG WYRQAPGKQRELVAAIHGFSTIYADSVKGRFTISR DNAKNSIYLQMNSLRPEDTALYYCNKVPWGDYH PGNVYWGQGTQVTVSS	
405	02B04	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMG WYRQAPGKQRELVAAIHGFSTIYADSVKGRFTISR DNAKNSIYLQMNSLRPEDTALYYCNKVPWGDYH PLNVYWGQGTQVTVSS	
406	01H11	EVQLVESGGGLVQPGRSLTLSCVASTNIFSTSPMG WYRQAPGKQRELVAAIHGFSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
407	02E06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSDSPMG WYRQAPGKQRELVAAIHGFSTFYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
408	01E08	EVQLVESGGGLVQPGRSLTLSCAASTNIFSQSPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVCWGQGTQVTVSS	
409	02A04	EVQLVESGGGLVQPGRSLTLSCAASTNIFSQSPMG WYRQAPGKQRELVAAIHGKSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPSNVYWGKGTQVTVSS	
410	02A08	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPGNVYWGQGTQVTVSS	
411	02E05	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMG WYRQAPGKQRELVAAIHGISTLYADSVKGRFTISR DNAKNSIYLQMNSLRPEDTALYYCNKVPWGDYH PGNVYWGQGTQVTVSS	
412	02H09	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
413	02G06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSGSPMG WYRQAPGKQRELVAAIHGNSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	

414	01B09	EVQLVESGGGLVQPGRSLTLSCAASSNIFSISPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
415	02F03	evqlvesgggLVQPGRSLTLSCAASTNIFSIYPMGWYR QAPGKQRELVAAIHGSSTLYADSVKGRFTISRDN AKNSIYLQMNSLRPEDTALYYCNKVPWGDYHPK NVYWGQGTQVTVSS	
416	02F02	evqlvesgggLVQPGRSLTLSCAASTNIFSKSPMGWYR QAPGKQRELVAAIHGSSTLYADSVKGRFTISRDN AKNSIYLQMNSLRPEDTALYYCNKVPWGDYHPG NVYWGQGTQVTVSS	
417	02H01	evqlvesgggLVQPGRSLTLSCAASTNIFSKSPMGWYR QAPGKQRELVAAIHGSSTLYADSVKGRFTISRDN AKNSIYLQMNSLRPEDTALYYCNKVPWGDYHPR NVYWGQGTQVTVSS	
418	01G10	EVQLVESGGGLVQPGRSLTLSCAASTNEFSISPMG WYRQAPGKQRELVAAIHGLSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGAY HPRNVYWGQGTQVTVSS	
419	02D11	EVQLVESGGGLVQPGRSLTLSCAASTNEFSISPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
420	01B01	evqlvesgggLVQPGRSLTLSCAASTNIPSISPMGWYR QAPGKQRELVAAIHGESTLYADSVKGRFTISRDN AKNSIYLQMNSLRPEDTALYYCNKVPWGDYHPR NVAWGQGTQVTVSS	
421	01G11	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMG WYRQAPGKQRELVAAIHGASTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVAWGQGTQVTVSS	
422	01H10	evqlvesgggLVQPGRSLTLSCAASTNIPSISPMGWYR QAPGKQRELVAAIHGESTLYADSVKGRFTISRDN AKNSIYLQMNSLRPEDTALYYCNKVPWGDYHPR NVYWGQGTQVTVSS	
423	01C04	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVYWGQGTQVTVSS	
424	01D04	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMG WYRQAPGKQRELVAAIHGVSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVQWGQGTQVTVSS	
425	01E07	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMG WYRQAPGKQRELVAAIHGQSTLYADSVKGRFTIS	

		RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVQWGQGTQVTVSS	
426	02B11	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVSWGQGTQVTVSS	
427	01F10	EVQLVESGGGLVQPGRSLTLSCAASSNIFSISPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVTWGQGTQVTVSS	
428	02G08	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVTWGQGTQVTVSS	
429	02G11	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVTWGQGTQVTVSS	
430	02H06	evqlvesgggLVQPGRSLTLSCAASTNIRSISPMGWYR QAPGKQRELVAAIHGSSTLYADSVKGRFTISRDN AKNSIYLQMNSLRPEDTALYYCNKVPWGDYHPR NVVWGQGTQVTVSS	
431	01B02	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMG WYRQAPGKQRELVAAISGFSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNEVPWGDY HPRNVYWGQGTQVTVSS	
432	02H11	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVYWGQGTQVTVSS	
433	01F08	EVQLVESGGGLVQPGRSLTLSCAASTNITSVSPMG WYRQAPGKQRELVAAIHGPSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPTNVYWGQGTQVTVSS	
434	01H01	EVQLVESGGGLVQPGRSLTLSCAASTNIGSISPMG WYRQAPGKQRELVAAIHGQSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPQNVYWGQGTQVTVSS	
435	01E10	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMG WYRQAPGKQRELVAAIHGKSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRRVYWGQGTQVTVSS	
436	01G01	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRRVYWGQGTQVTVSS	
437	01G04	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMG WYRQAPGKQRELVAAIHGNSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRMVYWGQGTQVTVSS	

438	01A04	EVQLVESGGGLVQPGRSLTLSCAASTNIFMISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
439	01F12	EVQLVESGGGLVQPGRSLTLSCAASTNIFRISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
440	01B06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGEY HPRNVYWGQGTQVTVSS	
441	01C06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPMG WYRQAPGKQRELVAAIHGDSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGKY HPRNVYWGQGTQVTVSS	
442	01B08	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMG WYRQAPGKQRELVAAIHGSSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
443	01C02	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMG WYRQAPGKQRELVAAIHGNSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
444	01C10	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMG WYRQAPGKQRELVAAIHGFSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGYY HPRNVYWGQGTQVTVSS	
445	01F09	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMG WYRQAPGKQRELVAAIHGHSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
446	02D06	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMG WYRQAPGKQRELVAAIHGFSTVYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
447	01A06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSIRPMG WYRQAPGKQRELVAAIHGFSTVYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVYWGQGTQVTVSS	
448	01C07	EVQLVESGGGLVQPGRSLTLSCAASTNIFSIYPMG WYRQAPGKQRELVAAIHGFSTYYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGSY HPRNVYWGQGTQVTVSS	
449	01G09	EVQLVESGGGLVQPGRSLTLSCAASTNIFNISPMG WYRQAPGKQRELVAAIHGFSTYYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
450	01F05	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMG WYRQAPGKQRELVAAIHGFSTWYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	

451	02B12	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMG WYRQAPGKQRELVAAIHGFDTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVYWGQGTQVTVSS	
452	02G01	EVQLVESGGGLVQPGRSLTLSCAASTNIFSINPMG WYRQAPGKQRELVAAIHGFDTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRNVSWGQGTQVTVSS	
453	01A09	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMG WYRQAPGKQRELVAAIHGRSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGSY HPRNVYWGQGTQVTVSS	
454	01H05	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMG WYRQAPGKQRELVAAIHGTSTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
455	02F06	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGRY HPRNVYWGQGTQVTVSS	
456	02G07	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMG WYRQAPGKQRELVAAIHGESTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPRDVYWGQGTQVTVSS	
457	01F07-M34Y	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPYG WYRQAPGKQRELVAAIHGFSTIYADSVKGRFTISR DNAKNSIYLQMNSLRPEDTALYYCNKVPWGDYH PGNVYWGQGTQVTVSS	
458	01F01-M34G	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPGG WYRQAPGKQRELVAAIHGFSTIYADSVKGRFTISR DNAKNSIYLQMNSLRPEDTALYYCNKVPWGDYH PGNVYWGQGTQVTVSS	
459	02G02-M34Y	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPYG WYRQAPGKQRELVAAIHGASTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
460	02G02-M34G	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPGG WYRQAPGKQRELVAAIHGASTLYADSVKGRFTIS RDNAKNSIYLQMNSLRPEDTALYYCNKVPWGDY HPGNVYWGQGTQVTVSS	
461	253BH10 (llama anti-BCMA antibody)	QVQLVESGGGLVQPGESLRLSCAASTNIFSISPMG WYRQAPGKQRELVAAIHGFSTLYADSVKGRFTIS RDNAKNTIYLQMNSLKPEDTAVYYCNKVPWGDY HPRNVYWGQGTQVTVSS	

Table 11. PSMA binding protein sequences

SEQ ID NO:	**Description**	**Sequence**
462	CDR1 variant 1	RFMISEYHMH
463	CDR1 variant 2	RFMISPYSMH

464	CDR1 variant 3	RFMISPYHMH
465	CDR1 variant 4	RFMISEYSMH
466	CDR2 variant 1	DINPAGTTDYAESVKG
467	CDR2 variant 2	TINPAKTTDYAESVKG
468	CDR2 variant 3	TINPAGQTDYAESVKG
469	CDR2 variant 4	TINPAGTTDYAEYVKG
470	CDR2 variant 5	DINPAKTTDYAESVKG
471	CDR2 variant 6	DINPAGQTDYAESVKG
472	CDR2 variant 7	DINPAGTTDYAEYVKG
473	CDR2 variant 8	TINPAGTTDYAESVKG
474	CDR3 variant 1	DSYGY
475	CDR3 variant 2	DGYGY
476	wt anti-PSMA	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYSMHWVRQAP GKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLKPEDTAVYYCDGYGYRGQGTQVTVSS
477	Anti-PSMA clone 1	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYSMHWVRQAP GKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDGYGYRGQGTLVTVSS
478	Anti-PSMA clone 2	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYHMHWVRQAP GKGLEWVSDINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
479	Anti-PSMA clone 3	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYHMHWVRQAP GKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
480	Anti-PSMA clone 4	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYSMHWVRQAP GKGLEWVSTINPAKTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
481	Anti-PSMA clone 5	EVQLVESGGGLVQPGGSLRLSCAASRFMISPYSMHWVRQAP GKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDGYGYRGQGTLVTVSS
482	Anti-PSMA clone 6	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYSMHWVRQAP GKGLEWVSTINPAGQTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDGYGYRGQGTLVTVSS

483	Anti-PSMA clone 7	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYSMHWVRQAP GKGLEWVSTINPAGTTDYAEYVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDGYGYRGQGTLVTVSS
484	Anti-PSMA clone 8	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYHMHWVRQAP GKGLEWVSDINPAKTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
485	Anti-PSMA clone 9	EVQLVESGGGLVQPGGSLRLSCAASRFMISPYHMHWVRQAP GKGLEWVSDINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
486	Anti-PSMA clone 10	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYHMHWVRQAP GKGLEWVSDINPAGQTDYAESVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
487	Anti-PSMA clone 11	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYHMHWVRQAP GKGLEWVSDINPAGTTDYAEYVKGRFTISRDNAKNTLYLQM NSLRAEDTAVYYCDSYGYRGQGTLVTVSS
488	Anti-PSMA clone 12	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAP GKGLEWVSDINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLKPEDTAVYYCDSYGYRGQGTQVTVSS
489	Anti-PSMA clone 13	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAP GKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQM NSLKPEDTAVYYCDSYGYRGQGTQVTVSS

Table 12. MSLN binding protein sequences

SEQ ID NO:	**Description**	**Sequence**	Notes
490	9B1	GRTFSVRGMA	CDR1
491	9F3	GSIPSIEQMG	CDR1
492	7H2	GTTYTFDLMS	CDR1
493	3B4	GSTSNINNMR	CDR1
494	4A2	GSTFGINAMG	CDR1
495	12D1	ISAFRLMSVR	CDR1
496	3G1	GRPFSINTMG	CDR1
497	2A1	GSDFTEDAMA	CDR1
498	6F3	GSDFTEDAMA	CDR1
499	1H2	GFTFSSFGMS	CDR1
500	3F2	GLTYSIVAVG	CDR1
501	12C2	GLTFGVYGME	CDR1

502	2D1	TTSSINSMS	CDR1
503	6H2	GRTLSRYAMG	CDR1
504	5D2	GSIFSPNAMI	CDR1
505	7C4	GATSAITNLG	CDR1
506	5F2	GSTFRIRVMR	CDR1
507	2C2	GDTSKFKAVG	CDR1
508	5G2	GSTFGNKPMG	CDR1
509	9H2	GSTSSINTMY	CDR1
510	5D4	GRTDRITTMG	CDR1
511	2A4	GRTIGINDMA	CDR1
512	7F1	AIGSINSMS	CDR1
513	5C2	GSTSSINTMY	CDR1
514	2F4	TTFSINSMS	CDR1
515	2A2	GSTFSIRAMR	CDR1
516	11F3	GRTSTIDTMY	CDR1
517	10B3	GSTSSINTMY	CDR1
518	MH1	GGDWSANFMY	CDR1
519	MH2	GGDWSANFMY	CDR1
520	MH3	GSTSSINTMY	CDR1
521	MH4	GSTSSINTMY	CDR1
522	MH5	GSTSSINTMY	CDR1
523	MH6	GSTFSIRAMR	CDR1
524	MH7	GSTFSIRAMR	CDR1
525	MH8	GSTFSIRAMR	CDR1
526	MH9	GRTSTIDTMY	CDR1
527	MH10	GRTSTIDTMY	CDR1
528	MH11	GRTSTIDTMY	CDR1
529	9B1	TMNPDGFPNYADAVKGRFT	CDR2
530	9F3	ALTSGGRANYADSVKGRFT	CDR2
531	7H2	SISSDGRTSYADSVRGRFT	CDR2
532	3B4	VITRGGYAIYLDAVKGRFT	CDR2
533	4A2	VISRGGSTNYADSVKGRFT	CDR2

534	12D1	TIDQLGRTNYADSVKGRFA	CDR2
535	3G1	SISSSGDFTYTDSVKGRFT	CDR2
536	2A1	FVSKDGKRILYLDSVRGRFT	CDR2
537	6F3	FVSKDGKRILYLDSVRGRFT	CDR2
538	1H2	SISGSGSDTLYADSVKGRFT	CDR2
539	3F2	DISPVGNTNYADSVKGRFT	CDR2
540	12C2	SHTSTGYVYYRDSVKGRFT	CDR2
541	2D1	VITDRGSTSYADSVKGRFT	CDR2
542	6H2	AISRSGGTTRYSDSVKGRFT	CDR2
543	5D2	SINSSGSTNYGDSVKGRFT	CDR2
544	7C4	RISVREDKEDYEDSVKGRFT	CDR2
545	5F2	VISGSSTYYADSVKGRFT	CDR2
546	2C2	WINNSGVGNTAESVKGRFT	CDR2
547	5G2	VISSDGGSTRYAALVKGRFT	CDR2
548	9H2	FISSGGSTNVRDSVKGRFS	CDR2
549	5D4	TISNRGTSNYANSVKGRFT	CDR2
550	2A4	TITKGGTTDYADSVDGRFT	CDR2
551	7F1	VITDRGSTSYADSVKGRFT	CDR2
552	5C2	TINRGGSTNVRDSVKGRFS	CDR2
553	2F4	VITNRGTTSYADSVKGRFT	CDR2
554	2A2	VIYGSSTYYADAVKGRFT	CDR2
555	11F3	YVTSRGTSNVADSVKGRFT	CDR2
556	10B3	FISSGGSTNVRDSVKGRFS	CDR2
557	MH1	RISGRGVVDYVESVKGRFT	CDR2
558	MH2	RISGRGVVDYVESVKGRFT	CDR2
559	MH3	FISSGGSTNVRDSVKGRFT	CDR2
560	MH4	FISSGGSTNVRDSVKGRFT	CDR2
561	MH5	FISSGGSTNVRDSVKGRFT	CDR2
562	MH6	VIYGSSTYYADAVKGRFT	CDR2
563	MH7	VIYGSSTYYADAVKGRFT	CDR2
564	MH8	VIYGSSTYYADAVKGRFT	CDR2
565	MH9	YVTSRGTSNVADSVKGRFT	CDR2

566	MH10	YVTSRGTSNVADSVKGRFT	CDR2
567	MH11	YVTSRGTSNVADSVKGRFT	CDR2
568	9B1	GPY	CDR3
569	9F3	GRFKGDYAQRSGMDY	CDR3
570	7H2	QRSGVRAF	CDR3
571	3B4	DRVEGTSGGPQLRDY	CDR3
572	4A2	RTYTRHDY	CDR3
573	12D1	GGGPLGSRWLRGRH	CDR3
574	3G1	RRTYLPRRFGS	CDR3
575	2A1	APGAARNY	CDR3
576	6F3	APGAARNV	CDR3
577	1H2	GGSLSRSS	CDR3
578	3F2	VRGWLDERPGPGPIVY	CDR3
579	12C2	NRGSYEY	CDR3
580	2D1	IADWRGY	CDR3
581	6H2	RRRGWGRTLEY	CDR3
582	5D2	SDFRRGTQY	CDR3
583	7C4	QRWGRGPGTT	CDR3
584	5F2	DDSGIARDY	CDR3
585	2C2	YRRFGINKNY	CDR3
586	5G2	LRTYYLNDPVVFS	CDR3
587	9H2	YIPLRGTLHDY	CDR3
588	5D4	RKWGRNY	CDR3
589	2A4	KRREWAKDFEY	CDR3
590	7F1	IADWRGY	CDR3
591	5C2	YIPYGGTLHDF	CDR3
592	2F4	IADWRGY	CDR3
593	2A2	DTIGTARDY	CDR3
594	11F3	RTTSYPVDF	CDR3
595	10B3	YIPYGGTLHDF	CDR3
596	MH1	ASY	CDR3
597	MH2	ASY	CDR3

598	MH3	YIPYGGTLHDF	CDR3
599	MH4	YIPYGGTLHDF	CDR3
600	MH5	YIPYGGTLHDF	CDR3
601	MH6	DTIGTARDY	CDR3
602	MH7	DTIGTARDY	CDR3
603	MH8	DTIGTARDY	CDR3
604	MH9	RTTSYPVDF	CDR3
605	MH10	RTTSYPVDF	CDR3
606	MH11	RTTSYPVDF	CDR3
607	9B1	QVQLVESGGGLVQPGGSLRLSCAASGRTFSVRGMAWY RQAGNNRALVATMNPDGFPNYADAVKGRFTISWDIAEN TVYLQMNSLNSEDTTVYYCNSGPYWGQGTQVTVSS	
608	9F3	QVQLVESGGGLVQAGGSLRLSCAASGSIPSIEQMGWYR QAPGKQRELVAALTSGGRANYADSVKGRFTISGDNVRN MVYLQMNSLKPEDTAIYYCSAGRFKGDYAQRSGMDYW GKGTLVTVSS	
609	7H2	QVQLVESGGGLVQAGGSLRLSCAFSGTTYTFDLMSWYR QAPGKQRTVVASISSDGRTSYADSVRGRFTISGENGKNT VYLQMNSLKLEDTAVYYCLGQRSGVRAFWGQGTQVTV SS	
610	3B4	QVQLVESGGGLVQAGGSLRLSCVASGSTSNINNMRWYR QAPGKERELVAVITRGGYAIYLDAVKGRFTISRDNANNA IYLEMNSLKPEDTAVYVCNADRVEGTSGGPQLRDYFGQ GTQVTVSS	
611	4A2	QVQLVESGGGLVQAGGSLRLSCAASGSTFGINAMGWYR QAPGKQRELVAVISRGGSTNYADSVKGRFTISRDNAENT VSLQMNTLKPEDTAVYFCNARTYTRHDYWGQGTQVTV SS	
612	12D1	QVRLVESGGGLVQAGGSLRLSCAASISAFRLMSVRWYR QDPSKQREWVATIDQLGRTNYADSVKGRFAISKDSTRNT VYLQMNMLRPEDTAVYYCNAGGGPLGSRWLRGRHWG QGTQVTVSS	
613	3G1	QVRLVESGGGLVQAGESLRLSCAASGRPFSINTMGWYR QAPGKQRELVASISSSGDFTYTDSVKGRFTISRDNAKNT VYLQMNSLKPEDTAVYYCNARRTYLPRRFGSWGQGTQ VTVSS	
614	2A1	QVQPVESGGGLVQPGGSLRLSCVVSGSDFTEDAMAWYR QASGKERESVAFVSKDGKRILYLDSVRGRFTISRDIDKKT VYLQMDNLKPEDTGVYYCNSAPGAARNYWGQGTQVT VSS	
615	6F3	QVQPVESGGGLVQPGGSLRLSCVVSGSDFTEDAMAWYR QASGKERESVAFVSKDGKRILYLDSVRGRFTISRDIYKKT VYLQMDNLKPEDTGVYYCNSAPGAARNVWGQGTQVT VSS	

616	1H2	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVR QAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLVTVSS	
617	3F2	QVQIVESGGGLVQAGGSLRLSCVASGLTYSIVAVGWYR QAPGKEREMVADISPVGNTNYADSVKGRFTISKENAKN TVYLQMNSLKPEDTAVYYCHIVRGWLDERPGPGPIVYW GQGTQVTVSS	
618	12C2	QVQLVESGGGLVQTGGSLRLSCAASGLTFGVYGMEWFR QAPGKQREWVASHTSTGYVYYRDSVKGRFTISRDNAKS TVYLQMNSLKPEDTAIYYCKANRGSYEYWGQGTQVTV SS	
619	2D1	QVQLVESGGGLVQAGGSLRLSCAASTTSSINSMSWYRQ AQGKQREPVAVITDRGSTSYADSVKGRFTISRDNAKNTV YLQMNSLKPEDTAIYTCHVIADWRGYWGQGTQVTVSS	
620	6H2	QVQLVESGGGLVQAGGSLRLSCAASGRTLSRYAMGWF RQAPGKERQFVAAISRSGGTTRYSDSVKGRFTISRDNAA NTFYLQMNNLRPDDTAVYYCNVRRRGWGRTLEYWGQ GTQVTVSS	
621	5D2	QVQLGESGGGLVQAGGSLRLSCAASGSIFSPNAMIWHRQ APGKQREPVASINSSGSTNYGDSVKGRFTVSRDIVKNTM YLQMNSLKPEDTAVYYCSYSDFRRGTQYWGQGTQVTV SS	
622	7C4	QVQLVESGGGLVPSGGSLRLSCAASGATSAITNLGWYRR APGQVREMVARISVREDKEDYEDSVKGRFTISRDNTQNL VYLQMNNLQPHDTAIYYCGAQRWGRGPGTTWGQGTQ VTVSS	
623	5F2	QVQLVESGGGLVQAGGSLRLSCAASGSTFRIRVMRWYR QAPGTERDLVAVISGSSTYYADSVKGRFTISRDNAKNTL YLQMNNLKPEDTAVYYCNADDSGIARDYWGQGTQVTV SS	
624	2C2	QVQLVESGGGLVQAGESRRLSCAVSGDTSKFKAVGWY RQAPGAQRELLAWINNSGVGNTAESVKGRFTISRDNAK NTVYLQMNRLTPEDTDVYYCRFYRRFGINKNYWGQGT QVTVSS	
625	5G2	QVQLVESGGGLVQAGGSLRLSCAASGSTFGNKPMGWY RQAPGKQRELVAVISSDGGSTRYAALVKGRFTISRDNAK NTVYLQMESLVAEDTAVYYCNALRTYYLNDPVVFSWG QGTQVTVSS	
626	9H2	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYWYR QAPGKERELVAFISSGGSTNVRDSVKGRFSVSRDSAKNI VYLQMNSLTPEDTAVYYCNTYIPLRGTLHDYWGQGTQV TVSS	
627	5D4	QVQLVESGGGLVQAGGSLRLSCVASGRTDRITTMGWYR QAPGKQRELVATISNRGTSNYANSVKGRFTISRDNAKNT VYLQMNSLKPEDTAVYYCNARKWGRNYWGQGTQVTV SS	
628	2A4	QVQLVESGGGLVQARGSLRLSCTASGRTIGINDMAWYR QAPGNQRELVATITKGGTTDYADSVDGRFTISRDNAKNT VYLQMNSLKPEDTAVYYCNTKRREWAKDFEYWGQGT QVTVSS	

629	7F1	QVQLVESGGGLVQAGGSLRLSCAASAIGSINSMSWYRQAPGKQREPVAVITDRGSTSYADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAIYTCHVIADWRGYWGQGTQVTVSS	
630	5C2	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYWFRQAPGEERELVATINRGGSTNVRDSVKGRFSVSRDSAKNIVYLQMNRLKPEDTAVYYCNTYIPYGGTLHDFWGQGTQVTVSS	
631	2F4	QVQLVESGGGLVQAGGSLRLSCTTSTTFSINSMSWYRQAPGNQREPVAVITNRGTTSYADSVKGRFTISRDNARNTVYLQMDSLKPEDTAIYTCHVIADWRGYWGQGTQVTVSS	
632	2A2	QVQLVESGGGLVQAGGSLTLSCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNAKNTLYLQMNNLKPEDTAVYYCNADTIGTARDYWGQGTQVTVSS	
633	11F3	QVQLVESGGGLVQAGGSLRLSCVASGRTSTIDTMYWHRQAPGNERELVAYVTSRGTSNVADSVKGRFTISRDNAKNTAYLQMNSLKPEDTAVYYCSVRTTSYPVDFWGQGTQVTVSS	
634	10B3	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYWYRQAPGKERELVAFISSGGSTNVRDSVKGRFSVSRDSAKNIVYLQMNSLKPEDTAVYYCNTYIPYGGTLHDFWGQGTQVTVSS	
635	5H1	QVQLVESGGGLVQPGGSLRLSCAASGGDWSANFMYWYRQAPGKQRELVARISGRGVVDYVESVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCAVASYWGQGTQVTVSS	
636	MH1 (exemplary humanized version of 5H1)	EVQLVESGGGLVQPGGSLRLSCAASGGDWSANFMYWYRQAPGKQRELVARISGRGVVDYVESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVASYWGQGTLVTVSS	
637	MH2 (exemplary humanized version of 5H1)	EVQLVESGGGLVQPGGSLRLSCAASGGDWSANFMYWVRQAPGKGLEWVSRISGRGVVDYVESVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAVASYWGQGTLVTVSS	
638	MH3 (exemplary humanized version of 10B3)	EVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYWYRQAPGKERELVAFISSGGSTNVRDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNTYIPYGGTLHDFWGQGTLVTVSS	
639	MH4 (exemplary humanized version of 10B3)	EVQLVESGGGLVQPGGSLRLSCAASGSTSSINTMYWYRQAPGKERELVAFISSGGSTNVRDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNTYIPYGGTLHDFWGQGTLVTVSS	
640	MH5 (exemplary humanized version of 10B3)	EVQLVESGGGLVQPGGSLRLSCAASGSTSSINTMYWVRQAPGKGLEWVSFISSGGSTNVRDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNTYIPYGGTLHDFWGQGTLVTVSS	

641	MH6-GG (exemplary humanized version of 2A2)	QVQLVESGGGVVQAGGSLRLSCAASGSTFSIRAMRWYR QAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SSGG	
642	MH7-GG(exemplary humanized version of 2A2)	QVQLVESGGGVVQPGGSLRLSCAASGSTFSIRAMRWYR QAPGKERELVAVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SSGG	
643	MH8-GG (exemplary humanized version of 2A2)	QVQLVESGGGVVQPGGSLRLSCAASGSTFSIRAMRWVR QAPGKGLEWVSVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SSGG	
644	MH9 (exemplary humanized version of 11F3)	EVQLVESGGGLVQAGGSLRLSCVASGRTSTIDTMYWHR QAPGNERELVAYVTSRGTSNVADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCSVRTTSYPVDFWGQGTLVTV S	
645	MH10 (exemplary humanized version of 11F3)	EVQLVESGGGLVQPGGSLRLSCAASGRTSTIDTMYWHR QAPGKERELVAYVTSRGTSNVADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCSVRTTSYPVDFWGQGTLVTV SS	
646	MH11	EVQLVESGGGLVQPGGSLRLSCAASGRTSTIDTMYWVR QAPGKGLEWVSYVTSRGTSNVADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCSVRTTSYPVDFWGQGTLVT VSS	
647	Anti-MSLN-MH6T	QVQLVESGGGVVQAGGSLTLSCAASGSTFSIRAMRWYR QAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SS	
648	MH6 (exemplary humanized version of 2A2)	QVQLVESGGGVVQAGGSLRLSCAASGSTFSIRAMRWYR QAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SS	
649	MH7 (exemplary humanized version of 2A2)	QVQLVESGGGVVQPGGSLRLSCAASGSTFSIRAMRWYR QAPGKERELVAVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SS	
650	MH8 (exemplary humanized version of 2A2)	QVQLVESGGGVVQPGGSLRLSCAASGSTFSIRAMRWVR QAPGKGLEWVSVIYGSSTYYADAVKGRFTISRDNSKNTL YLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTV SS	

3505	Exemplary CDR2 of MSLN binding domain	INSSGSTNYG	
3506	Exemplary CDR3 of MSLN binding domain	NAGGGPLGSR	
3507	Exemplary CDR2 of MSLN binding domain	ISSGGSTNVR	
3508	Exemplary CDR3 of MSLN binding domain	NADTIGTARD	

Table 13. EGFR binding protein sequences

SEQ ID NO:	**Description**	**Sequence**	**Notes**
651	EL1	GSIAYIYTMD	CDR1
652	EL104	GRTDSWYVMG	CDR1
653	EL106	RTIISINAMT	CDR1
654	EL113	ARTLRLYAVG	CDR1
655	EL12	GSIAYIYTMD	CDR1
656	EL120	GSIAYIYTMD	CDR1
657	EL133	GRYQMA	CDR1
658	EL138	TRTLKLYAVG	CDR1
659	EL147	GSIAYIYTMD	CDR1
660	EL148	GSIAYIYTMD	CDR1
661	EL15	GSIAYIYTMD	CDR1
662	EL153	GRYQMA	CDR1
663	EL16	GSIVTINAMT	CDR1
664	EL162	RSIVSIKSMT	CDR1
665	EL165	GSTFRHHAMA	CDR1
666	EL17	GSIAYIYTMD	CDR1
667	EL171	GSIAYIYTMD	CDR1
668	EL172	VSIFSVNAVD	CDR1
669	EL176	GSIAYIYTMD	CDR1
670	EL178	GRYQLA	CDR1
671	EL18	GRYHMA	CDR1
672	EL187	GSIAYIYTMD	CDR1
673	EL27	GSIAYIYTMD	CDR1

674	EL30	GRYNMA	CDR1
675	EL33	GRYQMA	CDR1
676	EL35	GRYHLA	CDR1
677	EL4	GRSFSNYIMG	CDR1
678	EL40	GSIAYIYTMD	CDR1
679	EL43	GRYQMA	CDR1
680	EL44	GLTFSSYAMA	CDR1
681	EL51	GNIAYIYTMD	CDR1
682	EL56	GSIAYIYTMD	CDR1
683	EL6	GSIAYIYTMD	CDR1
684	EL64	GNDFVITDMH	CDR1
685	EL77	GAIAYIYGMG	CDR1
686	EL79	GRYHTA	CDR1
687	EL83	GNIAYIYTMN	CDR1
688	EL88	GNIAYIYTMG	CDR1
689	EH1	GSIAYIYTMD	CDR1
690	EH104	GRTDSWYVMG	CDR1
691	EH113	ARTLRLYAVG	CDR1
692	EH16	GSIVTINAMT	CDR1
693	EH18	GRYHMA	CDR1
694	EH38	GSTFRHHAMA	CDR1
695	EH4	GRSFSNYIMG	CDR1
696	EH44	GLTFSSYAMA	CDR1
697	EH60	VSIFSVNAVD	CDR1
698	EH64	GNDFVITDMH	CDR1
699	EH77	GAIAYIYGMG	CDR1
700	EL1	TSTRDGNVDYAESVKG	CDR2
701	EL104	VSWSYGNTYYADSVKG	CDR2
702	EL106	IITSGGETNYADSVKG	CDR2
703	EL113	GIGRSERTYYTDSVKG	CDR2
704	EL12	TSTHDGNTDYADSVKG	CDR2
705	EL120	TSTRDGNTDYADSVKG	CDR2
706	EL133	TISSGDSTWYTNSVKG	CDR2
707	EL138	GIGRSERIYYIDSVKG	CDR2
708	EL147	TSTHDGNTDYADSVKG	CDR2
709	EL148	TFTRDGNTDYADSVKG	CDR2
710	EL15	TSTHDGNTDYADSLKG	CDR2
711	EL153	TISSGDSTWYTNSLKG	CDR2
712	EL16	IITSGGETNYADSVKG	CDR2
713	EL162	LITSGGETNYSDSVKG	CDR2
714	EL165	AINDHGDRTKYLDSVRG	CDR2
715	EL17	TSTHDGNTDYADSVKG	CDR2
716	EL171	TSTHDGNTDYADSVKG	CDR2
717	EL172	IMTSDGSTNYGDSVKG	CDR2
718	EL176	TSTRDGNIDYADSVKG	CDR2
719	EL178	TISSGDSTWYTNSVKG	CDR2
720	EL18	TISSGDSTWYTNSVKG	CDR2
721	EL187	TSTHDGNTDYTDSVKG	CDR2

722	EL27	TSTRDANTDYAGSVKG	CDR2
723	EL30	TITSADSTWYTNSVKG	CDR2
724	EL33	TISSGDSTWYTNSVKG	CDR2
725	EL35	TITSADSTWYTNSVKG	CDR2
726	EL4	GLGWSPGNTYYADSVKG	CDR2
727	EL40	TSTHDGNTDYADSVKG	CDR2
728	EL43	TISSGDSTWYTNSVKG	CDR2
729	EL44	RITSGGTTDYADSVKG	CDR2
730	EL51	TSTHDGSTDYADSVKG	CDR2
731	EL56	TSTWDGNTDYADSVKG	CDR2
732	EL6	TSTHDGNTDYADSVKG	CDR2
733	EL64	TITRFATTNYADSVKG	CDR2
734	EL77	AISSGGSTDYADSVKG	CDR2
735	EL79	TISSGDSTWYTNSVKG	CDR2
736	EL83	TSTHAGNTDYADSVKG	CDR2
737	EL88	TSTHDGNSDYADSVKG	CDR2
738	EH1	TSTRDGNVDYADSVKG	CDR2
739	EH104	GVSWSYGNTYYADSVKG	CDR2
740	EH113	GIGRSERTYYTDSVKG	CDR2
741	EH16	IITSGGETNYADSVKG	CDR2
742	EH18	TISSGDSTWYTNSVKG	CDR2
743	EH38	AINDHGDRTKYLDSVKG	CDR2
744	EH4	GLGWSPGNTYYADSVKG	CDR2
745	EH44	RITSGGTTDYADSVKG	CDR2
746	EH60	IMTSDGSTNYDDSVKG	CDR2
747	EH64	TITRFATTNYADSVKG	CDR2
748	EH77	AISSGGSTDYADSVKG	CDR2
749	EL1	DLRTAVDLIRANY	CDR3
750	EL104	RVSREVIPTRWDLYNY	CDR3
751	EL106	VPPLGS	CDR3
752	EL113	TFQTTDMVDVPTTQHEYDY	CDR3
753	EL12	DLRTAVDLIRANY	CDR3
754	EL120	DLRTAVDLIRANY	CDR3
755	EL133	ALYYRDSRRAADYPY	CDR3
756	EL138	TFQTSDNVGVPTVQHEYDY	CDR3
757	EL147	DLRTAVDLIRANY	CDR3
758	EL148	DLRTAVDLIRANY	CDR3
759	EL15	DLRTAVDLIRANY	CDR3
760	EL153	ALYYRDSRRAADYPY	CDR3
761	EL16	VPPLGS	CDR3
762	EL162	VPPLGS	CDR3
763	EL165	GPLVDYLETTPLVYTY	CDR3
764	EL17	DLRTAVDLIRANY	CDR3
765	EL171	DLRTAVDLIRANY	CDR3
766	EL172	VPPRY	CDR3
767	EL176	DLRTAVDLIRANY	CDR3
768	EL178	ALYYRDSRRAADYPY	CDR3
769	EL18	ALYYGDSRRAADYPY	CDR3

770	EL187	DLRTAVDLIRANY	CDR3
771	EL27	DLRTAVDLIRANY	CDR3
772	EL30	ALYYGDSRRAADYPY	CDR3
773	EL33	ALYYRDSWRAADYPY	CDR3
774	EL35	ALYYGDSRRAADYPY	CDR3
775	EL4	RRGDVIYTTPWNYVY	CDR3
776	EL40	DLRTPVDLIRANY	CDR3
777	EL43	ALYYRDSRRAIDYPY	CDR3
778	EL44	DLTYRNLLLKLPHY	CDR3
779	EL51	DLRTPVDLIRANY	CDR3
780	EL56	DLRTAVDLIRANY	CDR3
781	EL6	DLRTAVDLIRANY	CDR3
782	EL64	IGLRGVPDVNRQFEV	CDR3
783	EL77	DVRTSRNLVRSDY	CDR3
784	EL79	ALYYGDSRRAGDYPY	CDR3
785	EL83	DLRTAVDLIRANY	CDR3
786	EL88	DLRTPVDRIRGNF	CDR3
787	EH1	DLRTAVDLIRANY	CDR3
788	EH104	RVSREVIPTRWDLYNY	CDR3
789	EH113	TFQTTDMVDVPTTQHEYDY	CDR3
790	EH16	VPPLGS	CDR3
791	EH18	ALYYGDSRRAADYPY	CDR3
792	EH38	GPLVDYLETTPLVYTY	CDR3
793	EH4	RRGDVIYTTPWNYVY	CDR3
794	EH44	DLTYRNLLLKLPHY	CDR3
795	EH60	VPPRY	CDR3
796	EH64	IGLRGVPDVNRQFEV	CDR3
797	EH77	DVRTSRNLVRSDY	CDR3
798	EL1	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQAPGKQRELVATSTRDGNVDYAESVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
799	EL104	QVQLQESGGGLVQAGDSLRLSCVVSGRTDSWYVMGWFRQAPGKDREFVAGVSWSYGNTYYADSVKGRFTASRDNAKNTAYLQMNSLNAEDTAVYYCAARVSREVIPTRWDLYNYWGQGTQVTVSS	
800	EL106	QVQLQESGGGSVQPGGSLRVSCVVSRTIISINAMTWYHQAPGKRRELVAIITSGGETNYADSVKGRFTISRDNAKNTAYLQMNNLKPEDTGVYYCNVVPPLGSWGQGTQVTVSS	
801	EL113	QVQLQESGGGRVQAGGSLRLSCSASARTLRLYAVGWFRQAPGKEREFVAGIGRSERTYYTDSVKGRFTLSRDNAKNTVFLEMNDLEPEDTAVYFCALTFQTTDMVDVPTTQHEYDYWGRGTQVTVSS	
802	EL12	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQAPGKQRELVATSTHDGNTDYADSVKGRFTISRDNVKNTVYLQMNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	

803	EL120	QVQLQESGGGLVQPGGSLRLSCAASGSIAYIYTMDWYRQAP GKQRELVATSTRDGNTDYADSVKGRFTISRDNAKDTVYLQ MNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
804	EL133	QVQLQESGGGLVQAGGSLTLSCAASGRYQMAWFRQAPEKE REFVGTISSGDSTWYTNSVKGRFAISRDSARNTVYLQMNDL KPEDTAIYYCAAALYYRDSRRAADYPYWGQGTQVTVSS	
805	EL138	QVQLQESGGGRVQAGESLRLSCSTSTRTLKLYAVGWFRQA PGKERDFVAGIGRSERIYYIDSVKGRFTLSRDNAKNTVFLEM NDLEPEDTAVYFCAATFQTSDNVGVPTVQHEYDYWGQGTQ VTVSS	
806	EL147	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYADSVKGRFTISRDNAKNTVTLQ MNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
807	EL148	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATFTRDGNTDYADSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYYCNTDLRTAVDLIRANYWGQGTQVTVS S	
808	EL15	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYADSLKGRFTISRDNAKNTVYLQ MNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
809	EL153	QVQLQESGGGSVQAGGSLRLSCAASGRYQMAWFRQAPEKE REFVGTISSGDSTWYTNSLKGRFAISRDSARDTVYLQMNDL KPEDTAVYYCAAALYYRDSRRAADYPYWGQGTQVTVSS	
810	EL16	QVQLQESGGGLVQTGGSLRLSCAVSGSIVTINAMTWYRQAP GKRRELVAIITSGGETNYADSVKGRFTISRDNAKNTAHLQM NSLNPEDTGVYYCNVVPPLGSWGQGTQVTVSS	
811	EL162	QVQLQESGGGLVQTGGSLRLSCAVSRSIVSIKSMTWYRQAP GKRRELVALITSGGETNYSDSVKGRFTISRDNAKNTVYLQM NSLKPEDTGVYYCNVVPPLGSWGQGTQVTVSS	
812	EL165	QVQLQESGGGLVETGGSLRLSCAGSGSTFRHHAMAWFRQT PGKEREFVSAINDHGDRTKYLDSVRGRFTISRDNTDNMVYL QMTDLRPEDTANYSCAAGPLVDYLETTPLVYTYWGHGTQV TVSS	
813	EL17	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYADSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTV SS	
814	EL171	QVQLQESGGGSVQAGGSLTLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYADSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTV SS	
815	EL172	QVQLQESGGGLVQPGGSLRLSCTASVSIFSVNAVDWYRQSP GKERELVAIMTSDGSTNYGDSVKGRFTISRDNAKNTVYLQ MNNLKPEDTAVYYCNTVPPRYWGQGTQVTVSS	
816	EL176	QVQLQESGGGLVQPGGSLRLSCAASGSIAYIYTMDWYRQAP GKQRELVATSTRDGNIDYADSVKGRFTISRDSAKNTVYLQM SSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
817	EL178	QVQLQESGGGLVQAGGSLTLSCAASGRYQLAWFRQAPEKV REFVGTISSGDSTWYTNSVKGRFAISRDSARNTVYLQMNDL KPEDTAVYYCAAALYYRDSRRAADYPYWGQGTQVTVSS	

818	EL18	QVQLQESGGGSVQAGGSLRLSCAASGRYHMAWFRQAPEKE REFVGTISSGDSTWYTNSVKGRFAISRDSARNTAYLQMNDL KPEDTAVYYCAAALYYGDSRRAADYPYWGQGTQVTVSS	
819	EL187	QVQLQESGGGSVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYTDSVKGRFTISRDNAKNTVYLQ MNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
820	EL27	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQT PGKQRELVATSTRDANTDYAGSVKGRFTISRDNAKDTVYL QMNSLKPEDTAVYYCHADLRTAVDLIRANYWGQGTQVTV SS	
821	EL30	QVQLQESGGGLVQAGGSLRLSCAASGRYNMAWFRQAPEK EREFVGTITSADSTWYTNSVKGRFAITQDSARNTVYLQMND LKPEDTAVYYCAAALYYGDSRRAADYPYWGQGTQVTVSS	
822	EL33	QVQLQESGGGLVQPGGSLRLSCAASGRYQMAWFRQAPEKE REFVGTISSGDSTWYTNSVKGRFAISRDSARTTVYLQMNDL KPEDTAVYYCAAALYYRDSWRAADYPYWGQGTQVTVSS	
823	EL35	QVQLQESGGGLVQPGESLRLSCAATGRYHLAWFRQAPEKE REFVGTITSADSTWYTNSVKGRFAITRDSARNTVYLQMNDL KPEDTAVYYCAAALYYGDSRRAADYPYWGQGTQVTVSS	
824	EL4	QVQLQESGGGLVQAGGSLKLSCADSGRSFSNYIMGWFRQA PGKEREFVAGLGWSPGNTYYADSVKGRFTISRDNAKNMVY LQMNSLNPEDTAVYYCAARRGDVIYTTPWNYVYWGQGTQ VTVSS	
825	EL40	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYADSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYYCNADLRTPVDLIRANYWGQGTQVTVS S	
826	EL43	QVQLQESGGGSVQAGGSLRLSCAAPGRYQMAWFRQAPEKE REFVGTISSGDSTWYTNSVKGRFAISRDSARNTVYLQMNDL KSEDTAVYYCAAALYYRDSRRAIDYPYWGQGTQVTVSS	
827	EL44	QVQLQESGGGSVQAGGSLRLSCAASGLTFSSYAMAWFRQA PGKQRELVARITSGGTTDYADSVKGRFTISRDNAKNTMYLQ MNSLKPEDTAVYYCAADLTYRNLLLKLPHYWGQGTQVTV SS	
828	EL51	QVQLQESGGGLVQAGGSLRLSCAASGNIAYIYTMDWYRQA PGKQRELVATSTHDGSTDYADSVKGRFTISRDNAKNTVYLQ MNSLKPEDTAVYYCNADLRTPVDLIRANYWGQGTQVTVSS	
829	EL56	QVQLQESGGGLVQPGGSLRLSCAASGSIAYIYTMDWYRQAP GKQRELVATSTWDGNTDYADSVKGRFTISRDNAKNTVYLQ MNSLKPEDTAVYYCNADLRTAVDLIRANYWGQGTQVTVSS	
830	EL6	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDWYRQA PGKQRELVATSTHDGNTDYADSVKGRFTISRDNAKNTVYL QMSSLKPDDTAVYYCNADLRTAVDLIRANYWGQGTQVTV SS	
831	EL64	QVQLQESGGGLVQAGESLSLSCAASGNDFVITDMHWYRQA PGKQREWVATITRFATTNYADSVKGRFTISRDNAKNTWYL QMNSLKPDDTAVYYCKAIGLRGVPDVNRQFEVWGQGTQV TVSS	

832	EL77	QVQLQESGGGLVQAGGSLRLSCAASGAIAYIYGMGWYRQA PGNQRELVAAISSGGSTDYADSVKGRFTISRDNAKNTVYLQ MSSLKPEDTAVYYCNADVRTSRNLVRSDYWGQGTQVTVSS	
833	EL79	QVQLQESGGGLVQAGGSLRLSCAASGRYHTAWFRQAPEKE REFVGTISSGDSTWYTNSVKGRFAISRDSARNTVYLQMNDL KPEDTAVYYCAAALYYGDSRRAGDYPYWGQGTQVTVSS	
834	EL83	QVQLQESGGGLVQAGGSLRLSCAASGNIAYIYTMNWYRQA PGKQRELVATSTHAGNTDYADSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYYCNVDLRTAVDLIRANYWGQGTQVTV SS	
835	EL88	QVQLQESGGGLVQPGGSLRLSCAASGNIAYIYTMGWYRQA PGKQRELVATSTHDGNSDYADSVKGRFTISRDNAKNTVYL QMNTLKPDDTAVYYCNADLRTPVDRIRGNFWGQGTQVTVS S	
836	EH1	EVQLLESGGGLVQPGGSLTLSCAASGSIAYIYTMDWYRQAP GKQRELVATSTRDGNVDYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCNADLRTAVDLIRANYWGLGTQVTVSS	
837	EH104	EVQLLESGGGLVQPGGSLTLSCAASGRTDSWYVMGWFRQA PGKDREFVAGVSWSYGNTYYADSVKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCAARVSREVIPTRWDLYNYWGLGT QVTVSS	
838	EH113	EVQLLESGGGLVQPGGSLTLSCAASARTLRLYAVGWFRQAP GKEREFVAGIGRSERTYYTDSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCALTFQTTDMVDVPTTQHEYDYWGLGT QVTVSS	
839	EH16	EVQLLESGGGLVQPGGSLTLSCAASGSIVTINAMTWYRQAP GKRRELVAIITSGGETNYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCNVVPPLGSWGLGTQVTVSS	
840	EH18	EVQLLESGGGLVQPGGSLTLSCAASGRYHMAWFRQAPGKE REFVGTISSGDSTWYTNSVKGRFTISRDNSKNTLYLQMNSLR AEDTAVYYCAAALYYGDSRRAADYPYWGLGTQVTVSS	
841	EH38	EVQLLESGGGLVQPGGSLTLSCAASGSTFRHHAMAWFRQTP GKEREFVSAINDHGDRTKYLDSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAAGPLVDYLETTPLVYTYWGLGTQVT VSS	
842	EH4	EVQLLESGGGLVQPGGSLTLSCAASGRSFSNYIMGWFRQAP GKEREFVAGLGWSPGNTYYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCAARRGDVIYTTPWNYVYWGLGTQVT VSS	
843	EH44	EVQLLESGGGLVQPGGSLTLSCAASGLTFSSYAMAWFRQAP GKQRELVARITSGGTTDYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAADLTYRNLLLKLPHYWGLGTQVTVSS	
844	EH60	EVQLLESGGGLVQPGGSLTLSCAASVSIFSVNAVDWYRQSP GKERELVAIMTSDGSTNYDDSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCNTVPPRYWGLGTQVTVSS	
845	EH64	EVQLLESGGGLVQPGGSLTLSCAASGNDFVITDMHWYRQA PGKQREWVATITRFATTNYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCKAIGLRGVPDVNRQFEVWGLGTQVT VSS	

846	EH77	EVQLLESGGGLVQPGGSLTLSCAASGAIAYIYGMGWYRQAP GKQRELVAAISSGGSTDYADSVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCNADVRTSRNLVRSDYWGLGTQVTVSS	

Table 14. EpCAM binding protein sequences

SEQ. ID NO.	Name	Sequence	Notes
847	EPL90	GFIFRAASMA	CDR1
848	EPL118	GFIFRAASMG	CDR1
849	EPL138	GFIFRAASMD	CDR1
850	EPL145	GFIFRAASMG	CDR1
851	EPL164	GFIFRAASMD	CDR1
852	EPL31	GDTFLRYAMG	CDR1
853	EPL55	GDTFLRYAMG	CDR1
854	EPL57	GDTFLRYAMG	CDR1
855	EPL136	GDTFLRYAMG	CDR1
856	EPL15	GFTFSSYYMS	CDR1
857	EPL34	GFTFSSYYMS	CDR1
858	EPL86	GFTFSDWAMS	CDR1
859	EPL153	GFTFSDWAMS	CDR1
860	EPL20	GNVFRAATMA	CDR1
861	EPL70	GNVFRAATMA	CDR1
862	EPL125	GNVFRAATMA	CDR1
863	EPL13	GFAFGNHWMY	CDR1
864	EPL129	GFAFGNHWMY	CDR1
865	EPL159	GFAFGNHWMY	CDR1
866	EPL120	GFIFRAASIS	CDR1
867	EPL126	GFIFRAASMG	CDR1
868	EPL60	EYILSMYRMA	CDR1
869	EPL156	EYILSMYRMA	CDR1
870	EPL2	ESISSFIAVG	CDR1
871	EPL43	ESISSFIAVG	CDR1
872	EPL10	GSVFRANVMG	CDR1
873	EPL49	GRTSSIFGMG	CDR1
874	EPL58	GPIFSDTIRTMG	CDR1
875	EPL74	GSIFGINAMG	CDR1
876	EPL78	ANRFNINVMG	CDR1
877	EPL82	GTILSTMA	CDR1
878	EPL83	GSIFSLNTLA	CDR1
879	EPL97	GIIFRGTTMG	CDR1
880	EPL109	GFTLDDYTIG	CDR1
881	EPL117	GNIVRMTNMA	CDR1
882	EPL127	GFAFNDHAIL	CDR1
883	EPL152	GSIFRASTMA	CDR1
884	EPL189	GRINSINTMG	CDR1
885	EPL90	SISSGAFTNYADSVKA	CDR2
886	EPL118	TVSSGDFTNYADSVKG	CDR2

887	EPL138	TISSGGFTNYADSVKG	CDR2
888	EPL145	TVSSGGFTNYADSVKG	CDR2
889	EPL164	TISSTGFTNYANSVKG	CDR2
890	EPL31	AITWNGGNTDYAGSLKG	CDR2
891	EPL55	AITWNGGNTDYAGSLKG	CDR2
892	EPL57	AITWNGGNTDYADSLKG	CDR2
893	EPL136	AITWNGGNTDYAGSLKG	CDR2
894	EPL15	GIHYTGDWTNYADSVKG	CDR2
895	EPL34	GIHYTGDWTNYADSVKG	CDR2
896	EPL86	GIHYGDHTTHYADFVKG	CDR2
897	EPL153	SIHYGDHTTHYADFVKG	CDR2
898	EPL20	TIASGGTTNYADFVKG	CDR2
899	EPL70	TIASGGTTNYADFVKG	CDR2
900	EPL125	TIASGGTTNYADFVKG	CDR2
901	EPL13	SISSGGSTNYVDSVKG	CDR2
902	EPL129	SISSGGSTNYVDSVKG	CDR2
903	EPL159	SISSGGSTNYVDSVKG	CDR2
904	EPL120	TINSGGFTNYADSVLG	CDR2
905	EPL126	TINSGGFTNYADSVKG	CDR2
906	EPL60	DMSSGGTTNYADFVKG	CDR2
907	EPL156	DMSSGGTTNYADFVKG	CDR2
908	EPL2	GINRSGFTYYTDSVKG	CDR2
909	EPL43	GINRSGFTYYTDSVKG	CDR2
910	EPL10	RIDPGGTTTYADPVKG	CDR2
911	EPL49	SINWSGGSTSYADSVKG	CDR2
912	EPL58	TIASFPSRTNYVDSVKG	CDR2
913	EPL74	FITIGGNTNYLDSVKG	CDR2
914	EPL78	TINIGGSTDYADSVKG	CDR2
915	EPL82	TISRGGTTNYSDSVKG	CDR2
916	EPL83	RITGGGTTVYADSVKG	CDR2
917	EPL97	SISPLGTTSYSGSVEG	CDR2
918	EPL109	CISRRDDSTYYADSVKG	CDR2
919	EPL117	TISAGGSTTYVDSVKD	CDR2
920	EPL127	EICRDGTTYYTDSVKG	CDR2
921	EPL152	QIMSGGGTNYAGSVKG	CDR2
922	EPL189	EITRGGTTNYADSVQG	CDR2
923	EPL90	TFLRSDGHHTI	CDR3
924	EPL118	TFVRSDGHHTI	CDR3
925	EPL138	TFLRSDGHHTI	CDR3
926	EPL145	TFVRSDGHHTI	CDR3
927	EPL164	TFLRSDGQHSI	CDR3
928	EPL31	DLTFGLASSHYQYDY	CDR3
929	EPL55	DLTFGLASSHYQYDY	CDR3
930	EPL57	DLTFGLASSHYQYDY	CDR3
931	EPL136	DLTFGLASSHYQYDY	CDR3
932	EPL15	GSD	CDR3
933	EPL34	GSD	CDR3
934	EPL86	GST	CDR3

935	EPL153	GTT	CDR3
936	EPL20	GYLTSLGPKNY	CDR3
937	EPL70	GYLTSLGPKNY	CDR3
938	EPL125	LYLTSLGPKSY	CDR3
939	EPL13	SDN	CDR3
940	EPL129	SDN	CDR3
941	EPL159	SDN	CDR3
942	EPL120	TFLRSDGQPPI	CDR3
943	EPL126	TFLRSDGQPPI	CDR3
944	EPL60	AGRTGPPSYDAFNN	CDR3
945	EPL156	AGRTGPPSYDAFNN	CDR3
946	EPL2	GGLYFSNAYTQGDY	CDR3
947	EPL43	GGLYFSNAYTQGDY	CDR3
948	EPL10	IILLSGGPKDY	CDR3
949	EPL49	AVLTNKPSWNF	CDR3
950	EPL58	DLASIPTKTY	CDR3
951	EPL74	NPPLILTAGGLY	CDR3
952	EPL78	KLRVSGPTGPNVY	CDR3
953	EPL82	PLTDYGMGYN	CDR3
954	EPL83	MVRHPSGSTYEY	CDR3
955	EPL97	IQVTNVGPRVY	CDR3
956	EPL109	TPRSYTLRCLGKFDF	CDR3
957	EPL117	GSILTNRGAIPGS	CDR3
958	EPL127	DRRRYYCSGNRAFSSDYYY	CDR3
959	EPL152	AQITSWGPKVY	CDR3
960	EPL189	QTFPTFSRPTGLDY	CDR3
961	EPL90	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASMAWYRQ SPGNERELVASISSGAFTNYADSVKARFTISRDNAKNTVYL QMNSLKPEDTAVYFCGATFLRSDGHHTINGQGTQVTVSS	
962	EPL118	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASMGWFRQ SPGNERELVATVSSGDFTNYADSVKGRFTISRDNAKNTVY LQMNSLKPEDTAVYFCGATFVRSDGHHTIYGQGTQVTVS S	
963	EPL138	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASMDWYRQ FPGNERESIATISSGGFTNYADSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYFCGATFLRSDGHHTINGQGTQVTVSS	
964	EPL145	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASMGWFRQ SPGNERELVATVSSGGFTNYADSVKGRFTISRDNAKNTVY LQMNSLKPEDTAVYFCGATFVRSDGHHTIYGQGTQVTVS S	
965	EPL164	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASMDWYRQ SPGTQPELVATISSTGFTNYANSVKGRFTISRDNAKNTVYL QMNSLKPEDTAVYFCGATFLRSDGQHSIYGQGTQVTVSS	
966	EPL31	QVQLQESGGGLVHTGGSLRLSCAASGDTFLRYAMGWFRQ APGKEREFVAAITWNGGNTDYAGSLKGRFTISRDNTKNTV YLQMNSLKPEDTAVYYCAADLTFGLASSHYQYDYWGQG TQVTVSS	
967	EPL55	QVQLQESGGGLVQAGGSLRLSCAASGDTFLRYAMGWFR QAPGKEREFVAAITWNGGNTDYAGSLKGRFTISRDNTKNT	

		VYLQMNSLKPEDTAVYYCAADLTFGLASSHYQYDYWGQ GTQVTVSS	
968	EPL57	QVQLQESGGGLVHTGGSLRLSCAFSGDTFLRYAMGWFRQ APGKEREFVAAITWNGGNTDYADSLKGRFTISRDNTKNTV YLQMNSLRPEDTAVYYCAADLTFGLASSHYQYDYWGQG TQVTVSS	
969	EPL136	QVQLQESGGGLVQPGGSLRLSCAASGDTFLRYAMGWFRQ APGKEREFVAAITWNGGNTDYAGSLKGRFTISRDNTKNTV YLQMNSLKPEDTAVYYCAADLTFGLASSHYQYDYWGQG TQVTVSS	
970	EPL15	QVQLQESGGGSVLAGGSLRLSCAASGFTFSSYYMSWVRQ APGKGLEWVSGIHYTGDWTNYADSVKGRFTISRDNAKNE LYLEMNNLKPEDTAVYYCARGSDKGQGTQVTVSS	
971	EPL34	QVQLQESGGGSVQAGGSLRLSCAASGFTFSSYYMSWVRQ APGKGLEWVSGIHYTGDWTNYADSVKGRFTISRDNAKNE LYLEMNNLKPEDTAVYYCARGSDKGQGTQVTVSS	
972	EPL86	QVQLQESGGGLVQPGGSLRLSCAASGFTFSDWAMSWVRQ APGKGLEWVSGIHYGDHTTHYADFVKGRFTISRDDAKNT LYLQMNSLKPEDTAVYYCARGSTKGQGTQVTVSS	
973	EPL153	QVQLQESGGGLVQPGGSLRLSCAASGFTFSDWAMSWVRQ APGKGLEWVSSIHYGDHTTHYADFVKGRFTISRDDAKNTL YLQMNSLKPEDTAVYYCEKGTTRGQGTQVTVSS	
974	EPL20	QVQLQESGGGLVQAGGSLKLSCAASGNVFRAATMAWYR QAPEKQREMVATIASGGTTNYADFVKGRFTISRDNAKNT VYLQMNTLKPEDTAVYYCNAGYLTSLGPKNYWGQGTQV TVSS	
975	EPL70	QVQLQESGGGLVQPGGSLRLSCAASGNVFRAATMAWYR QAPEKXREMVATIASGGTTNYADFVKGRFTISRDNAKNT VYLQMNTLKPEDTAVYYCNAGYLTSLGPKNYWGQGTQV TVSS	
976	EPL125	QVQLQESGGGLVQAGGSLRLSCAASGNVFRAATMAWYR QVPEKQREMVATIASGGTTNYADFVKGRFTISRDNAKNT VYLQMNTLKPEDTAVYYCNALYLTSLGPKSYWGQGTQV TVSS	
977	EPL13	QVQLQESGGGLVQPGGSLRLSCAASGFAFGNHWMYWYR QAPGRGRELVASISSGGSTNYVDSVKGRFTISRDNARNTV YLQMYSLKPEDTAVYYCGTSDNWGQGTQVTVSS	
978	EPL129	QVQLQESGGGLVQAGGSLRLSCAASGFAFGNHWMYWYR QAPGRGRELVASISSGGSTNYVDSVKGRFTISRDNARNTV YLQMYSLRPEDTAVYYCGTSDNWGQGTQVTVSS	
979	EPL159	QVQLQESGGGLVQAGGSLRLSCAASGFAFGNHWMYWYR QAPGRGRELVASISSGGSTNYVDSVKGRFTISRDNARNTV YLQMYSLKPEDTAVYYCGTSDNWGQGTQVTVSS	
980	EPL120	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASISWYRQS PGNERELVATINSGGFTNYADSVLGRFTISRDNAKNTGYL QMNSLKPEDTAVYFCAATFLRSDGQPPIWGQGTQVTVSS	
981	EPL126	QVQLQESGGGLVQAGGSLRLSCAASGFIFRAASMGWYRQ SPGNERELVATINSGGFTNYADSVKGRFTISRDNAKNTGY LQMNSLKPEDTAVYFCAATFLRSDGQPPIWGQGTQVTVSS	
982	EPL60	QVQLQESGGGLVQAGGSLRLSCAASEYILSMYRMAWYR QAPGKVRELVADMSSGGTTNYADFVKGRFTISRDNDRNT	

		VYLQMNRLQPEDTAAYYCNVAGRTGPPSYDAFNNWGQG TQVTVSS	
983	EPL156	QVQLQESGGGLVQPGASLRVSCAASEYILSMYRMAWYRQ APGKVRELVADMSSGGTTNYADFVKGRFTISRDNDRNTV YLQMNRLQPEDTAAYYCNVAGRTGPPSYDAFNNWGQGT QVTVSS	
984	EPL2	QVQLQESGGGLVQPGGSLRLSCAASESISSFIAVGWYRQA PGKERELVAGINRSGFTYYTDSVKGRFSISRDNAKNTVLL QMTSLKPEDTAVYYCNAGGLYFSNAYTQGDYWGQGTQV TVSS	
985	EPL43	QVQLQESGGGLVQTGGSLRLSCAASESISSFIAVGWYRQA PGKERELVAGINRSGFTYYTDSVKGRFSISRDNAKNTVLL QMTSLKPEDTAVYYCNAGGLYFSNAYTQGDYWGQGTQV TVSS	
986	EPL10	QVQLQESGGGLVQAGGSLRLSCAASGSVFRANVMGWYR QAPGKQHELVARIDPGGTTTYADPVKGRFTISRDNAKKTV YLQMNSLKPDDTAVYYCNAIILLSGGPKDYWGQGTQVTV SS	
987	EPL49	QVQLQESGGGLVQAGGSLRLSCAPSGRTSSIFGMGWFRQ APGKEREFVASINWSGGSTSYADSVKGRFTISRDNAKNEM YLQMNSLKFEDTAVYVCAAAVLTNKPSWNFWGQGTQVT VSS	
988	EPL58	QVQLQESGGGLVQAGGSLRLSCAASGPIFSDTIRTMGWYR QAAGKQRELVATIASFPSRTNYVDSVKGRFTISRDIAKNTV YLQMDSLKPEDTAVYYCNVDLASIPTKTYWGQGTQVTVS S	
989	EPL74	QVQLQESGGGLVQAGGSLRLSCAASGSIFGINAMGWYRQ APGKQRESVAFITIGGNTNYLDSVKGRFTISRDNAKNTVY LQMNGLKPEDTAVYYCNTNPPLILTAGGLYWGQGTQVTV SS	
990	EPL78	QVQLQESGGGLVQPGGSLRLSCATSANRFNINVMGWYRQ APGQQRELVATINIGGSTDYADSVKGRFTISRDNAKNTVY LQLSDLKPEDTAVYYCNVKLRVSGPTGPNVYWGQGTQVT VSS	
991	EPL82	QVQLQESGGGLVQAGGSLKLSCTASGTILSTMAWYRQAP GKQRELVATISRGGTTNYSDSVKGRFAISRDSTKNTVYLQ MNSLKPEDTAVYYCNTPLTDYGMGYNWGQGTQVTVSS	
992	EPL83	QVQLQESGGGLVQAGGSLRLSCAVSGSIFSLNTLAWYRQ APGRQRDLIARITGGGTTVYADSVKGRFTISRDNAKNTVY LQMNSLKPEDTAVYYCNLMVRHPSGSTYEYWGQGTQVT VSS	
993	EPL97	QVQLQESGGGLVQAGGSLRLSCAASGIIFRGTTMGWFRQ APGKQRESVASISPLGTTSYSGSVEGRFTVSRDNAKNTLFL QMNSLKSEDTAVYYCNAIQVTNVGPRVYWGQGTQVTVS S	
994	EPL109	QVQLQESGGGLVQPGGSLRLSCASSGFTLDDYTIGWFRQA PGKEREGVSCISRRDDSTYYADSVKGRFTISRDNAKNTVD LQMISLRPEDTAVYYCAATPRSYTLRCLGKFDFQGQGTQV TVSS	
995	EPL117	QVQLQESGGGLVQAGGSLRLSCAASGNIVRMTNMAWYR QAPGKQREFVATISAGGSTTYVDSVKDRFTISRDNTKNTV	

		YLQMNYLKPEDTAVYYCATGSILTNRGAIPGSWGHGTQV TVSS	
996	EPL127	QVQLQESGGGLVQAGGSLRLSCAAPGFAFNDHAILWFRQ APGKEREGVSEICRDGTTYYTDSVKGRFTISSDNAKNTVY LQMNSVKTDDTAVYYCAVDRRRYYCSGNRAFSSDYYYW GQGTQVTVSS	
997	EPL152	QVQLQESGGGLVQAGGSLRLSCVHSGSIFRASTMAWYRQ APGKQRELVAQIMSGGGTNYAGSVKGRFTISRDNANNTV YLQMNSLKPEDTAVYYCNAAQITSWGPKVYWGQGTQVT VSS	
998	EPL189	QVQLQESGGGLVQPGGSLRLSCAASGRINSINTMGWYRQ APGNQRELVAEITRGGTTNYADSVQGRYAISRDNAKNLV YLQMNSLKPEDTDVYYCNAQTFPTFSRPTGLDYWGQGTQ VTVSS	
999	H13	EVQLVESGGGLVQPGGSLTLSCAASGFAFGNHWMYWYR QAPGRGRELVASISSGGSTNYVDSVKGRFTISRDNAKNTL YLQMNSLRAEDTAVYYCGTSDNWGQGTLVTVSS	Humaniz ed Anti-EpCAM sequence
1000	H138	EVQLLESGGGLVQPGGSLTLSCAASGFIFRAASMDWYRQF PGNERESIATISSGGFTNYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCGATFLRSDGHHTINGQGTLVTVSS	Humaniz ed Anti-EpCAM sequence
1001	H90	EVQLLESGGGLVQPGGSLTLSCAASGFIFRAASMAWYRQS PGNERELVASISSGAFTNYADSVKARFTISRDNSKNTLYLQ MNSLRAEDTAVYYCGATFLRSDGHHTINGQGTLVTVSS	Humaniz ed Anti-EpCAM sequence
1002	H138.2	EVQLLESGGGLVQPGGSLTLSCAASGFIFRAASMDWYRQF PGNERESIATISSGGFTNYADSVKGRFTISRDNSKNTLYLQ MNSLRAEDTAVYYCGATFLRSDGHHTIWGQGTLVTVSS	
1003	H90.2	EVQLLESGGGLVQPGGSLTLSCAASGFIFRAASMAWYRQS PGNERELVASISSGAFTNYADSVKARFTISRDNSKNTLYLQ MNSLRAEDTAVYYCGATFLRSDGHHTIWGQGTLVTVSS	

Table 15. FLT3 binding protein sequences

SEQ ID NO.	Name	Sequence	Sequence descriptor
1004	FLL101	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWYR QAPGKQREWVAQITRDSNSFYADSVKGRFAISRDNAKN TVYLQMNNLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1005	FLL103	QVQLQESGGGLVQAGGSLRLSCEASGPTFSINYIDWYR QAPGKQREWVAQITRDSNSFYADSVKGRFAVSRDNAK NTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1006	FLL116	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWYR QAPGKQREWVAQITRDSNSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain

1007	FLL125	QVQLQESGGGLVQAGGSLRLSCAASGSTFSRNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1008	FLL129	QVQLQESGGGLVQAGGSLRLSCAASGVTFSASYIDWYR QAPGNEREWVAQITRGGDSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1009	FLL137	QVQLQESGGGLVQAGGSLRLSCAASGSTFNNYAMDWF RQAPGKQREWVAQITRDSSSFYADSVKGRFAISRDNAK NTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1010	FLL14	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWYR QAPGKQREWVAQITRDSNSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRLLSYWGQGTQVTVSS	FLT3 antibody variable domain
1011	FLL146	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWYR QAPGKQREWVAQITRDDTSFYADSVKGRFAISRDNAKN TVYLQMNNLRPEDTAVYYCRLLSFWGQGTQVTVSS	FLT3 antibody variable domain
1012	FLL158	QVQLQESGGGLVQPGGSLRLSCAASGSTFGRNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1013	FLL179	QVQLQESGGGLVQAGGSLRLSCKASGVTFSINYIDWYR QAPGKQREWVAQITRDGSSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRILSDWGQGTQVTVSS	FLT3 antibody variable domain
1014	FLL181	QVQLQESGGGLVQAGDSLRLSCAASGVTFSASYIDWYR QAPGNEREWVAQITRGGDSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1015	FLL187	QVQLQESGGGLVQPGGSLRLSCAASGVTFSINYIDWYR QAPGKQREWVAQITRDSNSFYADSVKGRFAISRENAKN TVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1016	FLL32	QVQLQESGGGLVQAGGSLRLSCQASGVTFNINYIDWYR QAPGRQREWVAQITRDSTRFYADSVKGRFAISRDNAKN MVYLQLNSLKPEDTAVYYCRILSYWGQGTQVTVSS	FLT3 antibody variable domain
1017	FLL51	QVQLQESGGGLVQPGGSLRLSCAASGFDFSISYIDWYR QAPGNEREWVAQITRGGDSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRILSYWGQGTQVTVSS	FLT3 antibody variable domain
1018	FLL55	QVQLQESGGGLVQAGGSLRLSCAASGSTFSRNYIDWYR QAPGKQREWVAQITSAGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1019	FLL77	QVQLQESGGGLVQPGGSLRLSCAASGVTFSISYIDWYR QAPGNEREWVAQITRGGDSFYADSVKGRFAISRDNAKN TVYLQMNSLKPEDTAVYYCRILSYWGQGTQVTVSS	FLT3 antibody variable domain

1020	FLL97	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWYR QAPGKQREWVAQITRDSNSFYADSVKGRFAVSRDNAK NTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTVSS	FLT3 antibody variable domain
1021	FLL21	QVQLQESGGGLVQPGGSLTLSCAASGSTFSRNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1022	FLL57	QVQLQESGGGLVQAGGSLRLSCAASGSTFSKNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1023	FLL62	QVQLQESGGGLVQAGGSLRLSCAASGSTSSRNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1024	FLL79	QVQLQESGGGLVQAGGSLRLSCSASGSTFSRNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1025	FLL86	QVQLQESGGGLVQPGDPLRLSCAASGSTFSRNYIDWYR QAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNAKN TAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVSS	FLT3 antibody variable domain
1026	FLL112	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWAGGRTHYEDSVKGRFTIHRDNAK NTVYLQMNSLKPEDTAVYYCAAQVSRAYDGIWYSGG DYWGQGTQVTVSS	FLT3 antibody variable domain
1027	FLL142	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWDGGRTHYADFVKGRFTISRDNAK NTVYLQMNSLKPEDTAVYYCAAQVARAYDSKWYSGG DYWGQGTQVTVSS	FLT3 antibody variable domain
1028	FLL143	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWVGGRTHYADSVKGRFTISRDNAK NTVYLQMNSLKPEDTAVYYCAAQVARAYDGNWYSGG DYWGQGTQVTVSS	FLT3 antibody variable domain
1029	FLL154	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWSGGRTHYADSVKGRFTISRDNAK NTVYLQMNSLKPEDTAVYYCAGQVARAYDGNWYSRG DYWGQGTQVTVSS	FLT3 antibody variable domain
1030	FLL168	QVQLQESGGGSVQAGGSLRLSCAFSGRTFSGFGTGWFR QAPEKEREFVAAISWDGGRTHYADSVKGRFTISRDNAK NTVYLQMDSLKPEDTAIYYCAAQVSRAYDGRWYSAVD YWGRGTQVTVSS	FLT3 antibody variable domain
1031	FLL170	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAK NTVYLQMNSLKPEDTAVYYCAGQVARAYDSSWYSRG DYWGQGTQVTVSS	FLT3 antibody variable domain
1032	FLL188	QVQLQESGGGLVQAGGSLGLSCAVSGRTFSGFGTGWF RQPPEKEREFVAAISWDGGRTHYADSVKGRFTISRDNA KNTVFLQMNSLKPEDTAVYYCAAQVARAYDSRWYSG GDYWGQGTQVTVSS	FLT3 antibody variable domain

1033	FLL40	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAK NTVSLVYLQMNSLKPDDTAVYYCAGQVARAYDSSWY SRGDYLGQGTQVTVSS	FLT3 antibody variable domain
1034	FLL6	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWDGGRTHYADSVKGRFTISRDNAA NTVYLQMNSLKPEDTAVYYCAGQVSRAYDSMWYGRD DYWGQGTQVTVSS	FLT3 antibody variable domain
1035	FLL75	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAK NTVNLVYLQMNDLRPEDTAVYYCAGQVARAYDSNWY SRGDYWGQGTQVTVSS	FLT3 antibody variable domain
1036	FLL83	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAE NTVYLEMNSLKPEDTAVYICAGQVSRAYDSNWYSRDD YWGQGTQVTVSS	FLT3 antibody variable domain
1037	FLL94	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPEKEREFVAAISWDGGRTHYADSVKGRFTISRDNAK NTVYLQMNSLKPEDTAIYYCAGQVARAYDTRWYSRGD YWGQGTQVTVSS	FLT3 antibody variable domain
1038	FLL99	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWDGGRTHYADFVKGRFTISRDNAK NTVYLQMNSLKPEDTAVYYCAAQVARAYDSRWYSGG DYWGQGTQVTVSS	FLT3 antibody variable domain
1039	FLL38	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAVSWSGGTTEIADSVKGRFTISRDNAK NTVYLQMSSLKPGDTAVYYCAGQVARAYDSRWYSRG DYWGQGTQVTVSS	FLT3 antibody variable domain
1040	FLL53	QVQLQESGGGLVQAGDSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAVSQSGGTTHYADSVKGRFTISRDNAK NTETLVYLQMNSLKPEDTAVYYCAGQVARAYDSSWY ARGDYWGQGTQVTVSS	FLT3 antibody variable domain
1041	FLL553	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGWFR QAPGKEREFVAAISWSGGTTHYADSVKGRFTISRDNAK NTVNLVYLQMNSLRPEDTAVYYCAGQVARAYDSNWY SRGDYWGQGTQVTVSS	FLT3 antibody variable domain
1042	FLL74	QVQLQESGGGLVQAGGSLRLSCRFSGRTFSGFGTGWFR QAPGKEREFVAAISWAGGRTHYEDSVKGRFTISRDNAK NTVYLQMNSLKPEDTAVYYCAVQVSRAYDGIWYSGG DYWGQGTQVTVSS	FLT3 antibody variable domain
1043	FLL102	QVQLQESGGGLVQAGGSLMVSCAASGGTWSSYATGW FRQVPGKERKLIAGISRSGGRTYYAESVKGRFTISRDNA KNTVYLQMNTLKPDDTAVYYCAAARYFTSSVVYTSGN DYDYWGQGTQVTVSS	FLT3 antibody variable domain
1044	FLL122	QVQLQESGGGLVQAGGSLMVSCAASGGTWSSYATGW FRQVPGKERELIAGISRSGGRTYYAESVKGRFTISRDNA KNTVYLQMNTLKPDDTAVYYCAAARYFTSSVVYTSGN DYDYWGQGTQVTVSS	FLT3 antibody variable domain
1045	FLL134	QVQLQESGGGLVQPGGSLRLSCAASGGTFSSYATGWFR QVPGKEREFIAGISRNSGRTYAESVKGRFTISRDNAKNT VYLQMNTLRPDDTAVYYCAAARYFTRDAIYTSGDDYD YWGQGTQVTASS	FLT3 antibody variable domain

1046	FLL153	QVQLQESGGGLVQVGGSLMVSCAASGGTFSSYATGWF RQVPGKEREFIAGVSRNSGRTYYAESVKGRFTISRDNAK NTVYLQMNTLKPDDTGVYYCAAARYFTRDAVYTSGD DYDYWGQGTQVTVSS	FLT3 antibody variable domain
1047	FLL41	QVQLQESGGGLVQLGDSLMVSCAASGGTFSSYATGWF RQVPGREREFIAGISRSGGRTYYAESVKGRFTISRDNAK NTVYLQMNTLKPDDTAVYYCAAARYFTTSVVYTSGDD YDYWGQGTQVTVSS	FLT3 antibody variable domain
1048	FLL67	QVQLQESGGGLVQLGDSLMVSCAASGGTFSSYATGWF RQVPGKEREFIAGISRSGGRTYYAESVKGRFTISRDNAK NTVYLQMNTLKPDDTAVYYCAAARYFTTSVVYTSGDD YDYWGQGTQVTVSS	FLT3 antibody variable domain
1049	FLL92	QVQLQESGGGLVQAGGSLMVSCAASGGTWSSYATGW FRQVPGKERELIAGISRSGGRTYYAESVKGRFTISRDNA KNTVYLQMNTLKSDDTAVYYCAAARYFTSSVVYTSGN DYDYWGQGTQVTVSS	FLT3 antibody variable domain
1050	FLL71	QVQLQESGGGLVQVGGSLMVSCAASGGTFSSYATGWF RQVPGKEREFIAGISRNSGRTYYAESVKGRFTISRDNAK NTVYLQMNTLKPDDTAVYYCAAARYFTRDAVYTSGD DYDYWGQGTQVTVSS	FLT3 antibody variable domain
1051	FLL8	QVQLQESGGGLVQVGGSLMVSCAASGGTFSSYATGWF RQVPGKEREFIAGISRNSGRTYYAESVKGRFTISRDNAK NTVYLQMNTLKPDDTAVYYCAAARYFTRDVVYTSGD DYDYWGQGTQVTVSS	FLT3 antibody variable domain
1052	FLL84	QVQLQESGGGLVQAGGSLMVSCAASGGTFSSYATGWF RQVPGKEREFIAGISRSGGRTYYAESVKGRFTISRDNAK NTVYLQMNTLKPDDTAVYYCAAARYFTTSVVYTSGDD YDYWGQGTQVTVSS	FLT3 antibody variable domain
1053	FLL107	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYAMGWF RQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDNA KNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTTTPVV KYWGQGTQVTVSS	FLT3 antibody variable domain
1054	FLL141	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYAMGWF RQAPGMEREFVAAISWSGYSTYYADSVKGRFTISRDDA KNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTTTPVV KYWGQGTQVTVSS	FLT3 antibody variable domain
1055	FLL34	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYALGWFR QAPGKEREFVAAISWSGGNTYYADSVKGRFTISRDDAK NTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTTTPVVK YWGQGTQVTVSS	FLT3 antibody variable domain
1056	FLL4	QVQLQESGGGLVQAGGSLRLSCAASERTFSSYTMGWF RQAPGKEREFVAAMSWSGGSTYYADSVKGRFTISRDN AKNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTTTPV VKYWGQGTQVTVSS	FLT3 antibody variable domain
1057	FLL61	QVQLQESGGGLVQAGGSLRLSCAASERTFSSYAMGWF RQAPGKEREFVAAISWSGGSTYYADSVKGRFTISRDNA KNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTTTPIV KYWGQGTQVTVSS	FLT3 antibody variable domain
1058	FLL78	QVQLQESGGGWVQAGGSLRLSCAASGRTFSSYAMGWF RQAPGKEREFVAAISWSGSSTYYADSVKGRFTISRDNA KNTVYLLMDSLKPEDTAVYYCAAGGSTRVVVTTTPVV KYWGQGTQVTVSS	FLT3 antibody variable domain

1059	FLL1	QVQLQESGGGLVQAGGSLRLSCAASGRTFSTLTVAWFR QAPGKEREFVVASIPSGSNTGYAESVKGRFTISRDIAKN TVYLQMNSLKPEDTAMYFCAARIYFGSSRGYDYWGQG TQVTVSS	FLT3 antibody variable domain
1060	FLL26	QVQLQESGGGLVQAGGSLRLSCAASGRTFTTYTVAWF RQAPGKEREFLVASIPTGSNTAYAESVKGRFTISRGNAK NTVYLQMNSLKPEDTAMYYCAARTYFGSSRGYDYWG QGTQVTVSS	FLT3 antibody variable domain
1061	FLL160	QVQLQESGGGLVQAGDSLRLSCATSGRTFNLYRVGWF RQAPGKEREFVARITWSADITQYADSVKGRFTISRDNA KNTVYLQMNSLKPEDTAIYYCATTLRKSSGIYHVDDYD DWGQGTQVTVSS	FLT3 antibody variable domain
1062	FLL173	QVQLQESGGGLVQAGGSLRLSCATSGRTFNLYRVGWF RQAPGKEREFVARITWSADITQYTDSVKGRFTISRDNAK NTVYLQMNSLKPEDTAIYYCATTLRKSSGIYHTDDYDY WGQGTQVTVSS	FLT3 antibody variable domain
1063	FLL178	QVQLQESGGGLVQPGGSLRLSCAASGFTFSDYAMSWV RQAPGKGLEWVSGISSGGYKIGYTDSTKGRFTISRDNAK NTLYLQMNSLTAEDTAVYYCAKGTQWSWSLRDNTSR GQGTQVTVSS	FLT3 antibody variable domain
1064	FLL27	QVQLQESGGGLVQPGGSLRLSCKASGFTFSSYAMSWVR QAPGKGLEWVSGISSGGYKIGYTDSTKGRFTISRDNAK NTLYLQMNSLNAEDTAVYYCAKGTQWSWALRDSTSR GQGTQVTVSS	FLT3 antibody variable domain
1065	FLL190	QVQLQESGGGLVQAGGSLTLSCTASGSTFSINHFSWYR QAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNDKNT AYLQMNGLKPEDTAVYYCYYRGFWGQGTQVTVSS	FLT3 antibody variable domain
1066	FLL43	QVQLQESGGGLVQPGGSLTLSCTASGSTFSINHFAWYR QAPGKQRELVAFISSDGRSTDVESVKGRFTISGDNDKNT AYLQMNGLKPEDTAVYYCYYRGSWGQGTQVTVSS	FLT3 antibody variable domain
1067	FLL15	QVQLQESGGGLVQAGGSLSLSCAASEGTISHAAMGWF RQAPGKERQFVAYDTWTGGSTNYADSVKDRFTITGDH AKNTVYLQMNSLKPEDTGVYYCAVRGRYSASYTYTNP ASYKYWGQGTQVTVSS	FLT3 antibody variable domain
1068	FLL45	QVQLQESGGGLVQAGGSLRLSCAASGGTFSSSAMGWF RQAPGKEREFVATITQNDVPTYYTHSVKGRFTISRDNA KNTMYLQMNSLKPEDTAVYYCAQRVAQASGWRTTIK DYGYWGQGTQVTVSS	FLT3 antibody variable domain
1069	FLL39	QVQLQESGGGLVQAGGSLRLSCAASGLTSSTYRMAWF RQAPGKEREFAAGISYSADSGGSTNYADSVKGRFTISRD NAKNTVYLQMSSLKPEDTAVYYCAAGRYSGTYNSPYS SSYVYWGQGTQVTVSS	FLT3 antibody variable domain
1070	FLL177	QVQLQESGGGLVQTGGSLRLSCAASGSTFSRNTMGWF RQAPGKERVFVLGISWSGIRSYYLDSAKARFTISRDNAK NTVYLQMNSLRPEDTAVYYCAAQEGSSPGPYKYWGQG TQVTVSS	FLT3 antibody variable domain
1071	FLL823	QVQLQESGGGVVQVGGSLRLSCAASGGTFGYYAVGWF RQAPGKEREFVAAVTWNGAYLYSDPVKGRFTISRDNA KNTVYLQMNSLKSEDTAVYYCGLDRWSAVVESTPSTR GQGTQVTVSS	FLT3 antibody variable domain

1072	FLL76	QVQLQESGGGLVQAGGSLRLSCAASGGAFSSYVMGWF RQAPGKEREFVAAVISWSGRITDYADSVKGRFSISRDNA KSTVYLQMNNLKPEDTAVYYCAAKTGMYIDLRTSTFD YWGQGTQVTVSS	FLT3 antibody variable domain
1073	FLL822	QVQLQESGGGSVQAGGSLRLSCTASGRTFTDYTMGWF RQAPGKEREFMLGISSNGYRRYYTGSMKDRFTISRDNV KKTVYLQMNDLKPEDTAVYYCAASEDHGAPRYDYWG QGTQVTVSS	FLT3 antibody variable domain
1074	FLH107	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFR QAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSK NTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVK YWGQGTLVTVSS	FLT3 antibody variable domain
1075	FLH141	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFR QAPGMEREFVAAISWSGYSTYYADSVKGRFTISRDNSK NTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVK YWGQGTLVTVSS	FLT3 antibody variable domain
1076	FLH19C	EVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQ APGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNTA YLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS	FLT3 antibody variable domain
1077	FLH34	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYALGWFR QAPGKEREFVAAISWSGGNTYYADSVKGRFTISRDNSK NTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVK YWGQGTLVTVSS	FLT3 antibody variable domain
1078	FLH4	EVQLLESGGGLVQPGGSLTLSCAASERTFSSYTMGWFR QAPGKEREFVAAMSWSGGSTYYADSVKGRFTISRDNSK NTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVK YWGQGTLVTVSS	FLT3 antibody variable domain
1079	FLH78	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFR QAPGKEREFVAAISWSGSSTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVKY WGQGTLVTVSS	FLT3 antibody variable domain
1080	FLL101	GVTFSINYID	CDR1
1081	FLL103	GPTFSINYID	CDR1
1082	FLL116	GVTFSINYID	CDR1
1083	FLL125	GSTFSRNYID	CDR1
1084	FLL129	GVTFSASYID	CDR1
1085	FLL137	GSTFNNYAMD	CDR1
1086	FLL14	GVTFSINYID	CDR1
1087	FLL146	GVTFSINYID	CDR1
1088	FLL158	GSTFGRNYID	CDR1
1089	FLL179	GVTFSINYID	CDR1
1090	FLL181	GVTFSASYID	CDR1
1091	FLL187	GVTFSINYID	CDR1
1092	FLL32	GVTFNINYID	CDR1
1093	FLL51	GFDFSISYID	CDR1
1094	FLL55	GSTFSRNYID	CDR1
1095	FLL77	GVTFSISYID	CDR1
1096	FLL97	GVTFSINYID	CDR1
1097	FLL21	GSTFSRNYID	CDR1

1098	FLL57	GSTFSKNYID	CDR1
1099	FLL62	GSTSSRNYID	CDR1
1100	FLL79	GSTFSRNYID	CDR1
1101	FLL86	GSTFSRNYID	CDR1
1102	FLL112	GRTFSGFGTG	CDR1
1103	FLL142	GRTFSGFGTG	CDR1
1104	FLL143	GRTFSGFGTG	CDR1
1105	FLL154	GRTFSGFGTG	CDR1
1106	FLL168	GRTFSGFGTG	CDR1
1107	FLL170	GRTFSGFGTG	CDR1
1108	FLL188	GRTFSGFGTG	CDR1
1109	FLL40	GRTFSGFGTG	CDR1
1110	FLL6	GRTFSGFGTG	CDR1
1111	FLL75	GRTFSGFGTG	CDR1
1112	FLL83	GRTFSGFGTG	CDR1
1113	FLL94	GRTFSGFGTG	CDR1
1114	FLL99	GRTFSGFGTG	CDR1
1115	FLL38	GRTFSGFGTG	CDR1
1116	FLL53	GRTFSGFGTG	CDR1
1117	FLL553	GRTFSGFGTG	CDR1
1118	FLL74	GRTFSGFGTG	CDR1
1119	FLL102	GGTWSSYATG	CDR1
1120	FLL122	GGTWSSYATG	CDR1
1121	FLL134	GGTFSSYATG	CDR1
1122	FLL153	GGTFSSYATG	CDR1
1123	FLL41	GGTFSSYATG	CDR1
1124	FLL67	GGTFSSYATG	CDR1
1125	FLL92	GGTWSSYATG	CDR1
1126	FLL71	GGTFSSYATG	CDR1
1127	FLL8	GGTFSSYATG	CDR1
1128	FLL84	GGTFSSYATG	CDR1
1129	FLL107	GRTFSSYAMG	CDR1
1130	FLL141	GRTFSSYAMG	CDR1
1131	FLL34	GRTFSSYALG	CDR1
1132	FLL4	ERTFSSYTMG	CDR1
1133	FLL61	ERTFSSYAMG	CDR1
1134	FLL78	GRTFSSYAMG	CDR1
1135	FLL1	GRTFSTLTVA	CDR1
1136	FLL26	GRTFTTYTVA	CDR1
1137	FLL160	GRTFNLYRVG	CDR1
1138	FLL173	GRTFNLYRVG	CDR1
1139	FLL178	GFTFSDYAMS	CDR1
1140	FLL27	GFTFSSYAMS	CDR1
1141	FLL190	GSTFSINHFS	CDR1
1142	FLL43	GSTFSINHFA	CDR1
1143	FLL15	EGTISHAAMG	CDR1
1144	FLL45	GGTFSSSAMG	CDR1
1145	FLL39	GLTSSTYRMA	CDR1

1146	FLL177	GSTFSRNTMG	CDR1
1147	FLL823	GGTFGYYAVG	CDR1
1148	FLL76	GGAFSSYVMG	CDR1
1149	FLL822	GRTFTDYTMG	CDR1
1150	FLH107	GRTFSSYAMG	CDR1
1151	FLH141	GRTFSSYAMG	CDR1
1152	FLH19C	GSTFSINHFS	CDR1
1153	FLH34	GRTFSSYALG	CDR1
1154	FLH4	ERTFSSYTMG	CDR1
1155	FLH78	GRTFSSYAMG	CDR1
1156	FLL101	QITRDSNSFYADSVKG	CDR2
1157	FLL103	QITRDSNSFYADSVKG	CDR2
1158	FLL116	QITRDSNSFYADSVKG	CDR2
1159	FLL125	QITSGGNTHYEPSLKG	CDR2
1160	FLL129	QITRGGDSFYADSVKG	CDR2
1161	FLL137	QITRDSSSFYADSVKG	CDR2
1162	FLL14	QITRDSNSFYADSVKG	CDR2
1163	FLL146	QITRDDTSFYADSVKG	CDR2
1164	FLL158	QITSGGNTHYEPSLKG	CDR2
1165	FLL179	QITRDGSSFYADSVKG	CDR2
1166	FLL181	QITRGGDSFYADSVKG	CDR2
1167	FLL187	QITRDSNSFYADSVKG	CDR2
1168	FLL32	QITRDSTRFYADSVKG	CDR2
1169	FLL51	QITRGGDSFYADSVKG	CDR2
1170	FLL55	QITSAGNTHYEPSLKG	CDR2
1171	FLL77	QITRGGDSFYADSVKG	CDR2
1172	FLL97	QITRDSNSFYADSVKG	CDR2
1173	FLL21	QITSGGNTHYEPSLKG	CDR2
1174	FLL57	QITSGGNTHYEPSLKG	CDR2
1175	FLL62	QITSGGNTHYEPSLKG	CDR2
1176	FLL79	QITSGGNTHYEPSLKG	CDR2
1177	FLL86	QITSGGNTHYEPSLKG	CDR2
1178	FLL112	AISWAGGRTHYEDSVKG	CDR2
1179	FLL142	AISWDGGRTHYADFVKG	CDR2
1180	FLL143	AISWVGGRTHYADSVKG	CDR2
1181	FLL154	AISWSGGRTHYADSVKG	CDR2
1182	FLL168	AISWDGGRTHYADSVKG	CDR2
1183	FLL170	AISWSGGTTHYADSVKG	CDR2
1184	FLL188	AISWDGGRTHYADSVKG	CDR2
1185	FLL40	AISWSGGTTHYADSVKG	CDR2
1186	FLL6	AISWDGGRTHYADSVKG	CDR2
1187	FLL75	AISWSGGTTHYADSVKG	CDR2
1188	FLL83	AISWSGGTTHYADSVKG	CDR2
1189	FLL94	AISWDGGRTHYADSVKG	CDR2
1190	FLL99	AISWDGGRTHYADFVKG	CDR2
1191	FLL38	AVSWSGGTTEIADSVKG	CDR2
1192	FLL53	AVSQSGGTTHYADSVKG	CDR2
1193	FLL553	AISWSGGTTHYADSVKG	CDR2

1194	FLL74	AISWAGGRTHYEDSVKG	CDR2
1195	FLL102	GISRSGGRTYYAESVKG	CDR2
1196	FLL122	GISRSGGRTYYAESVKG	CDR2
1197	FLL134	GISRNSGRTYAESVKG	CDR2
1198	FLL153	GVSRNSGRTYYAESVKG	CDR2
1199	FLL41	GISRSGGRTYYAESVKG	CDR2
1200	FLL67	GISRSGGRTYYAESVKG	CDR2
1201	FLL92	GISRSGGRTYYAESVKG	CDR2
1202	FLL71	GISRNSGRTYYAESVKG	CDR2
1203	FLL8	GISRNSGRTYYAESVKG	CDR2
1204	FLL84	GISRSGGRTYYAESVKG	CDR2
1205	FLL107	AISWSGSNTYYADSVKG	CDR2
1206	FLL141	AISWSGYSTYYADSVKG	CDR2
1207	FLL34	AISWSGGNTYYADSVKG	CDR2
1208	FLL4	AMSWSGGSTYYADSVKG	CDR2
1209	FLL61	AISWSGGSTYYADSVKG	CDR2
1210	FLL78	AISWSGSSTYYADSVKG	CDR2
1211	FLL1	ASIPSGSNTGYAESVKG	CDR2
1212	FLL26	ASIPTGSNTAYAESVKG	CDR2
1213	FLL160	RITWSADITQYADSVKG	CDR2
1214	FLL173	RITWSADITQYTDSVKG	CDR2
1215	FLL178	GISSGGYKIGYTDSTKG	CDR2
1216	FLL27	GISSGGYKIGYTDSTKG	CDR2
1217	FLL190	FISSDGVSIDVESVKG	CDR2
1218	FLL43	FISSDGRSTDVESVKG	CDR2
1219	FLL15	YDTWTGGSTNYADSVKD	CDR2
1220	FLL45	TITQNDVPTYYTHSVKG	CDR2
1221	FLL39	AGISYSADSGGSTNYADSVKG	CDR2
1222	FLL177	GISWSGIRSYYLDSAKA	CDR2
1223	FLL823	AVTWNGAYLYSDPVKG	CDR2
1224	FLL76	AVISWSGRITDYADSVKG	CDR2
1225	FLL822	GISSNGYRRYYTGSMKD	CDR2
1226	FLH107	ISWSGSNTYYADSVKG	CDR2
1227	FLH141	ISWSGYSTYYADSVKG	CDR2
1228	FLH19C	ISSDGVSIDVESVKG	CDR2
1229	FLH34	ISWSGGNTYYADSVKG	CDR2
1230	FLH4	MSWSGGSTYYADSVKG	CDR2
1231	FLH78	ISWSGSSTYYADSVKG	CDR2
1232	FLL101	LSY	CDR3
1233	FLL103	LSY	CDR3
1234	FLL116	LSY	CDR3
1235	FLL125	LDY	CDR3
1236	FLL129	LSY	CDR3
1237	FLL137	LSY	CDR3
1238	FLL14	LSY	CDR3
1239	FLL146	LSF	CDR3
1240	FLL158	LDY	CDR3
1241	FLL179	LSD	CDR3

1242	FLL181	LSY	CDR3
1243	FLL187	LSY	CDR3
1244	FLL32	LSY	CDR3
1245	FLL51	LSY	CDR3
1246	FLL55	LDY	CDR3
1247	FLL77	LSY	CDR3
1248	FLL97	LSY	CDR3
1249	FLL21	LDY	CDR3
1250	FLL57	LDY	CDR3
1251	FLL62	LDY	CDR3
1252	FLL79	LDY	CDR3
1253	FLL86	LDY	CDR3
1254	FLL112	AQVSRAYDGIWYSGGDY	CDR3
1255	FLL142	AQVARAYDSKWYSGGDY	CDR3
1256	FLL143	AQVARAYDGNWYSGGDY	CDR3
1257	FLL154	GQVARAYDGNWYSRGDY	CDR3
1258	FLL168	AQVSRAYDGRWYSAVDY	CDR3
1259	FLL170	GQVARAYDSSWYSRGDY	CDR3
1260	FLL188	AQVARAYDSRWYSGGDY	CDR3
1261	FLL40	GQVARAYDSSWYSRGDY	CDR3
1262	FLL6	GQVSRAYDSMWYGRDDY	CDR3
1263	FLL75	GQVARAYDSNWYSRGDY	CDR3
1264	FLL83	GQVSRAYDSNWYSRDDY	CDR3
1265	FLL94	GQVARAYDTRWYSRGDY	CDR3
1266	FLL99	AQVARAYDSRWYSGGDY	CDR3
1267	FLL38	GQVARAYDSRWYSRGDY	CDR3
1268	FLL53	GQVARAYDSSWYARGDY	CDR3
1269	FLL553	GQVARAYDSNWYSRGDY	CDR3
1270	FLL74	VQVSRAYDGIWYSGGDY	CDR3
1271	FLL102	ARYFTSSVVYTSGNDYDY	CDR3
1272	FLL122	ARYFTSSVVYTSGNDYDY	CDR3
1273	FLL134	ARYFTRDAIYTSGDDYDY	CDR3
1274	FLL153	ARYFTRDAVYTSGDDYDY	CDR3
1275	FLL41	ARYFTTSVVYTSGDDYDY	CDR3
1276	FLL67	ARYFTTSVVYTSGDDYDY	CDR3
1277	FLL92	ARYFTSSVVYTSGNDYDY	CDR3
1278	FLL71	ARYFTRDAVYTSGDDYDY	CDR3
1279	FLL8	ARYFTRDVVYTSGDDYDY	CDR3
1280	FLL84	ARYFTTSVVYTSGDDYDY	CDR3
1281	FLL107	AGGSTRVVVTTTPVVKY	CDR3
1282	FLL141	AGGSTRVVVTTTPVVKY	CDR3
1283	FLL34	AGGSTRVVVTTTPVVKY	CDR3
1284	FLL4	AGGSTRVVVTTTPVVKY	CDR3
1285	FLL61	AGGSTRVVVTTTPIVKY	CDR3
1286	FLL78	AGGSTRVVVTTTPVVKY	CDR3
1287	FLL1	RIYFGSSRGYDY	CDR3
1288	FLL26	RTYFGSSRGYDY	CDR3
1289	FLL160	TLRKSSGIYHVDDYDD	CDR3

1290	FLL173	TLRKSSGIYHTDDYDY	CDR3
1291	FLL178	GTQWSWSLRDNTS	CDR3
1292	FLL27	GTQWSWALRDSTS	CDR3
1293	FLL190	RGF	CDR3
1294	FLL43	RGS	CDR3
1295	FLL15	RGRYSASYTYTNPASYKY	CDR3
1296	FLL45	RVAQASGWRTTIKDYGY	CDR3
1297	FLL39	GRYSGTYNSPYSSSYVY	CDR3
1298	FLL177	AQEGSSPGPYKY	CDR3
1299	FLL823	DRWSAVVESTPST	CDR3
1300	FLL76	AKTGMYIDLRTSTFDY	CDR3
1301	FLL822	SEDHGAPRYDY	CDR3
1302	FLH107	GGSTRVVVTTTPVVKY	CDR3
1303	FLH141	GGSTRVVVTTTPVVKY	CDR3
1304	FLH19C	RGF	CDR3
1305	FLH34	GGSTRVVVTTTPVVKY	CDR3
1306	FLH4	GGSTRVVVTTTPVVKY	CDR3
1307	FLH78	GGSTRVVVTTTPVVKY	CDR3
3495	FLH92a	EVQLLESGGGLVQPGGSLTLSCAASGGTWSSYATGWFR QAPGKERELIAGISRSGGRTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAAARYFTSSVVYTSGNDY DYWGQGTLVTVSS	FLT3 antibody variable domain
3496	FLH92b	EVQLLESGGGLVQPGGSLTLSCAASGGTWSSYATGWFR QAPGKERELIAGISRSGGRTYYADSVKGRFTISRDNSKN TVYLQMNSLRAEDTAVYYCAKARYFTSSVVYTSGNDY DYWGQGTLVTVSS	FLT3 antibody variable domain
3497	FLH92a	GGTWSSYATG	CDR1
3498	FLH92b	GGTWSSYATG	CDR1
3499	FLH92a	GISRSGGRTYYADSVKG	CDR2
3500	FLH92b	GISRSGGRTYYADSVKG	CDR2
3501	FLH92a	ARYFTSSVVYTSGNDYDY	CDR3
3502	FLH92b	ARYFTSSVVYTSGNDYDY	CDR3

Table 16. DLL3 binding protein sequences

SEQ. ID NO.	Name	Sequence	
1308	DL1	QVQLQESGGGLVQAGGSLRLSCAASGSIFSIASMGWYRQAPG KQRELVAVITSFSSTNYADSVKGRFTISRDNAKNTVYLQMNSL KPEDTGVYYCNARYFERTDWGQGTQVTVSS	
1309	DL74	QVQLQESGGGLVQAGGSLRLSCAAPGSIFSIASMGWYRQAPG KQRELVAVITSFSSTNYADSVKGRFTISRDNAKNTVYLQMNSL KPEDTGVYYCNARYFERTDWGQGTQVTVSS	
1310	DL31	QVQLQESGGGLVQAGGSLRLSCAASGSIFSIASMAWYRQAPG KQRELVAAITSFSSTNYADSVKGRFTISRDNAKNTVYLQMNSL KPEDTGVYYCNARYFERTDWGQGTQVTVSS	

1311	DL3	QVQLQESGGGLVQAGGSLRLSCAASESIFSINVMAWHRQAPG KQRELVARITSGGSTNYADSVKGRFTISRDNAKNTVYLQMNSL KPEDTGVYYCGAYQGLYAYWGQGTQVTVSS	
1312	DL80	QVQLQESGGGLVQAGGSLRLSCVASGSSFSITSMAWYRQAPG KQRDLVAAITSFGSTNYADSVKDRFTISRDNAKNTVYLQMNSL KPEDTAVYYCNGRVFDHVYWGQGTQVTVSS	
1313	DL18	QVQLQESGGGLVQAGGSLKLSCAASSSIFSISSMSWYRQAPGK QRELVAAITTFDYTNYADSVKGRFTISRDNAKNMMYLQMNSL KPEDTAVYLCNARAFGRDYWGQGTQVTVSS	
1314	DL94	QVQLQESGGGLVQAGGSLKLSCAASSSIFSISSMSWYRQAPGK QRELVAAITSFGSTNYADSVKGRFTISRDNAKNMMYLQMNSL KPEDTAVYRCNARTMGRDYWGQGTQVTVSS	
1315	DL17	QVQLQESGGGLVQPGGSLRLSCAASGSTLNIKIMAWHRQAPG KQRELVATLTSGGNTNYADSVKGRFTISRDNAKNTVYLQMNS LQPEDTAVYYCGLWDGVGGAYWGRGTQVTVSS	
1316	DL46	QVQLQESGGGLVQPGGSLRISCAASGSTLNIKIMAWHRQAPGK QRELVATLTSGGNTNYADSVKGRFTISRDNAKNTVYLQMNSL QPEDTAVYYCGLWDGVGGAYWGRGTQVTVSS	
1317	DL15	QVQLQESGGGLVQAGGSLRLSCAASGSTFNIKTMAWHRQAPG NQRELVATLTSGGNTNYADSVKGRFTISRDNAKNTVYLQMNS LKPEDTAVYYCGLWNGVGGAYWGRGTQVTVSS	
1318	DL26	QVQLQDGGGLVQPGGSLRLSCAASGSTFNIKLMAWHRQAPGN QRELVATLTSGGNTNYADSVKGRFTISRDNASNIVYLQMNSLK PEDTAVYYCGLWDGVGGAYWGRGTQVTVSS	
1319	DL83	QVQLQESGGGLVQAGGSLRLSCAASGSTFNFKIMAWHRQAPG KQRELVASLTSEGLTNYRDSVKGRFTISRDNAKNTVYLQMNN LKPEDTAVYYCGLWDGVGGAYWGRGTQVTVSS	
1320	DL5	QVQLQESGGGLVQPGGSLRLSCAASGFMFSSYSMSWYRQAPG KQRELVAAITTWGSTNYADSVKGRFTISRDNAKNTVWLQMNS LEPEDTAVYFCNARSWNNYWGQGTQVTVSS	
1321	DL22	QVQLQESGGGLVQVGGSLRLSCAASGFMFSSYSMSWYRQAPG KQRELVAAITSYGSTNYADSVKGRFTISRDNAKNTVWLQMNS LKPEDTAVYFCNARSWNNYWGQGTQVTVSS	
1322	DL85	QVQLQESGGGLVQPGGSLRLSCAASGFTFSSHSMSWYRQAPG KQRELVAAITTYGSTNYIDSVKGRFTISRDNTKNTVYLQMNSL KPEDTAVYFCNARSWNNYWGQGTQVTVSS	
1323	DL69	QVQLQESGGGLVQAGGSLRLSCVASGSSFSHNTMGWYRQAP GKQRDLVARITTFGTTNYADSVKGRFTISRDNAKNTVYLQMN SLKPEDTAVYYCNGESFGRIWYNWGQGTQVTVSS	
1324	DL27	QVQLQESGGGLVQAGASLRLTCTASGGRFSYATMGWSRQAP GKQREMVARITSSGFSTNYADSVKGRFTISRDNAKNAVYLQM DSLKPEDTAVYYCNAQHFGTDSWGQGTQVTVSS	
1325	DL51	QVQLQESGGGLVQAGASLRLTCTASGSRFSYATMGWSRQAPG KQRELVARITSSGFSTNYADSVKGRFTISRDNAKNAVYLQMDS LKPEDTAVYYCNAQQFGTDSWGQGTQVTVSS	
1326	DL54	QVQLQESGGGLVQAGGSLRLSCAASGSTFTSNVMGWHRQAP GKQRELVANMHSGGSTNYADSVKGRFTISRDNAKNIVYLQMN NLKIEDTAVYYCRWYGIQRAEGYWGQGTQVTVSS	

1327	DL11	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTVSRDNAKNTVYLQMNS LQPEDTAVYYCYAYRWVGRDTYWGQGTQVTVSS	
1328	DL19	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTISRDNAKNTVYLQMNS LQPEDTAVYYCYAYRWVGRDTYWGQGTQVTVSS	
1329	DL68	QVQLQESGGGLVVSGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTISRDNAKNTVYLQMNS LQPEDTAAYYCYAYRWVGRDTYWGQGTQVTVSS	
1330	DL14	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTISRDNAENTVYLQMNS LQPEDTAVYYCYAYRWEGRDTYWGQGTQVTVSS	
1331	DL67	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTISRDNAENTVYLQMNS LQPEDTAVYYCYAYRWEGRNTYWGQGTQVTVSS	
1332	DL56	QVQLQESGGGLVQPGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGSTNYVDSVKGRFTISRDNAKNTVYLQMNS LQPEDTAVYYCYAYRWVGRYTYWGQGTQVTVSS	
1333	DL13	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGTTNYVDSVKDRFTISRDNAKNTVYLQMNS LQPEDTAAYYCYAYRWVGRDTYWGQGTQVTVSS	
1334	DL77	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSIAWYRQAPG KKRELVAGISTDGTTNYVDSVKDRFTISRDNAKNTVYLQMNS LQPEDTAAYYCYAYRWVGRDTYWGQGTQVTVSS	
1335	DL79	QVQLQESGGGLVQAGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGTTNYVDSVKDRFTISRDNAKNTVYLQMNS LQPEDTAAYYCYAYRWVGRDTYWGQGTQVTVSS	
1336	DL20	QVQLQESGGGLVQAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGSTNYADSVKGRFTISEGNAKNTVDLQMNSL QPEDTAVYYCYAYRWVDRYTYWGQGTQVTVSS	
1337	DL41	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGSTNYADSVKGRFTISEDNAKNTVDLQMNSL QPEDTAVYYCYAYRWIDRYTYWGQGTQVTVSS	
1338	DL59	QVQLQESGGGLVQPGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGSTNYADSVKGRFTISEDNAKNTVDLQMNSL QPEDTAVYYCYAYRWVDRYTYWGQGTQVTVSS	
1339	DL16	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISSDGSTNYVDSVKGRFTISRDNAKNIVFLQMNSL QPQDTAVYYCYAYRWVGRDTYWGQGTQVTVSS	
1340	DL6	QVQLQESGGGLVVAGGSLRLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDSANNTMYLQMNSL QPEDTAVYYCYAYRWTTRYTYWGQGTQVTVSS	
1341	DL84	QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWYRQAPG KKRELVAGISSDGSTHYVDSVKGRFAISRDNAENTVYLQMND LQPDDTAVYYCYAYRWVGGYTYWGQGTQVTVSS	
1342	DL2	QVQLQESGGGLVQAGGSLRLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKNYADSVKGRFTISRDNAKNTVYLQMNS LKPEDTAVYYCYYFRTVAASSMQYWGQGTQVTVSS	

1343	DL43	QVQLQESGGGLVQAGGSLRLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNTVYLQMNS LKPEDTAVFYCYYFRTVSGSSMRYWGQGTQVTVSS	
1344	DL92	QVQLQESGGGLVQAGGSLRLSCAASGITSSVYSMGWYRQAPG KQRELVAGSSSDGSTHYVDSVRGRFTISRDNAKNTVYLQMSSL KPEDTAVYYCYANRGFAGAPSYWGQGTQVTVSS	
1345	DL10	QVQLQESGGGLVQAGGSLRLSCAASGRTSMFNSMGWHRQAP GKQRELVAIIRSGGSSNYADTVKGRFTISRDNTKNTVYLQMND LKPEDTAVYYCFYYFQSSYWGQGTQVTVSS	
1346	DL82	QVQLQESGGGLVQAGGSLRLSCAASGRTSMVNSMGWHRQAP GKQRELVALITSGGSSNYADTVKGRFTISRDNTKNTVYLQMN DLKPEDTAVYYCFYYFQSSYWGQGTQVTVSS	
1347	DL23	QVQLQESGGGLVQAGGSLRLSCAASGSVSMFNSMGWHRQPP GKQRELVAIITSGGSSNYADTVKGRFTISRDNTKNTVYLQMND LKPEDTAVYYCFYYFQSSYWGQGTQVTVSS	
1348	DL42	QVQLQESGGGLVQAGGSLRLSCTASGSIFSIAVMGWYRQVPG KRREWVATIFDGSYTNYADSVKGRFTISRDNARNKVYLQMNN LKPEDTAVYYCQTHWTQGSVPKESWGQGTQVTVSS	
1349	DL45	QVQLQESGGGLVQAGGSLRLSCVASSGIFSDMSMVWYRQAPG KQRELVASITTFGSTNYADPVKGRFTISRDNAKNTVYLQMNSL KPEDTAVYYCSGRSYSSDYWGRGTQVTVSS	
1350	DL58	QVQLQESGGGLVQAGGSLRLSCVASGSISSIIVMGWSRQAPGK QRESVATITRDGTRNYADSLKGRFTISRDNAKNTSYLQINSLKP EDTAVYSCYARYGDINYWGKGTQVTVSS	
1351	DL70	QVQLQESGGGLVQAGGSLRLSCVASGSISSIIVMGWSRQAPGK QRESLATISRGGTRTYADSVKGRFTISRDNAKNTSYLQMNSLK PEDTAVYSCYARYGDINYWGKGTQVTVSS	
1352	DL89	QVQLQESGGGLVQAGGSLRLSCVASGSIFTTNSMGWHRQGPG KQRELVALIGSAGSTKYADSVKGRFTISRDNAKNTVSLQMDSL KPEDTAVYYCFYYDSRSYWGQGTQVTVSS	
1353	DL38	QVQLQESGGGMVQPGGSLRLSCAASGSREISTMGWHRQAPGK QRELAARITSGGITKYADSVKGRFTISRDNAKKTVYLQMNSLK SEDTAVYYCFAYDNINAYWGQGTQVTVSS	
1354	DL52	QVQLQESGGGWVQAGGSLRLSCAASGSREISTMGWHRQAPG KQRELAARITSGGITKYADSVKGRFTISRDNAKKTVYLQMNSL KSEDTAVYYCFAYDNINAYWGQGTQVTVSS	
1355	DL64	QVQLQESGGGWVQAGGSLRLSCTASGSREISTMGWHRQAPG KQRELAARITSGGITKYADSVKGRFTISRDNAKKTVYLQMDSL KSEDTAVYYCFAYDNINAYWGQGTQVTVSS	
1356	DL33	QVQLQESGGGSVQAGRSLGLSCAASGSREISTMGWHRQAPGK QRELAARITSGGITKYADSVKGRFTISRDNAKKTVYLQMNSLK SEDTAVYYCFAYDNINAYWGQGTQVTVSS	
1357	DL12	QVQLQESGGGLVQAGGSLRLSCTASGSIFRGAAMYWHRQAPG KQRELVAAITTSGNTSYADSVKGRFTISRDNAKNTMYLQIISLK PEDTAVYYCAFWIAGKAYWGQGTQVTVSS	
1358	DL29	QVQLQESGGGLVQPGGSLRLSCAASGSISSFNFMSWHRQAPGK ERELAGVITRGGATNYADSVKGRFTISRDNVKNTVYLQMNGL KPEDTAVYYCHGRSQLGSTWGQGTQVTVSS	

1359	DL61	QVQLQESGGGLVQAGGSLRLSCLASGTIFTASTMGWHRQPPG KQRELVASIAGDGRTNYAESTEGRFTISRDDAKNTMYLQMNS LKPEDTAVYYCYAYYLDTYAYWGQGTQVTVSS	
1360	DH1	EVQLVESGGGLVQPGGSLTLSCAASGSIFSIASMGWYRQAPGK QRELVAVITSFSSTNYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCNARYFERTDWGQGTLVTVSS	
1361	DH10	EVQLVESGGGLVQPGGSLTLSCAASGRTSMFNSMGWHRQAPG KQRELVAIIRSGGSSNYADTVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCFYYFQSSYWGQGTLVTVSS	
1362	DH11	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWVGRDTYWGQGTLVTVSS	
1363	DH12	EVQLVESGGGLVQPGGSLTLSCTASGSIFRGAAMYWHRQAPG KQRELVAAITTSGNTSYADSVKGRFTISRDNAKNSMYLQMNS LRAEDTAVYYCAFWIAGKAYWGQGTLVTVSS	
1364	DH15	EVQLVESGGGLVQPGGSLTLSCAASGSTFNIKTMAWHRQAPG NQRELVATLTSGGNTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCGLWNGVGGAYWGQGTLVTVSS	
1365	DH17	EVQLVESGGGLVQPGGSLTLSCAASGSTLNIKIMAWHRQAPG KQRELVATLTSGGNTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCGLWDGVGGAYWGQGTLVTVSS	
1366	DH18	EVQLVESGGGLVQPGGSLTLSCAASSSIFSISSMSWYRQAPGKQ RELVAAITTFDYTNYADSVKGRFTISRDNAKNSMYLQMNSLR AEDTAVYYCNARAFGRDYWGQGTLVTVSS	
1367	DH2	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVAASSMQYWGQGTLVTVSS	
1368	DH22	EVQLVESGGGLVQPGGSLTLSCAASGFMFSSYSMSWYRQAPG KQRELVAAITSYGSTNYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCNARSWNNYWGQGTLVTVSS	
1369	DH23	EVQLVESGGGLVQPGGSLTLSCAASGSVSMFNSMGWHRQPPG KQRELVAIITSGGSSNYADTVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCFYYFQSSYWGQGTLVTVSS	
1370	DH27	EVQLVESGGGLVQPGGSLTLSCTASGGRFSYATMGWSRQAPG KQREMVARITSSGFSTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCNAQHFGTDSWGQGTLVTVSS	
1371	DH29	EVQLVESGGGLVQPGGSLTLSCAASGSISSFNFMSWHRQAPGK ERELAGVITRGGATNYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCHGRSQLGSTWGQGTLVTVSS	
1372	DH3	EVQLVESGGGLVQPGGSLTLSCAASESIFSINVMAWHRQAPGK QRELVARITSGGSTNYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCGAYQGLYAYWGQGTLVTVSS	
1373	DH38	EVQLVESGGGLVQPGGSLTLSCAASGSREISTMGWHRQAPGK QRELAARITSGGITKYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCFAYDNINAYWGQGTLVTVSS	
1374	DH42	EVQLVESGGGLVQPGGSLTLSCTASGSIFSIAVMGWYRQVPGK RREWVATIFDGSYTNYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCQTHWTQGSVPKESWGQGTLVTVSS	

1375	DH43	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1376	DH45	EVQLVESGGGLVQPGGSLTLSCVASSGIFSDMSMVWYRQAPG KQRELVASITTFGSTNYADPVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCSGRSYSSDYWGQGTLVTVSS	
1377	DH5	EVQLVESGGGLVQPGGSLTLSCAASGFMFSSYSMSWYRQAPG KQRELVAAITTWGSTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCNARSWNNYWGQGTLVTVSS	
1378	DH51	EVQLVESGGGLVQPGGSLTLSCTASGSRFSYATMGWSRQAPG KQRELVARITSSGFSTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCNAQQFGTDSWGQGTLVTVSS	
1379	DH54	EVQLVESGGGLVQPGGSLTLSCAASGSTFTSNVMGWHRQAPG KQRELVANMHSGGSTNYADSVKGRFTISRDNAKNSVYLQMN SLRAEDTAVYYCRWYGIQRAEGYWGQGTLVTVSS	
1380	DH56	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGSTNYVDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWVGRYTYWGQGTLVTVSS	
1381	DH58	EVQLVESGGGLVQPGGSLTLSCVASGSISSIIVMGWSRQAPGK QRESVATITRDGTRNYADSLKGRFTISRDNAKNSSYLQMNSLR AEDTAVYYCYARYGDINYWGQGTLVTVSS	
1382	DH6	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1383	DH61	EVQLVESGGGLVQPGGSLTLSCLASGTIFTASTMGWHRQPPGK QRELVASIAGDGRTNYAESTEGRFTISRDNAKNSMYLQMNSLR AEDTAVYYCYAYYLDTYAYWGQGTLVTVSS	
1384	DH67	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTNYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWEGRNTYWGQGTLVTVSS	
1385	DH69	EVQLVESGGGLVQPGGSLTLSCVASGSSFSHNTMGWYRQAPG KQRDLVARITTFGTTNYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCNGESFGRIWYNWGQGTLVTVSS	
1386	DH70	EVQLVESGGGLVQPGGSLTLSCVASGSISSIIVMGWSRQAPGK QRESLATISRGGTRTYADSVKGRFTISRDNAKNSSYLQMNSLR AEDTAVYYCYARYGDINYWGQGTLVTVSS	
1387	DH80	EVQLVESGGGLVQPGGSLTLSCVASGSSFSITSMAWYRQAPGK QRDLVAAITSFGSTNYADSVKDRFTISRDNAKNSVYLQMNSLR AEDTAVYYCNGRVFDHVYWGQGTLVTVSS	
1388	DH82	EVQLVESGGGLVQPGGSLTLSCAASGRTSMVNSMGWHRQAP GKQRELVALITSGGSSNYADTVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCFYYFQSSYWGQGTLVTVSS	
1389	DH83	EVQLVESGGGLVQPGGSLTLSCAASGSTFNFKIMAWHRQAPG KQRELVASLTSEGLTNYRDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCGLWDGVGGAYWGQGTLVTVSS	
1390	DH84	EVQLVESGGGLVQPGGSLTLSCAASGFTLDYYAIGWYRQAPG KKRELVAGISSDGSTHYVDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWVGGYTYWGQGTLVTVSS	

1391	DH89	EVQLVESGGGLVQPGGSLTLSCVASGSIFTTNSMGWHRQGPG KQRELVALIGSAGSTKYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCFYYDSRSYWGQGTLVTVSS	
1392	DH92	EVQLVESGGGLVQPGGSLTLSCAASGITSSVYSMGWYRQAPG KQRELVAGSSSDGSTHYVDSVRGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYANRGFAGAPSYWGQGTLVTVSS	
1393	DH94	EVQLVESGGGLVQPGGSLTLSCAASSSIFSISSMSWYRQAPGKQ RELVAAITSFGSTNYADSVKGRFTISRDNAKNSMYLQMNSLRA EDTAVYYCNARTMGRDYWGQGTLVTVSS	
1394	1A01	EVQLVESGGGLVQPGGSLTLSCVASGFTSSINAMGWYRRAPG KQRELVAGISSDGSFVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRHVSGSSMRYWGQGTLVTVSS	
1395	1A03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSSRYWGQGTLVTVSS	
1396	1A04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYEDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1397	1A05	EVQLVESGGGLVQPGGSLTLSCVASGSPSSINAMGWYRRAPG KQRELSAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVRGSSMSYWGQGTLVTVSS	
1398	1A06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELAAGISSDGSSVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSKRYWGQGTLVTVSS	
1399	1A07	EVQLVESGGGLVQPGGSLTLSCVASGSISSINAMGWYRRAPGK QRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRMVSGSSMRYWGQGTLVTVSS	
1400	1A09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKLYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVQGSSMRYWGQGTLVTVSS	
1401	1A010	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAYGWYRRAPGK QRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVYGSSMRYWGQGTLVTVSS	
1402	1A011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGSSYRYWGQGTLVTVSS	
1403	1A012	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVLGSSMRYWGQGTLVTVSS	
1404	1B01	EVQLVESGGGLVQPGGSLTLSCVASGSTSIINAMGWYRRAPGK QRELAAGISSDGSKVIADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRRVSGSSMRYWGQGTLVTVSS	
1405	1B02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKIYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1406	1B03	EVQLVESGGGLVQPGGSLTLSCVASGKTSSINAMAWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSARYWGQGTLVTVSS	

1407	1B04	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSLVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRIVRGSSMRYWGQGTLVTVSS	
1408	1B05	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYYRTVSGSSMRYWGQGTLVTVSS	
1409	1B07	EVQLVESGGGLVQPGGSLTLSCVASGSGSSINAMGWYRRAPG KQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRHVSGSSMRYWGQGTLVTVSS	
1410	1B08	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRFVSGSSMRYWGQGTLVTVSS	
1411	1B09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1412	1B010	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTKSGSSMRYWGQGTLVTVSS	
1413	1B011	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVYGSSMRYWGQGTLVTVSS	
1414	1C01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYRDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMGYWGQGTLVTVSS	
1415	1C02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRSWGQGTLVTVSS	
1416	1C03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDNSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVGGSSMRYWGQGTLVTVSS	
1417	1C04	EVQLVESGGGLVQPGGSLTLSCVASGNTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1418	1C05	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSHMRYWGQGTLVTVSS	
1419	1C06	EVQLVESGGGLVQPGGSLTLSCVASGSTSIINAMGWYRRAPGK QRELVAGISSDGSKVYEDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRAVSGSSMRYWGQGTLVTVSS	
1420	1C07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1421	1C08	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELPAGISSDGSKVYAVSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSPMRYWGQGTLVTVSS	
1422	1C010	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGVSSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMSYWGQGTLVTVSS	

1423	1C011	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVYEDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1424	1C012	EVQLVESGGGLVQPGGSLTLSCVASGITSSINAMGWYRRAPGK QRELVAGISSDGSKVYAGSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVRGSSMRYWGQGTLVTVSS	
1425	1D01	EVQLVESGGGLVQPGGSLTLSCVASGSTSDINAMGWYRRAPG KQRELVAGISSDKSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVRGSSMRYWGQGTLVTVSS	
1426	1D02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSNGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRQVSGSSMRYWGQGTLVTVSS	
1427	1D03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVLADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRIVSGSSMGYWGQGTLVTVSS	
1428	1D04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSKNAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGASMRYWGQGTLVTVSS	
1429	1D06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDNSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVHGSSMRYWGQGTLVTVSS	
1430	1D08	EVQLVESGGGLVQPGGSLTLSCVASGLTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRMVSGSSMRYWGQGTLVTVSS	
1431	1D09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTISGSSMRYWGQGTLVTVSS	
1432	1D010	EVQLVESGGGLVQPGGSLTLSCVASGSTSSNNAMAWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTRSGSSMRYWGQGTLVTVSS	
1433	1D011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDNSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGHSMRYWGQGTLVTVSS	
1434	1D012	EVQLVESGGGLVQPGGSLTLSCVASGSTSHINAMGWYRRAPG KQRELVAGISSDGSRVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGGSMRYWGQGTLVTVSS	
1435	1E02	EVQLVESGGGLVQPGGSLTLSCVASGQTSSINAMGWYRRAPG KQRELVAGISSDGSQVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTKSGSSMRYWGQGTLVTVSS	
1436	1E04	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINGMGWYRRAPG KQRELPAGISSDGSKAYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTASGTSMRYWGQGTLVTVSS	
1437	1E05	EVQLVESGGGLVQPGGSLTLSCVASGSTSVINAMAWYRRAPG KQRELAAGISSDGSKVYAKSAKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFNTVSGSSMRYWGQGTLVTVSS	
1438	1E07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYNDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVRGSSQRYWGQGTLVTVSS	

1439	1E08	EVQLVESGGGLVQPGGSLTLSCVASGKTSSINAMGWYRRAPG KQRELVAGISSDGSKVIADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVLGSSMRYWGQGTLVTVSS	
1440	1E09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTRSGSSMRYWGQGTLVTVSS	
1441	1E010	EVQLVESGGGLVQPGGSLTLSCVASGSVSSINAMGWYRRAPG KQRELVAGISSDGSKVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGLSMRYWGQGTLVTVSS	
1442	1E011	EVQLVESGGGLVQPGGSLTLSCVASGNTSSINAMGWYRRAPG KQRELVAGISSDGSKVYYDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVRGSSQRYWGQGTLVTVSS	
1443	1E012	EVQLVESGGGLVQPGGSLTLSCVASGSTSSTNAMGWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMVYWGQGTLVTVSS	
1444	1F01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYGDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSRSSMRYWGQGTLVTVSS	
1445	1F02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELAAGISSDQSKVYADSAKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMSYWGQGTLVTVSS	
1446	1F04	EVQLVESGGGLVQPGGSLTLSCVASGGTSSINAMGWYRRAPG KQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSARYWGQGTLVTVSS	
1447	1F05	EVQLVESGGGLVQPGGSLTLSCVASGSTRSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFHTVSGSSMRYWGQGTLVTVSS	
1448	1F06	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVIADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVLGSSMRYWGQGTLVTVSS	
1449	1F07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVDADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1450	1F08	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYKDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRNVSGSSMRYWGQGTLVTVSS	
1451	1F09	EVQLVESGGGLVQPGGSLTLSCVASGNTSSINAMGWYRRAPG KQRELVAGISSNGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVTGSSMRYWGQGTLVTVSS	
1452	1F010	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGISSDGSKVYKDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1453	1F011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVKGSSMRYWGQGTLVTVSS	
1454	1F012	EVQLVESGGGLVQPGGSLTLSCVASGLTSSINAMGWYRRAPG KQRELVAGISSDGSKVYQDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTNSGSSMRYWGQGTLVTVSS	

1455	1G01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYAESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGASMRYWGQGTLVTVSS	
1456	1G04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSTNAMGWYRRAPG KQRELVAGISSDGSKVLADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVNLSSMRYWGQGTLVTVSS	
1457	1G05	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKYYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVTGSSMRYWGQGTLVTVSS	
1458	1G06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVYAVSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRKVSGSSARYWGQGTLVTVSS	
1459	1G07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVVADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTYSGSSMRYWGQGTLVTVSS	
1460	1G09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSKSSMRYWGQGTLVTVSS	
1461	1G011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFKTVSGSSMRYWGQGTLVTVSS	
1462	1H01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELAAGISSDNSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTRSGSSMRYWGQGTLVTVSS	
1463	1H02	EVQLVESGGGLVQPGGSLTLSCVASGSKSSINAMGWYRRAPG KQRELAAGISSDGSKVYAQSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTSSGSSMRYWGQGTLVTVSS	
1464	1H06	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRFLSGSSMRYWGQGTLVTVSS	
1465	1H07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAFGWYRRAPGK QRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1466	1H08	EVQLVESGGGLVQPGGSLTLSCVASGSTFSINAMGWYRRAPG KQRELVAGISSDGSKVLADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRLVSGSSMRYWGQGTLVTVSS	
1467	1H010	EVQLVESGGGLVQPGGSLTLSCVASGSTRSINAMGWYRRAPG KQRELVAGISSDGSKVYNDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMRFWGQGTLVTVSS	
1468	1H011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVYNDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTQSGSSMRYWGQGTLVTVSS	
1469	1H012	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMPYWGQGTLVTVSS	
1470	2A01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVVADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTLSGSSMRYWGQGTLVTVSS	

1471	2A03	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVYGDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSAMRYWGQGTLVTVSS	
1472	2A04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTTSGSSMRYWGQGTLVTVSS	
1473	2A05	EVQLVESGGGLVQPGGSLTLSCVASGRTSSINAMGWYRRAPG KQRELVAGISSDGSKVYNDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGTSMRYWGQGTLVTVSS	
1474	2A06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSRNAMGWYRRAPG KQRELVAGISSDGSKVTADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTRSGSSMRYWGQGTLVTVSS	
1475	2A08	EVQLVESGGGLVQPGGSLTLSCVASGSTKSINAMGWYRRAPG KQRELVAGISSDGSKVYRDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTSSGSSMRYWGQGTLVTVSS	
1476	2A09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSRNAMGWYRRAPG KQRELVAGISSNGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMSYWGQGTLVTVSS	
1477	2A011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRPVSGSSMRYWGQGTLVTVSS	
1478	2B01	EVQLVESGGGLVQPGGSLTLSCVASGSTSLINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRHVSGSSMRYWGQGTLVTVSS	
1479	2B02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTKSGSSMRYWGQGTLVTVSS	
1480	2B03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSLVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFTTVSGSSMRYWGQGTLVTVSS	
1481	2B05	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGTKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFHTVSGSSMRYWGQGTLVTVSS	
1482	2B07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAFGWYRRAPGK QRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVRGSSMRYWGQGTLVTVSS	
1483	2B010	EVQLVESGGGLVQPGGSLTLSCVASGSTSSRNAMGWYRRAPG KQRELVAGISSDGSKLYLDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVLGSSMRYWGQGTLVTVSS	
1484	2B011	EVQLVESGGGLVQPGGSLTLSCVASGNTSSINAMGWYRRAPG KQRELVAGISSDGSRVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRSWGQGTLVTVSS	
1485	2B012	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVYNDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVRGSSMRYWGQGTLVTVSS	
1486	2C01	EVQLVESGGGLVQPGGSLTLSCVASGSTASINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRYVSGSSMRYWGQGTLVTVSS	

1487	2C02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVYGSSMRYWGQGTLVTVSS	
1488	2C04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSRNAMGWYRRAPG KQRELVAGISSDGSKLYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVLGSSMRYWGQGTLVTVSS	
1489	2C06	EVQLVESGGGLVQPGGSLTLSCVASGSTNSINAMGWYRRAPG KQRELVAGISSDGSKVYKDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYYRTVSGSSMRYWGQGTLVTVSS	
1490	2C07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRSVSGSSMRYWGQGTLVTVSS	
1491	2C08	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGISSDGSKVYQDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRRVSGSSMRYWGQGTLVTVSS	
1492	2C09	EVQLVESGGGLVQPGGSLTLSCVPSGSTSNINAMGWYRRAPG KQRELPAGISSDGTKIYADSAKVPFTITRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGTSMRYWGQGTLVTVSS	
1493	2C010	EVQLVESGGGLVQPGGSLTLSCVASGSTSKINAMGWYRRAPG KQRELVAGISSDRSKVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVAGSSMRYWGQGTLVTVSS	
1494	2D02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINALGWYRRAPGK QRELVAGISSDGSLVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRIVSGSSMRYWGQGTLVTVSS	
1495	2D03	EVQLVESGGGLVQPGGSLTLSCVASGKTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGVSMRYWGQGTLVTVSS	
1496	2D04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGSKVYRDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVQGSSMRYWGQGTLVTVSS	
1497	2D05	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTASGSSMRYWGQGTLVTVSS	
1498	2D06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSSRYWGQGTLVTVSS	
1499	2D07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGTKVYRDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVQGSSMRYWGQGTLVTVSS	
1500	2D09	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELAAGISSDGSKVYNDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVRGSSMRYWGQGTLVTVSS	
1501	2D010	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTKSGSSMRYWGQGTLVTVSS	
1502	2D011	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVWGSSMRYWGQGTLVTVSS	

1503	2D012	EVQLVESGGGLVQPGGSLTLSCVASGKTSSINAMGWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTRSGSSMRYWGQGTLVTVSS	
1504	2E01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPFK QGELPAGISPDGTKAYADSAKVRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFHTVCGTSMGYWGQGTLVTVSS	
1505	2E02	EVQLVESGGGLVQPGGSLTLSCVASGSTSAINAMGWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSQRYWGQGTLVTVSS	
1506	2E05	EVQLVESGGGLVQPGGSLTLSCVASGSPSSINAYGWYRRAPGK QRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGSSMSYWGQGTLVTVSS	
1507	2E06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYASSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVRGSSMRYWGQGTLVTVSS	
1508	2E08	EVQLVESGGGLVQPGGSLTLSCVASGSRSSINAMGWYRRAPG KQRELVAGISADGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTQSGSSMRYWGQGTLVTVSS	
1509	2E09	EVQLVESGGGLVQPGGSLTLSCVASGSVSSINAMGWYRRAPG KQRELVAGISSDGSKVYASSAKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTLSGSSMRYWGQGTLVTVSS	
1510	2E010	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFHTVSGSSMRYWGQGTLVTVSS	
1511	2E011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSSVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRRVSGSSMRYWGQGTLVTVSS	
1512	2F01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRLVSGSSMRYWGQGTLVTVSS	
1513	2F02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGSKVYAGSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGSYMRYWGQGTLVTVSS	
1514	2F03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELAAGISSDNSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVGGSSMRYWGQGTLVTVSS	
1515	2F06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAYGWYRRAPGK QRELVAGISSDGSAVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTHSGSSMRYWGQGTLVTVSS	
1516	2F07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGSSVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSTSSMRYWGQGTLVTVSS	
1517	2F08	EVQLVESGGGLVQPGGSLTLSCVASGSKSSINAMGWYRRAPG KQRELPAGISSNGTKVYADSAKVRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVLGTSMRYWGQGTLVTVSS	
1518	2F09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKLYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	

1519	2F11	EVQLVESGGGLVQPGGSLTLSCVASGSVSSINAMGWYRRAPG KQRELVAGISSDGSKVYKDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSMGYWGQGTLVTVSS	
1520	2G03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSLVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRAWGQGTLVTVSS	
1521	2G04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSLVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRILSGSSMRYWGQGTLVTVSS	
1522	2G07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVQGSSMRYWGQGTLVTVSS	
1523	2G08	EVQLVESGGGLVQPGGSLTLSCVASGSTSYINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGQSMGYWGQGTLVTVSS	
1524	2G09	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGVSSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSARYWGQGTLVTVSS	
1525	2G011	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELPAGISRDGSKVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRYVSGSSMRYWGQGTLVTVSS	
1526	2H010	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELAAGISSDGSKLYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSMRYWGQGTLVTVSS	
1527	2H011	EVQLVESGGGLVQPGGSLTLSCVASGSTSRINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRRVSGSSMRYWGQGTLVTVSS	
1528	2H02	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELAAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFHTVSGSSMRYWGQGTLVTVSS	
1529	2H03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRQVSGSSMRYWGQGTLVTVSS	
1530	2H04	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDTSKVYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSYMRYWGQGTLVTVSS	
1531	2H06	EVQLVESGGGLVQPGGSLTLSCVASGSTSTINAMGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTASGSSMRYWGQGTLVTVSS	
1532	2H07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGSTVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGHSMRYWGQGTLVTVSS	
1533	2H08	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELAAGISKDGSKVYADSAKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSSSRYWGQGTLVTVSS	
1534	2E05-M106Y	EVQLVESGGGLVQPGGSLTLSCVASGSPSSINAYGWYRRAPGK QRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGSSYSYWGQGTLVTVSS	

1535	2E05-M106Q	EVQLVESGGGLVQPGGSLTLSCVASGSPSSINAYGWYRRAPGKQRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYYFRTVSGSSQSYWGQGTLVTVSS	
1536	3A01	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPGKKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1537	3A02	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSLAWYRQAPGKKRELVAGISADGSTAYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1538	3A03	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPGKKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1539	3A04	EVQLVESGGGLVQPGGSLTLSCAASGSQVSFLSMAWYRQAPGKKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRYIYWGQGTLVTVSS	
1540	3A05	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPGKKRELVAGISEAGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1541	3A06	EVQLVESGGGLVQPGGSLTLRCAASGSKVSFLSMAWYRQAPGKKRELVAGISADGSTDYVDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1542	3A08	EVQLVESGGGLVQPGGSLTLSCAASGSSVGFLSMAWYRQAPGKKRELVAGISADGSTDYIRSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1543	3A09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPGKKRELVAGISADGSVDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRYIYWGQGTLVTVSS	
1544	3A010	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPGKKRELVAGISADGSTLYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1545	3A011	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSLAWYRQAPGKKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1546	3B01	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPGKKRELVAGISGDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1547	3B02	EVQLVESGGGLVQPGGSLTLSCAASGSSVQFLSMAWYRQAPGKKRELVAGISADGSTDYINSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1548	3B04	EVQLVESGGGLVQPGGSLTLSCAASGSNVSFLSMAWYRQAPGKKRELVAGISARGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYHWTTRYTYWGQGTLVTVSS	
1549	3B05	EVQLVESGGGLVQPGGSLTLSCVASGSSVKFLSMAWYRQAPGKKRELVAGISADGSTTYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1550	3B06	EVQLVESGGGLVQPGGSLTLSCAASGKSVSFLSMAWYRQAPGKKRELVAGISKDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLRAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	

1551	3B07	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1552	3B09	EVQLVESGGGLVQPGGSLTLSCAASGSHVSFLSMAWYRQAPG KKRELVAGISANGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYAYWGQGTLVTVSS	
1553	3B010	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWVTRYTYWGQGTLVTVSS	
1554	3B011	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSADYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWVTRYTYWGQGTLVTVSS	
1555	3C01	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISAHGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1556	3C02	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTIYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1557	3C03	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISRDGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRGTYWGQGTLVTVSS	
1558	3C04	EVQLVESGGGLVQPGGSLTLSCAASGSHVSFLSMAWYRQAPG KKRELVAGISADGPTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWDTRYTYWGQGTLVTVSS	
1559	3C05	EVQLVESGGGLVQPGGSLTLSCVASGTSVSFLSMAWYRQAPG KKRELVAGISADGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1560	3C06	EVQLVESGGGLVQPGGSLTLSCAASGTSVSFLSIAWYRQAPGK KRELVAGISADGSTDYIASVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1561	3C08	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISLDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTGRYTYWGQGTLVTVSS	
1562	3C09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTIYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1563	3C011	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISAHGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1564	3D01	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWITRYTYWGQGTLVTVSS	
1565	3D02	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWITRYTYWGQGTLVTVSS	
1566	3D03	EVQLVESGGGLVQPGGSLTLSCAASGSSVVFLSMAWYRQAPG KKRELVAGISADGSMDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	

1567	3D05	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1568	3D07	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWTTRYTYWGQGTLVTVSS	
1569	3D08	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISANGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTNRYTYWGQGTLVTVSS	
1570	3D09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSRLSMAWYRQAPG KKRELVAGISANGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYRYWGQGTLVTVSS	
1571	3D010	EVQLVESGGGLVQPGGSLTLSCAASGSSKSFLSMAWYRQAPG KKRELVAGISADGSTSYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1572	3D011	EVQLVESGGGLVQPGGSLTLSCAASGSSVSRLSMAWYRQAPG KKRELVAGISADGSRDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYKYWGQGTLVTVSS	
1573	3E01	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTMYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWHTRYTYWGQGTLVTVSS	
1574	3E02	EVQLVESGGGLVQPGGSLTLSCAASGSGVRFLSMAWYRQAPG KKRELVAGISPDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1575	3E03	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISGDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWMTRYTYWGQGTLVTVSS	
1576	3E04	EVQLVESGGGLVQPGGSLTLSCAASGSSVHFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYRYWGQGTLVTVSS	
1577	3E09	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1578	3E011	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTFWGQGTLVTVSS	
1579	3F03	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1580	3F05	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1581	3F06	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTSYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWATRYTYWGQGTLVTVSS	
1582	3F08	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTLYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWHTRYTYWGQGTLVTVSS	

1583	3F09	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWGTRYTYWGQGTLVTVSS	
1584	3F010	EVQLVESGGGLVQPGGSLTLSCAASYSSVSRLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRNTYWGQGTLVTVSS	
1585	3F011	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1586	3G01	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTLYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYAYWGQGTLVTVSS	
1587	3G02	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGRTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1588	3G04	EVQLVESGGGLVQPGGSLTLSCVASGTSVSFLSMAWYRQAPG KKRELVAGISADGSTIYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1589	3G06	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTLYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1590	3G07	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTSRYTYWGQGTLVTVSS	
1591	3G08	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISKDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRVTYWGQGTLVTVSS	
1592	3G09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSVLSMAWYRQAPG KKRELVAGISADGSTDYIGSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRTTYWGQGTLVTVSS	
1593	3G010	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISVDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1594	3G011	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTGYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWATRYTYWGQGTLVTVSS	
1595	3H01	EVQLVESGGGLVQPGGSLTLSCVASGSSVKFLSMAWYRQAPG KKRELVAGISGDGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1596	3H03	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYALRWTTRYTYWGQGTLVTVSS	
1597	3H06	EVQLVESGGGLVQPGGSLTLSCAASGSSVSQLSMAWYRQAPG KKRELVAGISADGSTDYFDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRGTYWGQGTLVTVSS	
1598	3H07	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTSYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	

1599	3H09	EVQLVESGGGLVQPGGSLTLSCAASKSSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRATYWGQGTLVTVSS	
1600	3H010	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTAYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1601	3H011	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWPTRYTYWGQGTLVTVSS	
1602	4A01	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISQDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1603	4A02	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISNDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWKTRYTYWGQGTLVTVSS	
1604	4A04	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISARGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1605	4A05	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSLAWYRQAPGK KRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWKTRRTYWGQGTLVTVSS	
1606	4A06	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1607	4A07	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISADGSTLYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYRYWGQGTLVTVSS	
1608	4A08	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTNYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1609	4A010	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYKYWGQGTLVTVSS	
1610	4A011	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISADGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWKTRYTYWGQGTLVTVSS	
1611	4A09	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTDYIGSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRVTYWGQGTLVTVSS	
1612	4B01	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRFTYWGQGTLVTVSS	
1613	4B02	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRFTYWGQGTLVTVSS	
1614	4B04	EVQLVESGGGLVQPGGSLTLSCAASGSSVLFLSMAWYRQAPG KKRELVAGVSSDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	

1615	4B05	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGHTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTHWGQGTLVTVSS	
1616	4B06	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTDYFDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1617	4B07	EVQLVESGGGLVQPGGSLTLSCAASGSSVGFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1618	4B08	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFMSMAWYRQAPG KKRELVAGISADGSTDYIASVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRSTYWGQGTLVTVSS	
1619	4B09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTDYISSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWTTRYTYWGQGTLVTVSS	
1620	4B011	EVQLVESGGGLVQPGGSLTLSCAASGSSVTFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRGTYWGQGTLVTVSS	
1621	4C01	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWKTRYTYWGQGTLVTVSS	
1622	4C02	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISADGSTTYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRFTYWGQGTLVTVSS	
1623	4C03	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFMSMAWYRQAPG KKRELVAGISVDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1624	4C05	EVQLVESGGGLVQPGGSLTLSCAASGSSVSNLSMAWYRQAPG KKRELVAGISADGSTAYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1625	4C06	EVQLVESGGGLVQPGGSLTLSCAASNSSVSKLSMAWYRQAPG KKRELVAGISADGSTAYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1626	4C07	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISADGSKDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRLTYWGQGTLVTVSS	
1627	4C08	EVQLVESGGGLVQPGGSLTLSCVASGSQVSFLSMAWYRQAPG KKRELVAGISADGSTDYFDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1628	4C010	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFMSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRLTYWGQGTLVTVSS	
1629	4C011	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1630	4D01	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	

1631	4D02	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISARGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYQWTTRYTYWGQGTLVTVSS	
1632	4D03	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISATGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1633	4D04	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSIAWYRQAPGK KRELVAGISKDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWTTRMTYWGQGTLVTVSS	
1634	4D05	EVQLVESGGGLVQPGGSLTLSCAASGSSSSFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1635	4D06	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISPDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYRYWGQGTLVTVSS	
1636	4D08	EVQLVESGGGLVQPGGSLTLSCAASGSSVNFLSMAWYRQAPG KKRELVAGISADGSTHYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWLTRYTYWGQGTLVTVSS	
1637	4D09	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTDYILSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYEWTTRYTYWGQGTLVTVSS	
1638	4D010	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIHSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1639	4D011	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISVDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1640	4E01	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSVAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1641	4E02	EVQLVESGGGLVQPGGSLTLSCAASGSQVSFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1642	4E06	EVQLVESGGGLVQPGGSLTLSCAASGTSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIRSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRLTYWGQGTLVTVSS	
1643	4E07	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTMYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRLTYWGQGTLVTVSS	
1644	4E08	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYKWTTRYTYWGQGTLVTVSS	
1645	4E09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSSAWYRQAPGK KRELVAGISADGSTLYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWTTRSTYWGQGTLVTVSS	
1646	4E010	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	

1647	4E011	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISATGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1648	4F02	EVQLVESGGGLVQPGGSLTLSCAASGSTVSFLSMAWYRQAPG KKRELVAGISHDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1649	4F03	EVQLVESGGGLVQPGGSLTLSCAASGSSVQFLSMAWYRQAPG KKRELVAGISYDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1650	4F04	EVQLVESGGGLVQPGGSLTLSCAASRSSVSFLSMAWYRQAPG KKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWLTRYTYWGQGTLVTVSS	
1651	4F08	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISADGSTAYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1652	4F09	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTDYIESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1653	4F010	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISIDGSTDYIKSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWTTRYRYWGQGTLVTVSS	
1654	4F011	EVQLVESGGGLVQPGGSLTLSCAASGSKVSFLSMAWYRQAPG KKRELVAGISADGSKDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1655	4G01	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWPTRYTYWGQGTLVTVSS	
1656	4G02	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISRDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRHTYWGQGTLVTVSS	
1657	4G03	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTDYIHSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTRRYTYWGQGTLVTVSS	
1658	4G05	EVQLVESGGGLVQPGGSLTLSCAASGSSVSILSMAWYRQAPG KKRELVAGISADGSTIYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWHTRYTYWGQGTLVTVSS	
1659	4G07	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSVAWYRQAPG KKRELVAGISANGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTNRYTYWGQGTLVTVSS	
1660	4G08	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISTDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYRYWGQGTLVTVSS	
1661	4G09	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISYDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRRTYWGQGTLVTVSS	
1662	4G010	EVQLVESGGGLVQPGGSLTLSCAASGHSVSFLSMAWYRQAPG KKRELVAGISADGSTDYIASVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	

1663	4G011	EVQLVESGGGLVQPGGSLTLSCAASGSSVRFLSMAWYRQAPG KKRELVAGISADGSTDYIGSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1664	4H01	EVQLVESGGGLVQPGGSLTLSCAASGSSVSFLSMAWYRQAPG KKRELVAGISANGSTDYYDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWRTRYTYWGQGTLVTVSS	
1665	4H03	EVQLVESGGGLVQPGGSLTLSCAASGSRVSFLSMAWYRQAPG KKRELVAGISADGSTSYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1666	4H04	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGVSADGSTDYIDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYEWTTRYTYWGQGTLVTVSS	
1667	4H05	EVQLVESGGGLVQPGGSLTLSCAASGSSVSRLSMAWYRQAPG KKRELVAGISARGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRSTYWGQGTLVTVSS	
1668	4H06	EVQLVESGGGLVQPGGSLTLSCAASGRSVSFLSMAWYRQAPG KKRELVAGISADGSTIYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWTTRYTYWGQGTLVTVSS	
1669	4H07	EVQLVESGGGLVQPGGSLTLSCAASGRSVSFLSMAWYRQAPG KKRELVAGISANGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1670	4H08	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSMAWYRQAPG KKRELVAGISADGSTDYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWSTRYTYWGQGTLVTVSS	
1671	4H09	EVQLVESGGGLVQPGGSLTLSCAASGSSVSKLSMAWYRQAPG KKRELVAGISADGSTDYRDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWTYRYTYWGQGTLVTVSS	
1672	4H011	EVQLVESGGGLVQPGGSLTLSCAASGSSVSRLSMAWYRQAPG KKRELVAGISVDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRLTYWGQGTLVTVSS	
1673	4D09-M34L	EVQLVESGGGLVQPGGSLTLSCAASGSSVKFLSLAWYRQAPG KKRELVAGISADGSTDYILSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYEWTTRYTYWGQGTLVTVSS	
1674	4H11-M34L	EVQLVESGGGLVQPGGSLTLSCAASGSSVSRLSLAWYRQAPG KKRELVAGISVDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTTRLTYWGQGTLVTVSS	
1675	41B11	EVQLVESGGGLVQPGGSLTLSCVASGTSSSINAMGWYRRAPG KQRELVAGISSDGSKVFNESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRPAAGSPMRYWGQGTLVTVSS	
1676	41C02	EVQLVESGGGLVQPGGSLTLSCVASGTTSSINAIGWYRRAPGK QRELVAGISSDGSEVYTDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVDGSPLRYWGQGTLVTVSS	
1677	41D01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDDSNVYYESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSKRYWGQGTLVTVSS	
1678	41D02	EVQLVESGGGLVQPGGSLTLSCVASGQTYRVNAFGWYRRAPG KQRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFSAGSGTEMSYWGQGTLVTVSS	

1679	41D03	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMAWYRRAPG KQRELVAGISSDESTLYVDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFGSLSGSSTTYWGQGTLVTVSS	
1680	41D07	EVQLVESGGGLVQPGGSLTLSCVASGSASLTNATGWYRRAPG KQRELVAGISSDDSKVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFGSVSGSWTRYWGQGTLVTVSS	
1681	41E01	EVQLVESGGGLVQPGGSLTLSCVASGYPSLNNAMGWYRRAPG KQRELVAGISSDGSQVYGASVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRLVSGSSMSYWGQGTLVTVSS	
1682	41E02	EVQLVESGGGLVQPGGSLTLSCVASGSSSTINAIGWYRRAPGK QRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTGSGTSKSYWGQGTLVTVSS	
1683	41F07	EVQLVESGGGLVQPGGSLTLSCVASGSTSYINAMGWYRRAPG KQRELVAGISSDGSNMYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFSNMSGTTRRYWGQGTLVTVSS	
1684	41G01	EVQLVESGGGLVQPGGSLTLSCVASGSTSSVNALGWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVPGSAMGYWGQGTLVTVSS	
1685	42A03	EVQLVESGGGLVQPGGSLTLSCVASGSTSLSNAVGWYRRAPG KQRELVAGISSDGSKVSAESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRAESGSSMGYWGQGTLVTVSS	
1686	42A06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSTNAIGWYRRAPGK QRELVAGISSDGSKVYDDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTLYGSSRSYWGQGTLVTVSS	
1687	42A07	EVQLVESGGGLVQPGGSLTLSCVASGLTSTINAMGWYRRAPG KQRELVAGISSDGSKVYDDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFSPFSGSDTGYWGQGTLVTVSS	
1688	42A08	EVQLVESGGGLVQPGGSLTLSCVASGVSPSKNAIGWYRRAPG KQRELVAGISSDGSAVYVGSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFSTFSGSSISYWGQGTLVTVSS	
1689	42A11	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAVGWYRRAPGK QRELVAGISSDGSYVYSESVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTLAGSEMRYWGQGTLVTVSS	
1690	42B06	EVQLVESGGGLVQPGGSLTLSCVASGSTTMNNAMAWYRRAP GKQRELVAGISSDSSHVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVSGSGVRYWGQGTLVTVSS	
1691	42B10	EVQLVESGGGLVQPGGSLTLSCVASGSTSKINAIGWYRRAPGK QRELVAGISSDSSIVYTDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRPGAGHSNSYWGQGTLVTVSS	
1692	42C01	EVQLVESGGGLVQPGGSLTLSCVASGQTTALNAMGWYRRAP GKQRELVAGISSDGSEVNTDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRRASGTAMSYWGQGTLVTVSS	
1693	42C03	EVQLVESGGGLVQPGGSLTLSCVASGATSSINAIGWYRRAPGK QRELVAGISSDGSKLSSDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFTSASGTDLSYWGQGTLVTVSS	
1694	42C07	EVQLVESGGGLVQPGGSLTLSCVASGSTSTINAMGWYRRAPG KQRELVAGISSDNSKVYADSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRSANGSSKRYWGQGTLVTVSS	

1695	42C08	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAMGWYRRAPG KQRELVAGISSDGSRVYFDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFKTIAGAGMRYWGQGTLVTVSS	
1696	42C10	EVQLVESGGGLVQPGGSLTLSCVASGSTSLVNAMGWYRRAPG KQRELVAGISSDGSLVYAESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRYGSGSSLSYWGQGTLVTVSS	
1697	42C11	EVQLVESGGGLVQPGGSLTLSCVASGSTSLNNAIGWYRRAPG KQRELVAGISSDGSVVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVPGASMKYWGQGTLVTVSS	
1698	42D05	EVQLVESGGGLVQPGGSLTLSCVASGSTSPVNAMAWYRRAPG KQRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYYFRTVDGSAISYWGQGTLVTVSS	
1699	42D06	EVQLVESGGGLVQPGGSLTLSCVASGTTSSMNAIGWYRRAPG KQRELVAGISSDGSKLYDESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVKGSGGSYWGQGTLVTVSS	
1700	42D07	EVQLVESGGGLVQPGGSLTLSCVASGETSSINAMAWYRRAPG KQRELVAGISSDYSKLYADSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVSGSSRGYWGQGTLVTVSS	
1701	42D08	EVQLVESGGGLVQPGGSLTLSCVASGSTSTINAIGWYRRAPGK QRELVAGISSDSSKVYTESVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRPGPGSQMAYWGQGTLVTVSS	
1702	42E01	EVQLVESGGGLVQPGGSLTLSCVASGSTYSMNAMGWYRRAP GKQRELVAGISSDGSQVYVDSVKGRFTISRDNAKNSVYLQMN SLRAEDTAVYYCYYFRTVAGSASGYWGQGTLVTVSS	
1703	42E02	EVQLVESGGGLVQPGGSLTLSCVASGSPSSINAYGWYRRAPGK QRELVAGISSDGSKVYSDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGSSYSYWGQGTLVTVSS	
1704	42E05	EVQLVESGGGLVQPGGSLTLSCVASGSTSTINAIGWYRRAPGK QRELVAGISSDGSKVYVDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFINLKGSSMAYWGQGTLVTVSS	
1705	42E06	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDGSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRMVTGSYGGYWGQGTLVTVSS	
1706	42E07	EVQLVESGGGLVQPGGSLTLSCVASGSISSINAMGWYRRAPGK QRELVAGISSDGSSVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFKSSYGLPMRYWGQGTLVTVSS	
1707	42F01	EVQLVESGGGLVQPGGSLTLSCVASGSTQVNNAMAWYRRAP GKQRELVAGISSDGSQVYYGSVKGRFTISRDNAKNSVYLQMN SLRAEDTAVYYCYYFKTVSGQSLRYWGQGTLVTVSS	
1708	42F08	EVQLVESGGGLVQPGGSLTLSCVASGSTASFNAMAWYRRAPG KQRELVAGISSDGSKVYTDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRTVTGRAARYWGQGTLVTVSS	
1709	42F10	EVQLVESGGGLVQPGGSLTLSCVASGSPLSINAIGWYRRAPGK QRELVAGISSDGSKVSADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFGPAIGASRTYWGQGTLVTVSS	
1710	42G05	EVQLVESGGGLVQPGGSLTLSCVASGSTTFINAIGWYRRAPGK QRELVAGISSDGSKVYEDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTVSGAPKSYWGQGTLVTVSS	

1711	42G07	EVQLVESGGGLVQPGGSLTLSCVASGSTSSINAIGWYRRAPGK QRELVAGISSDRSKVYADSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFHTVSGSSMSYWGQGTLVTVSS	
1712	42H05	EVQLVESGGGLVQPGGSLTLSCVASGETDTINAVGWYRRAPG KQRELVAGISSDGSKVYAESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFRRLEGYSNRYWGQGTLVTVSS	
1713	42H08	EVQLVESGGGLVQPGGSLTLSCVASGSTSPINAIGWYRRAPGK QRELVAGISSDGSVVTTESVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYYFRTGSGSSMGYWGQGTLVTVSS	
1714	42H11	EVQLVESGGGLVQPGGSLTLSCVASGSITSSNAMGWYRRAPG KQRELVAGISSDGSHVHQESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYYFTTVTGSSMSYWGQGTLVTVSS	
1715	51A01	EVQLVESGGGLVQPGGSLTLSCAASRYSVSNLSMAWYRQAPG KKRELVAGISADGSTVYVESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYYWTERRPYWGQGTLVTVSS	
1716	51A02	EVQLVESGGGLVQPGDSLTLSCAASMSTVSVLSMAWYRQAPG KKRELVAGISSDGSTVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAIYYCYAYSWDDAHPYWGQGTLVTVSS	
1717	51A03	EVQLVESGGGLVQPGGSLTLSCAASDSYVSLLSMAWYRQAPG KKRELVAGISVDGSTHYVASVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWMTRLTYWGQGTLVTVSS	
1718	51A05	EVQLVESGGGLVQPGGSLTLSCAASDSAVSVLSIAWYRQAPG KKRELVAGISTDGSKHYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYDWADAQPYWGQGTLVTVSS	
1719	51B01	EVQLVESGGGLVQPGGSLTLSCAASHSSVTSLSLAWYRQAPG KKRELVAGISYDGSKYYAESVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYSWTDRLPYWGQGTLVTVSS	
1720	51B04	EVQLVESGGGLVQPGGSLTLSCAASDSVVKFLSMAWYRQAPG KKRELVAGISANGSRTYMESVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYRWATRLPYWGQGTLVTVSS	
1721	51B11	EVQLVESGGGLVQPGGSLTLSCAASDPSVWNLSMAWYRQAP GKKRELVAGISPDGSTDYVDSVKGRFTISRDNAKNSVYLQMN SLRAEDTAVYYCYAYKWSNRLPYWGQGTLVTVSS	
1722	51C02	EVQLVESGGGLVQPGGSLTLSCAASGTSVMLLSLAWYRQAPG KKRELVAGISPNGSAVYTESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYGWKTRQPYWGQGTLVTVSS	
1723	51D01	EVQLVESGGGLVQPGGSLTLSCAASSSPVSNLSLAWYRQAPGK KRELVAGISPDGSTAYMESVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWPNRRGYWGQGTLVTVSS	
1724	51D03	EVQLVESGGGLVQPGGSLTLSCAASWRSVLLLSVAWYRQAPG KKRELVAGISNDGSTDYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYDWTTRQRYWGQGTLVTVSS	
1725	51E02	EVQLVESGGGLVQPGGSLTLSCAASSSSVQYLSMAWYRQAPG KKRELVAGISTDGSAVYFDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYNWSYAQPYWGQGTLVTVSS	
1726	51E03	EVQLVESGGGLVQPGGSLTLSCAASGTSVSLLSLAWYRQAPG KKRELVAGISTGGSTHYIESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYNWTDSLQYWGQGTLVTVSS	

1727	51E05	EVQLVESGGGLVQPGGSLTLSCAASLSSVSNLSIAWYRQAPGK KRELVAGISTDGSTVYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYSWTTSLPYWGQGTLVTVSS	
1728	51F01	EVQLVESGGGLVQPGGSLTLSCAASMYSVSFLSMAWYRQAPG KKRELVAGISNEGSTYYMDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYKWRSRSTYWGQGTLVTVSS	
1729	51F02	EVQLVESGGGLVQPGGSLTLSCAASKSSVSHLSLAWYRQAPG KKRELVAGISADGSHVYTNSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYSQTTRDPYWGQGTLVTVSS	
1730	51F03	EVQLVESGGGLVQPGGSLTLSCAASYTSVLDLSIAWYRQAPGK KRELVAGISDDGSRYYTDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWTARDTYWGQGTLVTVSS	
1731	51F04	EVQLVESGGGLVQPGGSLTLSCAASMSDVSFLSMAWYRQAPG KKRELVAGISAEGSTLYMESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWTSRLSYWGQGTLVTVSS	
1732	51G02	EVQLVESGGGLVQPGGSLTLSCAASESSVSFLSSAWYRQAPGK KRELVAGISTDGSTVYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYSWTTRSRYWGQGTLVTVSS	
1733	51G04	EVQLVESGGGLVQPGGSLTLSCAASGDSVSLLSMAWYRQAPG KKRELVAGISANGSTSYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYNWTSRYRYWGQGTLVTVSS	
1734	51G10	EVQLVESGGGLVQPGGSLTLSCAASGSDVWYLSLAWYRQAPG KKRELVAGISDDGSRHYIESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWKTRFPYWGQGTLVTVSS	
1735	51H04	EVQLVESGGGLVQPGGSLTLSCAASKSAVAFLSIAWYRQAPG KKRELVAGISPDGSTVYIESVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWTTRYPYWGQGTLVTVSS	
1736	51H05	EVQLVESGGGLVQPGGSLTLSCAASFSAVAYLSMAWYRQAPG KKRELVAGISDDGSTVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYEWTNALPYWGQGTLVTVSS	
1737	52B01	EVQLVESGGGLVQPGGSLTLSCAASVYSVYDLSTAWYRQAPG KKRELVAGISDDGSTVYFDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWITRSPYWGQGTLVTVSS	
1738	52C04	EVQLVESGGGLVQPGGSLTLSCAASGDSVSFLSMAWYRQAPG KKRELVAGISDEGSTVYIGSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWTTRRQYWGQGTLVTVSS	
1739	52D04	EVQLVESGGGLVQPGGSLTLSCAASSSSVSLLSLAWYRQAPGK KRELVAGISDDGSIVYMDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYSWITRSPYWGQGTLVTVSS	
1740	53A04	EVQLVESGGGLVQPGGSLTLSCAASADSVSFLSIAWYRQAPGK KRELVAGISDDGSKHYFDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWEESRQYWGQGTLVTVSS	
1741	53A05	EVQLVESGGGLVQPGGSLTLSCAASASSVTLLSIAWYRQAPGK KRELVAGISTDGSTDYLHSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYTWTTRLPYWGQGTLVTVTS	
1742	53A09	EVQLVESGGGLVQPGGSLTLSCAASADSVSFLSIAWYRQAPGK KRELVAGISDDGSKHYFDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYRWEESRQYWGQGTLVTVSS	

1743	53B05	EVQLVESGGGLVQPGGSLTLSCAASGTSVWLLSMAWYRQAP GKKRELVAGISYDGSTVYVESVKGRFTISRDNAKNSVYLQMN SLRAEDTAVYYCYAYSWTTRQPYWGQGTLVTVSS	
1744	53B06	EVQLVESGGGLVQPGGSLTLSCAASGSSVSILSIAWYRQAPGK KRELVAGISDDGSTVYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYVWGTRLPYWGQGTLVTVSS	
1745	53C03	EVQLVESGGGLVQPGGSLTLSCAASGTAVSNLSIAWYRQAPG KKRELVAGISDDGSTVYVDSVKGRFTISRDNAKNSVYLQMNS LRAEDTAVYYCYAYEWTNALPYWGQGTLVTVSS	
1746	53C04	EVQLVESGGGLVQPGGSLTLSCAASGSAVSMLSLAWYRQAPG KKRELVAGISDDGSQVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYRWEDALTYWGQGTLVTVSS	
1747	53H03	EVQLVESGGGLVQPGGSLTLSCAASGMTVFFLSMAWYRQAPG KKRELVAGISVDGSTVYSDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWTTRYPYWGQGTLVTVSS	
1748	53H04	EVQLVESGGGLVQPGGSLTLSCAASQYSVTFLSVAWYRQAPG KKRELVAGISDDGSNVYIDSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWIDSLRYWGQGTLVTVSS	
1749	54B05	EVQLVESGGGLVQPGGSLTLSCAASGETVSFLSLAWYRQAPG KKRELVAGISTDGSTVYFVSVKGRFTISRDNAKNSVYLQMNSL RAEDTAVYYCYAYSWTTPRAYWGQGTLVTVSS	
1750	51X5	EVQLVESGGGLVQPGGSLTLSCAASLSSVSVLSIAWYRQAPGK KRELVAGISTDGSTVYIDSVKGRFTISRDNAKNSVYLQMNSLR AEDTAVYYCYAYSWTTSLPYWGQGTLVTVSS	
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1755	DL80	GSSFSITSMA	CDR1
1756	DL18	SSIFSISSMS	CDR1
1757	DL94	SSIFSISSMS	CDR1
1758	DL17	GSTLNIKIMA	CDR1
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1787	DL92	GITSSVYSMG	CDR1
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1795	DL89	GSIFTTNSMG	CDR1
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2879	3B06	YRWTTRYTY	CDR3
2880	3B07	YRWTTRYTY	CDR3
2881	3B09	YRWTTRYAY	CDR3
2882	3B010	YRWVTRYTY	CDR3
2883	3B011	YRWVTRYTY	CDR3
2884	3C01	YRWSTRYTY	CDR3
2885	3C02	YRWRTRYTY	CDR3
2886	3C03	YRWTTRGTY	CDR3
2887	3C04	YRWDTRYTY	CDR3
2888	3C05	YRWTTRRTY	CDR3
2889	3C06	YRWRTRYTY	CDR3
2890	3C08	YRWTGRYTY	CDR3
2891	3C09	YRWRTRYTY	CDR3
2892	3C011	YRWRTRYTY	CDR3
2893	3D01	YRWITRYTY	CDR3
2894	3D02	YRWITRYTY	CDR3
2895	3D03	YRWRTRYTY	CDR3
2896	3D05	YRWTRRYTY	CDR3
2897	3D07	YSWTTRYTY	CDR3
2898	3D08	YRWTNRYTY	CDR3
2899	3D09	YRWTTRYRY	CDR3
2900	3D010	YRWTTRYTY	CDR3

2901	3D011	YRWTTRYKY	CDR3
2902	3E01	YRWHTRYTY	CDR3
2903	3E02	YRWTRRYTY	CDR3
2904	3E03	YRWMTRYTY	CDR3
2905	3E04	YRWTTRYRY	CDR3
2906	3E09	YRWSTRYTY	CDR3
2907	3E011	YRWTTRYTF	CDR3
2908	3F03	YRWRTRYTY	CDR3
2909	3F05	YRWTTRRTY	CDR3
2910	3F06	YRWATRYTY	CDR3
2911	3F08	YRWHTRYTY	CDR3
2912	3F09	YRWGTRYTY	CDR3
2913	3F010	YRWTTRNTY	CDR3
2914	3F011	YRWRTRYTY	CDR3
2915	3G01	YRWTTRYAY	CDR3
2916	3G02	YRWRTRYTY	CDR3
2917	3G04	YRWTTRRTY	CDR3
2918	3G06	YRWTTRRTY	CDR3
2919	3G07	YRWTSRYTY	CDR3
2920	3G08	YRWTTRVTY	CDR3
2921	3G09	YRWTTRTTY	CDR3
2922	3G010	YRWRTRYTY	CDR3
2923	3G011	YRWATRYTY	CDR3
2924	3H01	YRWTTRRTY	CDR3
2925	3H03	LRWTTRYTY	CDR3
2926	3H06	YRWTTRGTY	CDR3
2927	3H07	YRWRTRYTY	CDR3
2928	3H09	YRWTTRATY	CDR3
2929	3H010	YRWTTRRTY	CDR3
2930	3H011	YRWPTRYTY	CDR3
2931	4A01	YRWRTRYTY	CDR3
2932	4A02	YRWKTRYTY	CDR3
2933	4A04	YRWSTRYTY	CDR3
2934	4A05	YRWKTRRTY	CDR3
2935	4A06	YRWTTRRTY	CDR3
2936	4A07	YRWTTRYRY	CDR3
2937	4A08	YRWRTRYTY	CDR3
2938	4A010	YRWTTRYKY	CDR3
2939	4A011	YRWKTRYTY	CDR3
2940	4A09	YRWTTRVTY	CDR3
2941	4B01	YRWTTRFTY	CDR3

2942	4B02	YRWTTRFTY	CDR3
2943	4B04	YRWRTRYTY	CDR3
2944	4B05	YRWTTRYTH	CDR3
2945	4B06	YRWTRRYTY	CDR3
2946	4B07	YRWTTRYTY	CDR3
2947	4B08	YRWTTRSTY	CDR3
2948	4B09	YSWTTRYTY	CDR3
2949	4B011	YRWTTRGTY	CDR3
2950	4C01	YRWKTRYTY	CDR3
2951	4C02	YRWTTRFTY	CDR3
2952	4C03	YRWRTRYTY	CDR3
2953	4C05	YRWTTRRTY	CDR3
2954	4C06	YRWSTRYTY	CDR3
2955	4C07	YRWTTRLTY	CDR3
2956	4C08	YRWTRRYTY	CDR3
2957	4C010	YRWTTRLTY	CDR3
2958	4C011	YRWTRRYTY	CDR3
2959	4D01	YRWTTRRTY	CDR3
2960	4D02	YQWTTRYTY	CDR3
2961	4D03	YRWTRRYTY	CDR3
2962	4D04	YRWTTRMTY	CDR3
2963	4D05	YRWTTRRTY	CDR3
2964	4D06	YRWTTRYRY	CDR3
2965	4D08	YRWLTRYTY	CDR3
2966	4D09	YEWTTRYTY	CDR3
2967	4D010	YRWRTRYTY	CDR3
2968	4D011	YRWRTRYTY	CDR3
2969	4E01	YRWRTRYTY	CDR3
2970	4E02	YRWSTRYTY	CDR3
2971	4E06	YRWTTRLTY	CDR3
2972	4E07	YRWTTRLTY	CDR3
2973	4E08	YKWTTRYTY	CDR3
2974	4E09	YRWTTRSTY	CDR3
2975	4E010	YRWRTRYTY	CDR3
2976	4E011	YRWSTRYTY	CDR3
2977	4F02	YRWTTRYTY	CDR3
2978	4F03	YRWRTRYTY	CDR3
2979	4F04	YRWLTRYTY	CDR3
2980	4F08	YRWRTRYTY	CDR3
2981	4F09	YRWTTRYTY	CDR3
2982	4F010	YRWTTRYRY	CDR3
2983	4F011	YRWTTRYTY	CDR3

2984	4G01	YRWPTRYTY	CDR3
2985	4G02	YRWTTRHTY	CDR3
2986	4G03	YRWTRRYTY	CDR3
2987	4G05	YRWHTRYTY	CDR3
2988	4G07	YRWTNRYTY	CDR3
2989	4G08	YRWTTRYRY	CDR3
2990	4G09	YRWTTRRTY	CDR3
2991	4G010	YRWSTRYTY	CDR3
2992	4G011	YRWSTRYTY	CDR3
2993	4H01	YRWRTRYTY	CDR3
2994	4H03	YRWTTRYTY	CDR3
2995	4H04	YEWTTRYTY	CDR3
2996	4H05	YRWTTRSTY	CDR3
2997	4H06	YRWTTRYTY	CDR3
2998	4H07	YRWSTRYTY	CDR3
2999	4H08	YRWSTRYTY	CDR3
3000	4H09	YRWTYRYTY	CDR3
3001	4H011	YRWTTRLTY	CDR3
3002	4D09-M34L	YEWTTRYTY	CDR3
3003	4H11-M34L	YRWTTRLTY	CDR3
3004	41B11	FRPAAGSPMRY	CDR3
3005	41C02	FRTVDGSPLRY	CDR3
3006	41D01	FRTVSGSSKRY	CDR3
3007	41D02	FSAGSGTEMSY	CDR3
3008	41D03	FGSLSGSSTTY	CDR3
3009	41D07	FGSVSGSWTRY	CDR3
3010	41E01	FRLVSGSSMSY	CDR3
3011	41E02	FRTGSGTSKSY	CDR3
3012	41F07	FSNMSGTTRRY	CDR3
3013	41G01	FRTVPGSAMGY	CDR3
3014	42A03	FRAESGSSMGY	CDR3
3015	42A06	FRTLYGSSRSY	CDR3
3016	42A07	FSPFSGSDTGY	CDR3
3017	42A08	FSTFSGSSISY	CDR3
3018	42A11	FRTLAGSEMRY	CDR3
3019	42B06	FRTVSGSGVRY	CDR3
3020	42B10	FRPGAGHSNSY	CDR3
3021	42C01	FRRASGTAMSY	CDR3
3022	42C03	FTSASGTDLSY	CDR3
3023	42C07	FRSANGSSKRY	CDR3
3024	42C08	FKTIAGAGMRY	CDR3
3025	42C10	FRYGSGSSLSY	CDR3
3026	42C11	FRTVPGASMKY	CDR3
3027	42D05	FRTVDGSAISY	CDR3

3028	42D06	FRTVKGSGGSY	CDR3
3029	42D07	FRTVSGSSRGY	CDR3
3030	42D08	FRPGPGSQMAY	CDR3
3031	42E01	FRTVAGSASGY	CDR3
3032	42E02	FRTVSGSSYSY	CDR3
3033	42E05	FINLKGSSMAY	CDR3
3034	42E06	FRMVTGSYGGY	CDR3
3035	42E07	FKSSYGLPMRY	CDR3
3036	42F01	FKTVSGQSLRY	CDR3
3037	42F08	FRTVTGRAARY	CDR3
3038	42F10	FGPAIGASRTY	CDR3
3039	42G05	FRTVSGAPKSY	CDR3
3040	42G07	FHTVSGSSMSY	CDR3
3041	42H05	FRRLEGYSNRY	CDR3
3042	42H08	FRTGSGSSMGY	CDR3
3043	42H11	FTTVTGSSMSY	CDR3
3044	51A01	YYWTERRPY	CDR3
3045	51A02	YSWDDAHPY	CDR3
3046	51A03	YRWMTRLTY	CDR3
3047	51A05	YDWADAQPY	CDR3
3048	51B01	YSWTDRLPY	CDR3
3049	51B04	YRWATRLPY	CDR3
3050	51B11	YKWSNRLPY	CDR3
3051	51C02	YGWKTRQPY	CDR3
3052	51D01	YRWPNRRGY	CDR3
3053	51D03	YDWTTRQRY	CDR3
3054	51E02	YNWSYAQPY	CDR3
3055	51E03	YNWTDSLQY	CDR3
3056	51E05	YSWTTSLPY	CDR3
3057	51F01	YKWRSRSTY	CDR3
3058	51F02	YSQTTRDPY	CDR3
3059	51F03	YRWTARDTY	CDR3
3060	51F04	YRWTSRLSY	CDR3
3061	51G02	YSWTTRSRY	CDR3
3062	51G04	YNWTSRYRY	CDR3
3063	51G10	YSWKTRFPY	CDR3
3064	51H04	YSWTTRYPY	CDR3
3065	51H05	YEWTNALPY	CDR3
3066	52B01	YSWITRSPY	CDR3
3067	52C04	YSWTTRRQY	CDR3
3069	52D04	YSWITRSPY	CDR3
3070	53A04	YRWEESRQY	CDR3
3071	53A05	YTWTTRLPY	CDR3
3072	53A09	YRWEESRQY	CDR3
3073	53B05	YSWTTRQPY	CDR3
3074	53B06	YVWGTRLPY	CDR3
3075	53C03	YEWTNALPY	CDR3
3076	53C04	YRWEDALTY	CDR3

3077	53H03	YSWTTRYPY	CDR3
3078	53H04	YSWIDSLRY	CDR3
3079	54B05	YSWTTPRAY	CDR3
3080	51X5 CDR3	YSWTTSLPY	CDR3

Table 17. Linker sequences

SEQ ID NO:	**Description**	**Sequence**
3859	Exemplary linker sequence	(GS)n
3860	Exemplary linker sequence	(GGS)n
3861	Exemplary linker sequence	(GGGS)n
3862	Exemplary linker sequence	(GGSG)n
3863	Exemplary linker sequence	(GGSGG)n
3864	Exemplary linker sequence	(GGGGS)n
3865	Exemplary linker sequence	(GGGGG)n
3866	Exemplary linker sequence	(GGG)n
3867	Exemplary linker sequence	(GGGGS)4
3868	Exemplary linker sequence	(GGGGS)3
3869	Exemplary linker sequence	LPETG
3870	6X his Tag	HHHHHH
3871	Exemplary linker sequence	GGGGSGGGS
3872	Exemplary linker sequence	SGGG
3879	Exemplary linker sequence	VVGGGG

Table 18. CD3 sequences

SEQ ID NO:	**Description**	**Sequence**
3081	wt anti-CD3 HC CDR1	GFTFNKYAMN
3082	wt anti-CD3 HC CDR2	RIRSKYNNYATYYADSVK
3083	wt anti-CD3 HC CDR3	HGNFGNSYISYWAY
3084	wt anti-CD3 LC CDR1	GSSTGAVTSGNYPN

3085	wt anti-CD3 LC CDR2	GTKFLAP
3086	wt anti-CD3 LC CDR3	VLWYSNRWV
3087	HC CDR1 variant 1	GNTFNKYAMN
3088	HC CDR1 variant 2	GFEFNKYAMN
3089	HC CDR1 variant 3	GFMFNKYAMN
3090	HC CDR1 variant 4	GFTYNKYAMN
3091	HC CDR1 variant 5	GFTFNNYAMN
3092	HC CDR1 variant 6	GFTFNGYAMN
3093	HC CDR1 variant 7	GFTFNTYAMN
3094	HC CDR1 variant 8	GFTFNEYAMN
3095	HC CDR1 variant 9	GFTFNKYPMN
3096	HC CDR1 variant 10	GFTFNKYAVN
3097	HC CDR1 variant 11	GFTFNKYAIN
3098	HC CDR1 variant 12	GFTFNKYALN
3099	HC CDR2 variant 1	RIRSGYNNYATYYADSVK
3100	HC CDR2 variant 2	RIRSKSNNYATYYADSVK
3101	HC CDR2 variant 3	RIRSKYNKYATYYADSVK
3102	HC CDR2 variant 4	RIRSKYNNYETYYADSVK
3103	HC CDR2 variant 5	RIRSKYNNYATEYADSVK
3104	HC CDR2 variant 6	RIRSKYNNYATYYKDSVK
3105	HC CDR2 variant 7	RIRSKYNNYATYYADEVK
3106	HC CDR2 variant 8	RIRSKYNNYATYYADAVK
3108	HC CDR2 variant 9	RIRSKYNNYATYYADQVK
3109	HC CDR2 variant 10	RIRSKYNNYATYYADDVK
3110	HC CDR3 variant 1	HANFGNSYISYWAY

3111	HC CDR3 variant 2	HTNFGNSYISYWAY
3112	HC CDR3 variant 3	HGNFNNSYISYWAY
3113	HC CDR3 variant 4	HGNFGDSYISYWAY
3114	HC CDR3 variant 5	HGNFGNSHISYWAY
3115	HC CDR3 variant 6	HGNFGNSPISYWAY
3116	HC CDR3 variant 7	HGNFGNSQISYWAY
3117	HC CDR3 variant 8	HGNFGNSLISYWAY
3118	HC CDR3 variant 9	HGNFGNSGISYWAY
3119	HC CDR3 variant 10	HGNFGNSYISYWAT
3120	LC CDR1 variant 1	ASSTGAVTSGNYPN
3121	LC CDR1 variant 2	GESTGAVTSGNYPN
3122	LC CDR1 variant 3	GSYTGAVTSGNYPN
3123	LC CDR1 variant 4	GSSFGAVTSGNYPN
3124	LC CDR1 variant 5	GSSKGAVTSGNYPN
3125	LC CDR1 variant 6	GSSSGAVTSGNYPN
3126	LC CDR1 variant 7	GSSTGYVTSGNYPN
3127	LC CDR1 variant 8	GSSTGAVVSGNYPN
3128	LC CDR1 variant 9	GSSTGAVTDGNYPN
3129	LC CDR1 variant 10	GSSTGAVTKGNYPN
3130	LC CDR1 variant 11	GSSTGAVTHGNYPN
3131	LC CDR1 variant 12	GSSTGAVTVGNYPN
3132	LC CDR1 variant 13	GSSTGAVTSGYYPN
3133	LC CDR2 variant 1	GIKFLAP
3134	LC CDR2 variant 2	GTEFLAP
3135	LC CDR2 variant 3	GTYFLAP

3136	LC CDR2 variant 4	GTSFLAP
3137	LC CDR2 variant 5	GTNFLAP
3138	LC CDR2 variant 6	GTKLLAP
3139	LC CDR2 variant 7	GTKELAP
3140	LC CDR2 variant 8	GTKILAP
3141	LC CDR2 variant 9	GTKMLAP
3142	LC CDR2 variant 10	GTKVLAP
3143	LC CDR2 variant 11	GTKFNAP
3144	LC CDR2 variant 12	GTKFGAP
3145	LC CDR2 variant 13	GTKFLVP
3146	LC CDR3 variant 1	TLWYSNRWV
3147	LC CDR3 variant 2	ALWYSNRWV
3148	LC CDR3 variant 3	VLWYDNRWV
3149	LC CDR3 variant 4	VLWYANRWV
3150	LC CDR3 variant 5	VLWYSNSWV
3151	LC CDR3 variant 6	VLWYSNRWI
3152	LC CDR3 variant 7	VLWYSNRWA
3153	Anti-CD3, clone 2B2	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPG KGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSS GGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTG AVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL
3154	Anti-CD3, clone 9F2	EVQLVESGGGLVQPGGSLKLSCAASGFEFNKYAMNWVRQAP GKGLEWVARIRSKYNKYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSFG AVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYDNRWVFGGGTKLTVL

3155	Anti-CD3, clone 5A2	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSHISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG YVTSGNYPNWVQQKPGQAPRGLIGGTSFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWIFGGGTKLTVL
3156	Anti-CD3, clone 6A2	EVQLVESGGGLVQPGGSLKLSCAASGFMFNKYAMNWVRQAP GKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWATWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSFG AVTSGNYPNWVQQKPGQAPRGLIGGTKLLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNSWVFGGGTKLTVL
3157	Anti-CD3, clone 2D2	EVQLVESGGGLVQPGGSLKLSCAASGFTFNTYAMNWVRQAP GKGLEWVARIRSKYNNYATYYKDSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSPISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVVSGNYPNWVQQKPGQAPRGLIGGTEFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3158	Anti-CD3, clone 3F2	EVQLVESGGGLVQPGGSLKLSCAASGFTYNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADEVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSPISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSKG AVTSGNYPNWVQQKPGQAPRGLIGGTKELAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL
3159	Anti-CD3, clone 1A2	EVQLVESGGGLVQPGGSLKLSCAASGNTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYETYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHTNFGNSYISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTSGYYPNWVQQKPGQAPRGLIGGTYFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3160	Anti-CD3, clone 1C2	EVQLVESGGGLVQPGGSLKLSCAASGFTFNNYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADAVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSQISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTDGNYPNWVQQKPGQAPRGLIGGIKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3161	Anti-CD3, clone 2E4	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAVNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSS GGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGESTG AVTSGNYPNWVQQKPGQAPRGLIGGTKILAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3162	Anti-CD3, clone 10E4	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYPMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKNEDTAVYYCVRHGNFNNSYISYWAYWGQGTLVTVSS GGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTKGNYPNWVQQKPGQAPRGLIGGTKMLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCALWYSNRWVFGGGTKLTVL

3163	Anti-CD3, clone 2H2	EVQLVESGGGLVQPGGSLKLSCAASGFTFNGYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADEVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSPISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVVSGNYPNWVQQKPGQAPRGLIGGTEFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3164	Anti-CD3, clone 2A4	EVQLVESGGGLVQPGGSLKLSCAASGNTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGDSYISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTHGNYPNWVQQKPGQAPRGLIGGTKVLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3165	Anti-CD3, clone 10B2	EVQLVESGGGLVQPGGSLKLSCAASGFTFNNYAMNWVRQAP GKGLEWVARIRSGYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSYT GAVTSGNYPNWVQQKPGQAPRGLIGGTKFNAPGTPARFSGSL LGGKAALTLSGVQPEDEAEYYCVLWYANRWVFGGGTKLTVL
3166	Anti-CD3, clone 1G4	EVQLVESGGGLVQPGGSLKLSCAASGFEFNKYAMNWVRQAP GKGLEWVARIRSKYNNYETYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSLISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSSG AVTSGNYPNWVQQKPGQAPRGLIGGTKFGAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3167	wt anti-CD3	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
3168	Anti-CD3, clone 2G5	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYALNWVRQAPG KGLEWVARIRSKYNNYATEYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSPISYWAYWGQGTLVTVSS GGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTSGNYPNWVQQKPGQAPRGLIGGTNFLAPGTPERFSGSLLG GKAALTLSGVQPEDEAEYYCVLWYSNRWAFGGGTKLTVL
3169	Anti-CD3, clone 8A5	EVQLVESGGGLVQPGGSLKLSCAASGFTFNEYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADDVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHGNFGNSGISYWAYWGQGTLVTVS SGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTG AVTVGNYPNWVQQKPGQAPRGLIGGTEFLAPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL

Table 19. HSA sequences

SEQ ID NO:	**Description**	**Sequence**
3170	wt anti-HSA CDR1	GFTFSSFGMS
3171	wt anti-HSA CDR2	SISGSGSDTLYADSVK

3172	wt anti-HSACDR3	GGSLSR
3173	CDR1 variant 1	GFTFSRFGMS
3174	CDR1 variant 2	GFTFSKFGMS
3175	CDR1 variant 3	GFTYSSFGMS
3176	CDR2 variant 1	SISGSGADTLYADSLK
3177	CDR2 variant 2	SISGSGTDTLYADSVK
3178	CDR2 variant 3	SISGSGRDTLYADSVK
3179	CDR2 variant 4	SISGSGSDTLYAESVK
3180	CDR2 variant 5	SISGSGTDTLYAESVK
3181	CDR2 variant 6	SISGSGRDTLYAESVK
3182	CDR3 variant 1	GGSLSK
3183	CDR3 variant 2	GGSLSV
3184	wt anti-HSA	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGL EWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSS
3185	Anti-HSA sdAb clone 6C	EVQLVESGGGLVQPGNSLRLSCAASGFTFSRFGMSWVRQAPGKGL EWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSS
3186	Anti-HSA sdAb clone 7A	EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGADTLYADSLKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSKSSQGTLVTVSS
3187	Anti-HSA sdAb clone 7G	EVQLVESGGGLVQPGNSLRLSCAASGFTYSSFGMSWVRQAPGKGL EWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSKSSQGTLVTVSS
3188	Anti-HSA sdAb clone 8H	EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGTDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSS
3189	Anti-HSA sdAb clone 9A	EVQLVESGGGLVQPGNSLRLSCAASGFTFSRFGMSWVRQAPGKGL EWVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSKSSQGTLVTVSS

3190	Anti-HSA sdAb clone 10G	EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSS
3191	Anti-HSA sdAb clone 6CE	EVQLVESGGGLVQPGNSLRLSCAASGFTFSRFGMSWVRQAPGKGL EWVSSISGSGSDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSS
3192	Anti-HSA sdAb clone 8HE	EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGTDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSS
3193	Anti-HSA sdAb clone 10GE	EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYAESVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSS

Table 20. Antigen sequences

SEQ ID NO:	**Description**	**Sequence**
3201	Human BCMA	MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSV KGTNAILWTCLGLSLIISLAVFVLMFLLRKINSEPLKDEFKNTGSGLLGM ANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAME EGATILVTTKTNDYCKSLPAALSATEIEKSISAR
3202	Murine BCMA	MAQQCFHSEYFDSLLHACKPCHLRCSNPPATCQPYCDPSVTSSVKGTYT VLWIFLGLTLVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSAQLDKA DTELTRIRAGDDRIFPRSLEYTVEECTCEDCVKSKPKGDSDHFFPLPAME EGATILVTTKTGDYGKSSVPTALQSVMGMEKPTHTR
3203	Cynomolgus BCMA	MLQMARQCSQNEYFDSLLHDCKPCQLRCSSTPPLTCQRYCNASMTNSV KGMNAILWTCLGLSLIISLAVFVLTFLLRKMSSEPLKDEFKNTGSGLLGM ANIDLEKGRTGDEIVLPRGLEYTVEECTCEDCIKNKPKVDSDHCFPLPAM EEGATILVTTKTNDYCNSLSAALSVTEIEKSISAR
3204	Mesothelin protein sequence	MALPTARPLLGSCGTPALGSLLFLLFSLGWVQPSRTLAGETGQEAAPLD GVLANPPNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTE QLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANV DLLPRGAPERQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFV AESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTM DALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRRE VEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFT YEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLET LKALLEVNKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTA FYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFQ NMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTDAVLP LTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGG IPNGYLVLDLSMQEALSGTPCLLGPGPVLTVLALLLASTLA

3205	EFGR-Human	MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFL SLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERI PLENLQIIRGNMYYENSYALAVLSNYDANKTGLKELPMRNLQGQKCDP SCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCT GPRESDCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGA TCVKKCPRNYVVTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKV CNGIGIGEFKDSLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLD PQELDILKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQHGQFSLA VVSLNITSLGLRSLKEISDGDVIISGNKNLCYANTINWKKLFGTSGQKTKI ISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDK CNLLEGEPREFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDG PHCVKTCPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEG CPTNGPKIPSIATGMVGALLLLLVVALGIGLFMRRRHIVRKRTLRRLLQE RELVEPLTPSGEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEG EKVKIPVAIKELREATSPKANKEILDEAYVMASVDNPHVCRLLGICLTST VQLITQLMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRL VHRDLAARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWM ALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGER LPQPPICTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQ GDERMHLPSPTDSNFYRALMDEEDMDDVVDADEYLIPQQGFFSSPSTSR TPLLSSLSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSID DTFLPVPGEWLVWKQSCSSTSSTHSAAASLQCPSQVLPPASPEGETVADL QTQ
3206	EGFR-Mouse	MRPSGTARTTLLVLLTALCAAGGALEEKKVCQGTSNRLTQLGTFEDHFL SLQRMYNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERI PLENLQIIRGNALYENTYALAILSNYGTNRTGLRELPMRNLQEILIGAVRF SNNPILCNMDTIQWRDIVQNVFMSNMSMDLQSHPSSCPKCDPSCPNGSC WGGGEENCQKLTKIICAQQCSHRCRGRSPSDCCHNQCAAGCTGPRESDC LVCQKFQDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKKCP RNYVVTDHGSCVRACGPDYYEVEEDGIRKCKKCDGPCRKVCNGIGIGEF KDTLSINATNIKHFKYCTAISGDLHILPVAFKGDSFTRTPPLDPRELEILKT VKEITGFLLIQAWPDNWTDLHAFENLEIIRGRTKQHGQFSLAVVGLNITS LGLRSLKEISDGDVIISGNRNLCYANTINWKKLFGTPNQKTKIMNNRAEK DCKAVNHVCNPLCSSEGCWGPEPRDCVSCQNVSRGRECVEKCNILEGEP REFVENSECIQCHPECLPQAMNITCTGRGPDNCIQCAHYIDGPHCVKTCP AGIMGENNTLVWKYADANNVCHLCHANCTYGCAGPGLQGCEVWPSGP KIPSIATGIVGGLLFIVVVALGIGLFMRRRHIVRKRTLRRLLQERELVEPLT PSGEAPNQAHLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIPVA IKELREATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLM PYGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRLVHRDLAA RNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESILHR IYTHQSDVWSYGVTVWELMTFGSKPYDGIPASDISSILEKGERLPQPPICT IDVYMIMVKCWMIDADSRPKFRELILEFSKMARDPQRYLVIQGDERMHL PSPTDSNFYRALMDEEDMEDVVDADEYLIPQQGFFNSPSTSRTPLLSSLS ATSNNSTVACINRNGSCRVKEDAFLQRYSSDPTGAVTEDNIDDAFLPVPE YVNQSVPKRPAGSVQNPVYHNQPLHPAPGRDLHYQNPHSNAVGNPEYL NTAQPTCLSSGFNSPALWIQKGSHQMSLDNPDYQQDFFPKETKPNGIFK GPTAENAEYLRVAPPSSEFIGA
3207	EGFR-Cyno	MRPSGTAGAALLALLAALCPASRALEEKKVCQGTSNKLTQLGTFEDHFL SLQRMFNNCEVVLGNLEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERI PLENLQIIRGNMYYENSYALAVLSNYDANKTGLKELPMRNLQEILHGAV RFSNNPALCNVESIQWRDIVSSEFLSNMSMDFQNHLGSCQKCDPSCPNG

		SCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGCTGPRES DCLVCRKFRDEATCKDTCPPLMLYNPTTYQMDVNPEGKYSFGATCVKK CPRNYVVTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGI GEFKDTLSINATNIKHFKNCTSISGDLHILPVAFRGDSFTHTPPLDPQELDI LKTVKEITGFLLIQAWPENRTDLHAFENLEIIRGRTKQHGQFSLAVVSLNI TSLGLRSLKEISDGDVIISGNKNLCYANTINWKKLFGTSSQKTKIISNRGE NSCKATGQVCHALCSPEGCWGPEPRDCVSCQNVSRGRECVDKCNILEG EPREFVENSECIQCHPECLPQVMNITCTGRGPDNCIQCAHYIDGPHCVKT CPAGVMGENNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCARNGP KIPSIATGMVGALLLLLVVALGIGLFMRRRHIVRKRTLRRLLQERELVEP LTPSGEAPNQALLRILKETEFKKIKVLGSGAFGTVYKGLWIPEGEKVKIP VAIKELREATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQ LMPFGCLLDYVREHKDNIGSQYLLNWCVQIAKGMNYLEDRRLVHRDL AARNVLVKTPQHVKITDFGLAKLLGAEEKEYHAEGGKVPIKWMALESIL HRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPI CTIDVYMIMVKCWMIDADSRPKFRELIIEFSKMARDPQRYLVIQGDERM HLPSPTDSNFYRALMDEEDMDDVVDADEYLIPQQGFFSSPSTSRTPLLSS LSATSNNSTVACIDRNGLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLP VPEYINQSVPKRPAGSVQNPVYHNQPLNPAPSRDPHYQDPHSTAVGNPE YLNTVQPTCVNSTFDSPAHWAQKGSHQISLDNPDYQQDFFPKEAKPNGI FKGSTAENAEYLRVAPQSSEFIGA
3208	Human EpCAM	METKHLGRGGAGRAGPHLWRGPRPNCSAGAGGGEPTHSPNSRAVTHQ RAPAARECVCENYKLAVNCFVNNNRQCQCTSVGAQNTVICSKLAAKCL VMKAEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTS MCWCVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDSKSLR TALQKEITTRYQLDPKFITSILYENNVITIDLVQNSSQKTQNDVDIADVAY YFEKDVKGESLFHSKKMDLTVNGEQLDLDPGQTLIYYVDEKAPEFSMQ GLKAGVIAVIVVVVIAVVAGIVVLVISRKKRMAKYEKAEIKEMGEMHRE LNA
3209	Cynomolgus EpCAM	CVCENYKLAVNCFLNDNGQCQCTSIGAQNTVLCSKLAAKCLVMKAEM NGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSTCWCVN TAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALEEAI KTRYQLDPKFITNILYEDNVITIDLVQNSSQKTQNDVDIADVAYYFEKDV KGESLFHSKKMDLRVNGEQLDLDPGQTLIYYVDEKAPEFSMQGLKAGV IAVIVVVVIAIVAGIVVLVISRKKRMAKYEKAEIKEMGEIHRELNA
3210	Mouse EpCAM	MAGPQALAFGLLLAVVTATLAAAQRDCVCDNYKLATSCSLNEYGECQ CTSYGTQNTVICSKLASKCLAMKAEMTHSKSGRRIKPEGAIQNNDGLYD PDCDEQGLFKAKQCNGTATCWCVNTAGVRRTDKDTEITCSERVRTYWII IELKHKERESPYDHQSLQTALQEAFTSRYKLNQKFIKNIMYENNVITIDL MQNSSQKTQDDVDIADVAYYFEKDVKGESLFHSSKSMDLRVNGEPLDL DPGQTLIYYVDEKAPEFSMQGLTAGIIAVIVVVSLAVIAGIVVLVISTRKK SAKYEKAEIKEMGEIHRELNA
3211	Human EpCAM	MAPPQVLAFGLLLAAATATFAAAQEECVCENYKLAVNCFVNNNRQCQ CTSVGAQNTVICSKLAAKCLVMKAEMNGSKLGRRAKPEGALQNNDGL YDPDCDESGLFKAKQCNGTSMCWCVNTAGVRRTDKDTEITCSERVRTY WIIIELKHKAREKPYDSKSLRTALQKEITTRYQLDPKFITSILYENNVITID LVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKMDLTVNGEQLDL DPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAVVAGIVVLVISRKK RMAKYEKAEIKEMGEMHRELNA

3212	Human EpCAM extracellular domain sequence	QEECVCENYKLAVNCFVNNNRQCQCTSVGAQNTVICSKLAAKCLVMK AEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSMCW CVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDSKSLRTALQ KEITTRYQLDPKFITSILYENNVITIDLVQNSSQKTQNDVDIADVAYYFEK DVKGESLFHSKKMDLTVNGEQLDLDPGQTLIYYVDEKAPEFSMQGLK
3213	Cynomolgus EpCAM extracellular domain sequence	QKECVCENYKLAVNCFLNDNGQCQCTSIGAQNTVLCSKLAAKCLVMK AEMNGSKLGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSTCW CVNTAGVRRTDKDTEITCSERVRTYWIIIELKHKAREKPYDVQSLRTALE EAIKTRYQLDPKFITNILYEDNVITIDLVQNSSQKTQNDVDIADVAYYFE KDVKGESLFHSKKMDLRVNGEQLDLDPGQTLIYYVDEKAPEFSMQGLK
3214	Mouse EpCAM extracellular domain sequence	QRDCVCDNYKLATSCSLNEYGECQCTSYGTQNTVICSKLASKCLAMKA EMTHSKSGRRIKPEGAIQNNDGLYDPDCDEQGLFKAKQCNGTATCWCV NTAGVRRTDKDTEITCSERVRTYWIIIELKHKERESPYDHQSLQTALQEA FTSRYKLNQKFIKNIMYENNVITIDLMQNSSQKTQDDVDIADVAYYFEK DVKGESLFHSSKSMDLRVNGEPLDLDPGQTLIYYVDEKAPEFSMQGLT
3215	FLT3 protein UniProt ID: P36888	MPALARDGGQLPLLVVFSAMIFGTITNQDLPVIKCVLINHKNNDSSVGKS SSYPMVSESPEDLGCALRPQSSGTVYEAAAVEVDVSASITLQVLVDAPG NISCLWVFKHSSLNCQPHFDLQNRGVVSMVILKMTETQAGEYLLFIQSE ATNYTILFTVSIRNTLLYTLRRPYFRKMENQDALVCISESVPEPIVEWVLC DSQGESCKEESPAVVKKEEKVLHELFGTDIRCCARNELGRECTRLFTIDL NQTPQTTLPQLFLKVGEPLWIRCKAVHVNHGFGLTWELENKALEEGNY FEMSTYSTNRTMIRILFAFVSSVARNDTGYYTCSSSKHPSQSALVTIVEK GFINATNSSEDYEIDQYEEFCFSVRFKAYPQIRCTWTFSRKSFPCEQKGLD NGYSISKFCNHKHQPGEYIFHAENDDAQFTKMFTLNIRRKPQVLAEASA SQASCFSDGYPLPSWTWKKCSDKSPNCTEEITEGVWNRKANRKVFGQW VSSSTLNMSEAIKGFLVKCCAYNSLGTSCETILLNSPGPFPFIQDNISFYAT IGVCLLFIVVLTLLICHKYKKQFRYESQLQMVQVTGSSDNEYFYVDFRE YEYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSIQVAVK MLKEKADSSEREALMSELKMMTQLGSHENIVNLLGACTLSGPIYLIFEY CCYGDLLNYLRSKREKFHRTWTEIFKEHNFSFYPTFQSHPNSSMPGSREV QIHPDSDQISGLHGNSFHSEDEIEYENQKRLEEEEDLNVLTFEDLLCFAYQ VAKGMEFLEFKSCVHRDLAARNVLVTHGKVVKICDFGLARDIMSDSNY VVRGNARLPVKWMAPESLFEGIYTIKSDVWSYGILLWEIFSLGVNPYPGI PVDANFYKLIQNGFKMDQPFYATEEIYIIMQSCWAFDSRKRPSFPNLTSF LGCQLADAEEAMYQNVDGRVSECPHTYQNRRPFSREMDLGLLSPQAQV EDS

3216	DLL3 Protein UniProtKB Accession Q9NYJ7	MVSPRMSGLLSQTVILALIFLPQTRPAGVFELQIHSFGPGPGPGAPRSPCS ARLPCRLFF RVCLKPGLSEEAAESPCALGAALSARGPVYTEQPGAPAPDLPLPDGLLQ VPFRDAWPGTF SFIIETWREELGDQIGGPAWSLLARVAGRRRLAAGGPWARDIQRAGAW ELRFSYRARCEP PAVGTACTRLCRPRSAPSRCGPGLRPCAPLEDECEAPLVCRAGCSPEHGF CEQPGECRCL EGWTGPLCTVPVSTSSCLSPRGPSSATTGCLVPGPGPCDGNPCANGGSCS ETPRSFECTC PRGFYGLRCEVSGVTCADGPCFNGGLCVGGADPDSAYICHCPPGFQGSN CEKRVDRCSLQ PCRNGGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGRACANGGTCV EGGGAHRCSCALG FGGRDCRERADPCAARPCAHGGRCYAHFSGLVCACAPGYMGARCEFPV HPDGASALPAAP PGLRPGDPQRYLLPPALGLLVAAGVAGAALLLVHVRRRGHSQDAGSRL LAGTPEPSVHAL PDALNNLRTQEGSGDGPSSSVDWNRPEDVDPQGIYVISAPSIYAREVATP LFPPLHTGRA GQRQHLLFPYPSSILSVK
3217	DLL3 Protein Sequence	RSPCSARLPCRLFFRVCLKPGLSEEAAESPCALGAALSARGPVYTEQPGA PAPDLPLPDGLLQVPFRDAWPGTFSFIIETWREELGDQIGGPAWSLLARV AGRRRLAAGGPWARDIQRAGAWELRFSYRARCEPPAVGTACTRLCRPR SAPSRCGPGLRPCAPLEDECEAPLVCRAGCSPEHGFCEQPGECRCLEGW TGPLCTVPVSTSSCLSPRGPSSATTGCLVPGPGPCDGNPCANGGSCSETPR SFECTCPRGFYGLRCEVSGVTCADGPCFNGGLCVGGADPDSAYICHCPP GFQGSNCEKRVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCEHD LDDCAGRACANGGTCVEGGGAHRCSCALGFGGRDCRERADPCAARPC AHGGRCYAHFSGLVCACAPGYMGARCEFPVHPDGASALPAAPPGLRPG DPQRYL
3509	NP_058637.1 delta-like protein 3 isoform 1 precursor [Homo sapiens]	MVSPRMSGLLSQTVILALIFLPQTRPAGVFELQIHSFGPGPGPGAPRSPCS ARLPCRLFFRVCLKPGLSE EAAESPCALGAALSARGPVYTEQPGAPAPDLPLPDGLLQVPFRDAWPGT FSFIIETWREELGDQIGGPAW SLLARVAGRRRLAAGGPWARDIQRAGAWELRFSYRARCEPPAVGTACT RLCRPRSAPSRCGPGLRPCAPL EDECEAPLVCRAGCSPEHGFCEQPGECRCLEGWTGPLCTVPVSTSSCLSP RGPSSATTGCLVPGPGPCDG NPCANGGSCSETPRSFECTCPRGFYGLRCEVSGVTCADGPCFNGGLCVG GADPDSAYICHCPPGFQGSNC EKRVDRCSLQPCRNGGLCLDLGHALRCRCRAGFAGPRCEHDLDDCAGR ACANGGTCVEGGGAHRCSCALG FGGRDCRERADPCAARPCAHGGRCYAHFSGLVCACAPGYMGARCEFPV HPDGASALPAAPPGLRPGDPQR YLLPPALGLLVAAGVAGAALLLVHVRRRGHSQDAGSRLLAGTPEPSVH ALPDALNNLRTQEGSGDGPSSS VDWNRPEDVDPQGIYVISAPSIYAREVATPLFPPLHTGRAGQRQHLLFPY PSSILSVK

Table 21. TriTAC XR sequences

SEQ ID NO:	Description	AA Sequence
3600	QDGNEE:L001:aPSMA:aALB:aCD3	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH
3601	QDGNEE:NCLV:aPSMA:aALB:aCD3	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTL SCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH
3602	LDGNEE:NCLV:aPSMA:aALB:aCD3	LDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLS CAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH
3603	PDGNEE:NCLV:aPSMA:aALB:aCD3	PDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLS CAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH

3604	DDGNEE:NCLV:aPSMA:aALB:aCD3	DDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3605	EDGNEE:NCLV:aPSMA:aALB:aCD3	EDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3606	QEGNEE:NCLV:aPSMA:aALB:aCD3	QEGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3607	QDANEE:NCLV:aPSMA:aALB:aCD3	QDANEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH

3608	QDSNEE:NCLV:aPSMA:aALB:aCD3	QDSNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3609	stub:aPSMA:aALB:aCD3	SGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3610	aAlb-MASK027::NCLV:aPSMA:aALB:aCD3	EVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQGGGGGLDGNEEPGGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSGGGGSGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKTTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3611	stub:CD19-TAC	VVGGGGENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFS

		GSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL HHHHHH*
3612	stub:FLT3-H107-TAC	VVGGGGEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQ APGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQ APGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNS LRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIR SKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVY YCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCT LWYSNRWVFGGGTKLTVLHHHHHH*
3613	stub:FLT3-H19C-TAC	VVGGGGEVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQ APGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSL RAEDTAVYYCYYRGFWGQGTLVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG GSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYIS YWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGT KLTVLHHHHHH*
3614	NCLV CD33-ACT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSQVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAP GQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEIRN LGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSG GGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSP QPEDSATYYCQQSAHFPITFGQGTRLEIKHHHHHHH*

3615	NCLV CD33-ATC	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSQVQLVQSGAEVKKPGESVKVSCKASGYTFTNY GMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTS TSTAYMEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQ SVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGS GTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKGGGGSGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH*
3616	NCLV CD33-CAT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSQVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPG QGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEIRNL GGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGG GGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSL AWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQP EDSATYYCQQSAHFPITFGQGTRLEIKHHHHHH*
3617	NCLV CD33-CTA	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSQVQLVQSGAEVKKPGESVKVSCKASGYTFT NYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTT DTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQG TSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCK SSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSG SGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKGGGG SGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQA PGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*

3618	NCLV CD33-TAC	QDGNEEGGGGSGGGGSGGGGSGGGGQVQLVQSGAEVKKPGESVKV SCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADK FQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYYV YFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSL GERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRE SGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTR LEIKGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFG MSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTT LYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGS EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGL EWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLK TEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGG GSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWV QQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH*
3619	NCLV CD33-TCA	QDGNEEGGGGSGGGGSGGGGSGGGQVQLVQSGAEVKKPGESVKV SCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYADK FQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYYV YFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSL GERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRE SGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTR LEIKGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPG KGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3620	stub:CD33-ACT	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CTLWYSNRWVFGGGTKLTVLGGGGSGGGSQVQLVQSGAEVKKPG ESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEP TYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWS DGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPD SLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLS WASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPIT FGQGTRLEIKHHHHHH*
3621	stub:CD33-ATC	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSQVQLV QSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWM GWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAV YYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGG SDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQK

		PGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYY CQQSAHFPITFGQGTRLEIKGGGGSGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATY YADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK FLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWV FGGGTKLTVLHHHHHH*
3622	stub:CD33-CAT	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEV QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSQVQLVQSGAEVKK PGESVKVSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTG EPTYADKFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWS WSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQS PDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLL LSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHF PITFGQGTRLEIKHHHHHH*
3623	stub:CD33-CTA	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSQV QLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPGQGLE WMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEIRNLGGDD TAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGGGGSG GGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSLAWY QQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQPEDS ATYYCQQSAHFPITFGQGTRLEIKGGGGSGGGSEVQLVESGGGLVQ PGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL YADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVS SQGTLVTVSSHHHHHH*
3624	stub:CD33-TAC	VVGGGGQVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWV KQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYM EIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGG GGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSS TNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTL TIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKGGGGSGGGSEVQL VESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVS SISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYY CTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGS LKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATY YADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTK

		FLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWV FGGGTKLTVLHHHHHH*
3625	stub:CD33-TCA	VVGGGGQVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWV KQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYM EIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGG GGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSS TNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTL TIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL YADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVS SQGTLVTVSSHHHHHH*
3626	NCLV CD19-ACT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQA PRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQ GSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKP TQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDK RYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWS YYFDYWGQGTTVTVSSHHHHHH*
3627	NCLV CD19-ATC	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSENVLTQSPATLSVTPGEKATITCRASQSVSYMH WYQQKPGQAPRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEA EDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVT LRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEW LAHIWWDDDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTA TYYCARMELWSYYFDYWGQGTTVTVSSGGGGSGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRS KYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQ TVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL WYSNRWVFGGGTKLTVLHHHHHH*

3628	NCLV CD19-CAT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAP RLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQG SVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKPT QTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDKR YNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWS YYFDYWGQGTTVTVSSHHHHHH*
3629	NCLV CD19-CTA	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSENVLTQSPATLSVTPGEKATITCRASQSVSY MHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSL EAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQ VTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKAL EWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVD TATYYCARMELWSYYFDYWGQGTTVTVSSGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYC TIGGSLSVSSQGTLVTVSSHHHHHH*
3630	NCLV CD19-TAC	QDGNEEGGGGSGGGGSGGGGSGGGENVLTQSPATLSVTPGEKATI TCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGS GTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSG GGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVG WIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFL TMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSSGGGGS GGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAP GKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLR PEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSK YNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLW YSNRWVFGGGTKLTVLHHHHHH*
3631	NCLV CD19-TCA	QDGNEEGGGGSGGGGSGGGGSGGGENVLTQSPATLSVTPGEKATI TCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGS GTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSG GGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVG WIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFL TMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSSGGGGS GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP

		GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGG SGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYC TIGGSLSVSSQGTLVTVSSHHHHHH*
3632	stub:CD19-ACT	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CTLWYSNRWVFGGGTKLTVLGGGGSGGGSENVLTQSPATLSVTPG EKATITCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFS GSGSGTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGG GGSGGGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSG MGVGWIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSK NQVFLTMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSS HHHHHH*
3633	stub:CD19-ATC	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSENVLT QSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAPRLLIYDAS NRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQGSVYPFTFG QGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKPTQTLTLTCT FSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDKRYNPALKS RLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWSYYFDYWG QGTTVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGF TFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFT ISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW GQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTL TCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFS GSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL HHHHHH*
3634	stub:CD19-CAT	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEV QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSENVLTQSPATLSVT PGEKATITCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPS RFSGSGSGTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIK GGGGSGGGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLST SGMGVGWIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDT

		SKNQVFLTMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTV SSHHHHHH*
3635	stub:CD19-CTA	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEN VLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAPRLLIY DASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQGSVYPF TFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKPTQTLTL TCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDKRYNPAL KSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWSYYFDY WGQGTTVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTIS RDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHH HHHH*
3636	stub:CD19-TCA	VVGGGGENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKP GQAPRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYY CFQGSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPAL VKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWD DDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARM ELWSYYFDYWGQGTTVTVSSGGGGSGGGSEVQLVESGGGLVQPG GSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYAT YYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANF GNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEP SLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRW VFGGGTKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTIS RDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHH HHHH*
3637	NCLV FLT3-H107-ACT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQAPG KEREFVAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSHHHHHH*

3638	NCLV FLT3-H107-ATC	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYA MGWFRQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVT VSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLV TVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTG AVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH*
3639	NCLV FLT3-H107-CAT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQAPGK EREFVAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSHHHHHH*
3640	NCLV FLT3-H107-CTA	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLLESGGGLVQPGGSLTLSCAASGRTFSS YAMGWFRQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSK NTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTL VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKF GMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3641	NCLV FLT3-H107-TAC	QDGNEEGGGGSGGGGSGGGGSGGGEVQLLESGGGLVQPGGSLTLS CAASGRTFSSYAMGWFRQAPGKEREFVAAISWSGSNTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH *

3642	NCLV FLT3-H107-TCA	QDGNEEGGGGSGGGGSGGGGSGGGEVQLLESGGGLVQPGGSLTLS CAASGRTFSSYAMGWFRQAPGKEREFVAAISWSGSNTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3643	stub:FLT3-H107-ACT	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CTLWYSNRWVFGGGTKLTVLGGGGSGGGSEVQLLESGGGLVQPG GSLTLSCAASGRTFSSYAMGWFRQAPGKEREFVAAISWSGSNTYY ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGSTRVV VTTTPVVKYWGQGTLVTVSSHHHHHH*
3644	stub:FLT3-H107-ATC	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLL ESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQAPGKEREFVAA ISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CAAGGSTRVVVTTTPVVKYWGQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CTLWYSNRWVFGGGTKLTVLHHHHHH*
3645	stub:FLT3-H107-CAT	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEV QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLLESGGGLVQP GGSLTLSCAASGRTFSSYAMGWFRQAPGKEREFVAAISWSGSNTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGSTRV VVTTTPVVKYWGQGTLVTVSSHHHHHH*
3646	stub:FLT3-H107-CTA	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS

		GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEV QLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQAPGKEREF VAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3647	stub:FLT3-H107-TCA	VVGGGGEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQ APGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMN SLRAEDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQ APGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGG GGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG NYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTL SGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEVQ LVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3648	NCLV FLT3-H19C-ACT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSEVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGK QRELVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAED TAVYYCYYRGFWGQGTLVTVSSHHHHHH*
3649	NCLV FLT3-H19C-ATC	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLTLSCAASGSTFSINH FSWYRQAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNTAY LQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSSGGGGSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH*
3650	NCLV FLT3-H19C-CAT	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK

		TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGKQ RELVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAEDT AVYYCYYRGFWGQGTLVTVSSHHHHHH*
3651	NCLV FLT3-H19C-CTA	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGGSLTLSCAASGSTFSI NHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNT AYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3652	NCLV FLT3-H19C-TAC	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTL SCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRF TISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW VRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH*
3653	NCLV FLT3-H19C-TCA	QDGNEEGGGGSGGGGSGGGGSGGGEVQLVESGGGLVQPGGSLTL SCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRF TISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTV SSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGG SEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPED TAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3654	stub:FLT3-H19C-ACT	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTA VYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CTLWYSNRWVFGGGTKLTVLGGGGSGGGSEVQLVESGGGLVQPG GSLTLSCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVES VKGRFTISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTL VTVSSHHHHHH*

3655	stub:FLT3-H19C-ATC	VVGGGGEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVR QAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGKQRELVAFIS SDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAEDTAVYYCYY RGFWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSC AASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGT PARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH*
3656	stub:FLT3-H19C-CAT	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEV QLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQP GGSLTLSCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVE SVKGRFTISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGT LVTVSSHHHHHH*
3657	stub:FLT3-H19C-CTA	VVGGGGEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSG GGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTS GNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEV QLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGKQRELV AFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAEDTAVYY CYYRGFWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGT LVTVSSHHHHHH*
3658	stub:FLT3-H19C-TCA	VVGGGGEVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQ APGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSL RAEDTAVYYCYYRGFWGQGTLVTVSSGGGGSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSK YNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLW YSNRWVFGGGTKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSV KGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTL VTVSSHHHHHH*

3659	QEGNEE:NCLV:aMSLN:aALB:aCD3	QEGNEEGGGGSGGGGSGGGGSGGGGQVQLVESGGGVVQAGGSLTLSCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3660	QDANEE:NCLV:aMSLN:aALB:aCD3	QDANEEGGGGSGGGGSGGGGSGGGGQVQLVESGGGVVQAGGSLTLSCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3661	QDGNEE:NCLV:aMSLN:aALB:aCD3	QDGNEEGGGGSGGGGSGGGGSGGGGQVQLVESGGGVVQAGGSLTLSCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3662	stub:aMSLN:aALB:aCD3	SGGGQVQLVESGGGVVQAGGSLTLSCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH

3824	QDGNEE:L001:aPSMA:aALB:aCD3	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3825	LDGNEE:L001:aPSMA:aALB:aCD3	LDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3826	PDGNEE:L001:aPSMA:aALB:aCD3	PDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3827	DDGNEE:L001:aPSMA:aALB:aCD3	DDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH

3828	EDGNEE:L001:aPSMA:aALB:aCD3	EDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH
3829	QEGNEE:L001:aPSMA:aALB:aCD3	QEGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH
3830	QDANEE:L001:aPSMA:aALB:aCD3	QDANEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH
3831	QDSNEE:L001:aPSMA:aALB:aCD3	QDSNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTLS CAASRFMISEYHMHWVRQAPGKGLEWVSTINPAGTTDYAESVKG RFTISRDNAKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMS WVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH

3832	L001 CD33-ACT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSQVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAP GQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEIRN LGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSG GGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKN SLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSP QPEDSATYYCQQSAHFPITFGQGTRLEIKHHHHHH*
3833	L001 CD33-ATC	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSQVQLVQSGAEVKKPGESVKVSCKASGYTFTNY GMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTTDTS TSTAYMEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQGTSV TVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQ SVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGS GTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKGGGGSGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH*
3834	L001 CD33-CAT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSQVQLVQSGAEVKKPGESVKVSCKASGYTFTNYGMNWVKQAPG QGLEWMGWINTYTGEPTYADKFQGRVTMTTDTSTSTAYMEIRNL GGDDTAVYYCARWSWSDGYYVYFDYWGQGTSVTVSSGGGGSGG GGSGGGGSDIVMTQSPDSLTVSLGERTTINCKSSQSVLDSSTNKNSL AWYQQKPGQPPKLLLSWASTRESGIPDRFSGSGSGTDFTLTIDSPQP EDSATYYCQQSAHFPITFGQGTRLEIKHHHHHH*

3835	L001 CD33-CTA	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSQVQLVQSGAEVKKPGESVKVSCKASGYTFT NYGMNWVKQAPGQGLEWMGWINTYTGEPTYADKFQGRVTMTT DTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYYVYFDYWGQG TSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVSLGERTTINCK SSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTRESGIPDRFSG SGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGTRLEIKGGGG SGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQA PGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3836	L001 CD33-TAC	QDGNEEGGGGKPLGLQARVVGGGGQVQLVQSGAEVKKPGESVK VSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYAD KFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYY VYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVS LGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTR ESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGT RLEIKGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKF GMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNL KTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGG GGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH*
3837	L001 CD33-TCA	QDGNEEGGGGKPLGLQARVVGGGGQVQLVQSGAEVKKPGESVK VSCKASGYTFTNYGMNWVKQAPGQGLEWMGWINTYTGEPTYAD KFQGRVTMTTDTSTSTAYMEIRNLGGDDTAVYYCARWSWSDGYY VYFDYWGQGTSVTVSSGGGGSGGGGSGGGGSDIVMTQSPDSLTVS LGERTTINCKSSQSVLDSSTNKNSLAWYQQKPGQPPKLLLSWASTR ESGIPDRFSGSGSGTDFTLTIDSPQPEDSATYYCQQSAHFPITFGQGT RLEIKGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPG KGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3838	L001 CD19-ACT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST

		GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQA PRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQ GSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKP TQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDK RYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWS YYFDYWGQGTTVTVSSHHHHHH*
3839	L001 CD19-ATC	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSENVLTQSPATLSVTPGEKATITCRASQSVSYMH WYQQKPGQAPRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEA EDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVT LRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEW LAHIWWDDDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTA TYYCARMELWSYYFDYWGQGTTVTVSSGGGGSGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRS KYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYY CVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQ TVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTL WYSNRWVFGGGTKLTVLHHHHHH*
3840	L001 CD19-CAT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAP RLLIYDASNRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQG SVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQVTLRESGPALVKPT QTLTLTCTFSGFSLSTSGMGVGWIRQPPGKALEWLAHIWWDDDKR YNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCARMELWS YYFDYWGQGTTVTVSSHHHHHH*
3841	L001 CD19-CTA	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSENVLTQSPATLSVTPGEKATITCRASQSVSY MHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGSGTDHTLTISSL EAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSGGGGSGGGGSQ VTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGKAL EWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVD TATYYCARMELWSYYFDYWGQGTTVTVSSGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI

		SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYC TIGGSLSVSSQGTLVTVSSHHHHHH*
3842	L001 CD19-TAC	QDGNEEGGGGKPLGLQARVVGGGGENVLTQSPATLSVTPGEKATI TCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGS GTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSG GGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVG WIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFL TMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSSGGGGS GGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAP GKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLR PEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSK YNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLW YSNRWVFGGGTKLTVLHHHHHH*
3843	L001 CD19-TCA	QDGNEEGGGGKPLGLQARVVGGGGENVLTQSPATLSVTPGEKATI TCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGS GTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSG GGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVG WIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFL TMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSSGGGGS GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGG SGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYC TIGGSLSVSSQGTLVTVSSHHHHHH*
3844	L001 FLT3-H107-ACT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQAPG KEREFVAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMNSLRA EDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSHHHHHH*

3845	L001 FLT3-H107-ATC	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYA MGWFRQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSKNT LYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVT VSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLV TVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTG AVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH*
3846	L001 FLT3-H107-CAT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWFRQAPGK EREFVAAISWSGSNTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCAAGGSTRVVVTTTPVVKYWGQGTLVTVSSHHHHHH*
3847	L001 FLT3-H107-CTA	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLLESGGGLVQPGGSLTLSCAASGRTFSS YAMGWFRQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDNSK NTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTPVVKYWGQGTL VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKF GMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKT TLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3848	L001 FLT3-H107-TAC	QDGNEEGGGGKPLGLQARVVGGGGEVQLLESGGGLVQPGGSLTL SCAASGRTFSSYAMGWFRQAPGKEREFVAAISWSGSNTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH *
3849	L001 FLT3-H107-TCA	QDGNEEGGGGKPLGLQARVVGGGGEVQLLESGGGLVQPGGSLTL SCAASGRTFSSYAMGWFRQAPGKEREFVAAISWSGSNTYYADSVK GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP

		VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3850	L001 FLT3-H19C-ACT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASST GAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSG GGSEVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGK QRELVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAED TAVYYCYYRGFWGQGTLVTVSSHHHHHH*
3851	L001 FLT3-H19C-ATC	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVK GRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGGSLTLSCAASGSTFSINH FSWYRQAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNTAY LQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSSGGGGSGGGSEVQ LVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH*
3852	L001 FLT3-H19C-CAT	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGKQ RELVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAEDT AVYYCYYRGFWGQGTLVTVSSHHHHHH*
3853	L001 FLT3-H19C-CTA	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLKL SCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVS PGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVP GTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGG TKLTVLGGGGSGGGSEVQLVESGGGLVQPGGSLTLSCAASGSTFSI

		NHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNSKNT AYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3854	L001 FLT3-H19C-TAC	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRF TISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW VRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH*
3855	L001 FLT3-H19C-TCA	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRF TISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTV SSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGGGGSGGG SEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPED TAVYYCTIGGSLSVSSQGTLVTVSSHHHHHH*
3856	QEGNEE:L001:aMSLN:aALB:aCD3	QEGNEEGGGGKPLGLQARVVGGGGQVQLVESGGGVVQAGGSLTL SCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGR FTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGT LVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3857	QDANEE:L001:aMSLN:aALB:aCD3	QDANEEGGGGKPLGLQARVVGGGGQVQLVESGGGVVQAGGSLTL SCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGR FTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGT LVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPN

		WVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3858	QDGNEE:L001:aMSLN:aALB:aCD3	QDGNEEGGGGKPLGLQARVVGGGGQVQLVESGGGVVQAGGSLTL SCAASGSTFSIRAMRWYRQAPGTERDLVAVIYGSSTYYADAVKGR FTISRDNSKNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQGT LVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSK FGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAK TTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGG GSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNN LKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSG GGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQ PEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH
3873	aFLT3-19C L001 TriTAC-XR	QDGNEEGGGGKPLGLQARVVGGGGEVQLVESGGGLVQPGGSLTL SCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRF TISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW VRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH*
3874	aFLT3-19C L085 TriTAC-XR	QDGNEEGGGGKPLGLQAGVVGGGGEVQLVESGGGLVQPGGSLTL SCAASGSTFSINHFSWYRQAPGKQRELVAFISSDGVSIDVESVKGRF TISGDNSKNTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSW VRQAPGKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWV ARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH*
3875	aFLT3-19C TriTAC	EVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWYRQAPGKQRE LVAFISSDGVSIDVESVKGRFTISGDNSKNTAYLQMNSLRAEDTAV YYCYYRGFWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGN SLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQ GTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFT FNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW GQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTL TCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFS

		GSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVL HHHHHH*
3876	aCD19-MaL001 TriTAC-XR	QDGNEEGGGGKPLGLQARVVGGGGENVLTQSPATLSVTPGEKATI TCRASQSVSYMHWYQQKPGQAPRLLIYDASNRASGVPSRFSGSGS GTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGSG GGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVG WIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFL TMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSSGGGGS GGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAP GKGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLR PEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSK YNNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYC VRHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLW YSNRWVFGGGTKLTVLHHHHHH*
3877	aGFP TriTAC	QVQLVESGGALVQPGGSLRLSCAASGFPVNRYSMRWYRQAPGKE REWVAGMSSAGDRSSYEDSVKGRFTISRDDARNTVYLQMNSLKPE DTAVYYCNVNVGFEYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG GSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGSLKLS CAASGFTFNKYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYIS YWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLVPG TPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGT KLTVLHHHHHH*
3881	Stub:aCD20-9xxx TriTAC	VVGGGGEVQLLESGGGLVQPGGSLTLSCAASGRTFSNYNMGWFR QAPGKEREFVAAIDWSGGSPYYAASVKGRFTISRDNSKNTLYLQM NSLRAEDTAVYYCAAPLSYGSTWLADYWGQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPG KGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVARIRSKY NNYATYYADQVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCV RHANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTV VTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRG LIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCTLWY SNRWVFGGGTKLTVLHHHHHH
3882	aCD20-L001-9xxx TriTAC-XR	QDGNEEGGGGKPLGLQARVVGGGGEVQLLESGGGLVQPGGSLTL SCAASGRTFSNYNMGWFRQAPGKEREFVAAIDWSGGSPYYAASV KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAPLSYGSTWLAD YWGQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKGRF TISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSS GGGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW

		VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTLVTV SSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGA VTSGNYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH

Table 22. TriTAC sequences

SEQ ID NO:	Description	AA Sequence	Notes
3218	Exemplary BH2T TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPMGWYR QAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3219	Exemplary 01A01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTDIFSISPMGWYR QAPGKQRELVAAIHGGSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVAWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3220	Exemplary 02E09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNDFSISPMGWY RQAPGKQRELVAAIHGGSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVAW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3221	Exemplary 01B03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSKSPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVVW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3222	Exemplary 01B04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNDFSISPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVKW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3223	Exemplary 02H05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNQFSISPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVVW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3224	Exemplary 01A02 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAINGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVHW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3225	Exemplary 01A05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3226	Exemplary 01B12 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMGWY RQAPGKQRELVAAIHGFQTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVVW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3227	Exemplary 01G06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGFETLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVLW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3228	Exemplary 02C05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSESPMGWY RQAPGKQRELVAAIHGFTTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3229	Exemplary 02G09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSDSPMGWY RQAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVAW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3230	Exemplary 01C08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSNSPMGWY RQAPGKQRELVAAIHGGSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVHW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3231	Exemplary 02B01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSNSPMGWY RQAPGKQRELVAAIHGRSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVMW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3232	Exemplary 02E03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSNSPMGWY RQAPGKQRELVAAIHGPSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3233	Exemplary 01D03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSNSPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVRW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3234	Exemplary 01D06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3235	Exemplary 01H04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSKSPMGWY RQAPGKQRELVAAIHGQSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3236	Exemplary 02B07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAIHGHSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3237	Exemplary 01A08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRKVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3238	Exemplary 01B07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGIYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW	BCMA TriTAC

		AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3239	Exemplary 01F03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSESPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGTYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3240	Exemplary 02F05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSVSPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGKYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3241	Exemplary 02H04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSVSPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3242	Exemplary 02A07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSKSPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPREVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3243	Exemplary 01D05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSDSPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3244	Exemplary 01E05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGKYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3245	Exemplary 01F02 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSHSPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3246	Exemplary 02C06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3247	Exemplary 02F11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVQW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3248	Exemplary 01E06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSLSPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3249	Exemplary 01A03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPGGWYR QAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3250	Exemplary 02A11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNHFSISPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRVVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3251	Exemplary 01D07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSASPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVNW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3252	Exemplary 01D10 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSASPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3253	Exemplary 01A07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMGWYR QAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3254	Exemplary 02F12 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3255	Exemplary 02B05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPYGWYR QAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3256	Exemplary 01E04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIASISPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3257	Exemplary 02A05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIASISPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3258	Exemplary 02C03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIASISPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3259	Exemplary 01E03 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3260	Exemplary 01H09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIMSISPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3261	Exemplary 02G05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3262	Exemplary 01C01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMGWY RQAPGKQRELVAAIHGHSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3263	Exemplary 01D02 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3264	Exemplary 02D09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNVVSISPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPNNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3265	Exemplary 02C01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIISISPMGWYR QAPGKQRELVAAIHGASTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3266	Exemplary 02G02 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMGWY RQAPGKQRELVAAIHGASTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3267	Exemplary 01B05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMGWY RQAPGKQRELVAAIHGFETLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3268	Exemplary 01G08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIQSISPMGWY RQAPGKQRELVAAIHGFETLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3269	Exemplary 01H06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTSDFSISPMGWY RQAPGKQRELVAAIHGFETLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3270	Exemplary 01F04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMGWY RQAPGKQRELVAAIHGFQTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3271	Exemplary 01H08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIMSISPMGWY RQAPGKQRELVAAIHGFSTVYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3272	Exemplary 02F07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMGWY RQAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3273	Exemplary 01C05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAIHGFKTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTARYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3274	Exemplary 02F04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3275	Exemplary 02B06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSNSPMGWY RQAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3276	Exemplary 01F07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMGWY RQAPGKQRELVAAIHGFSTIYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3277	Exemplary 02B04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPMGWY RQAPGKQRELVAAIHGFSTIYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPLNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3278	Exemplary 01H11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCVASTNIFSTSPMGWY RQAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3279	Exemplary 02E06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSDSPMGWY RQAPGKQRELVAAIHGFSTFYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3280	Exemplary 01E08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSQSPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVCW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3281	Exemplary 02A04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSQSPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPSNVYW GKGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3282	Exemplary 02A08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3283	Exemplary 02E05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGISTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3284	Exemplary 02H09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSRSPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3285	Exemplary 02G06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSGSPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3286	Exemplary 01B09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASSNIFSISPMGWYR QAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3287	Exemplary 02F03 TriTAC sequence	evqlvesgggLVQPGRSLTLSCAASTNIFSIYPMGWYRQAP GKQRELVAAIHGSSTLYADSVKGRFTISRDNAKNSIYL QMNSLRPEDTALYYCNKVPWGDYHPKNVYWGQGT QVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSC AASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL YADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYY CTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW	BCMA TriTAC

		GQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3288	Exemplary 02F02 TriTAC sequence	evqlvesgggLVQPGRSLTLSCAASTNIFSKSPMGWYRQA PGKQRELVAAIHGSSTLYADSVKGRFTISRDNAKNSIY LQMNSLRPEDTALYYCNKVPWGDYHPGNVYWGQGT QVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSC AASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL YADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYY CTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW GQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3289	Exemplary 02H01 TriTAC sequence	evqlvesgggLVQPGRSLTLSCAASTNIFSKSPMGWYRQA PGKQRELVAAIHGSSTLYADSVKGRFTISRDNAKNSIY LQMNSLRPEDTALYYCNKVPWGDYHPRNVYWGQGT QVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSC AASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTL YADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYY CTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKG LEWVARIRSKYNNYATYYADQVKDRFTISRDDSKNT AYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAYW GQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLT VSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPR GLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDE AEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3290	Exemplary 01G10 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNEFSISPMGWY RQAPGKQRELVAAIHGLSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGAYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3291	Exemplary 02D11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNEFSISPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3292	Exemplary 01B01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMGWYR QAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVAWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3293	Exemplary 01G11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMGWYR QAPGKQRELVAAIHGASTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVAWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3294	Exemplary 01H10 TriTAC sequence	evqlvesgggLVQPGRSLTLSCAASTNIPSISPMGWYRQAP GKQRELVAAIHGESTLYADSVKGRFTISRDNAKNSIYL QMNSLRPEDTALYYCNKVPWGDYHPRNVYWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLE WVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ	BCMA TriTAC

		GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3295	Exemplary 01C04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMGWYR QAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3296	Exemplary 01D04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMGWY RQAPGKQRELVAAIHGVSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVQW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3297	Exemplary 01E07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIPSISPMGWYR QAPGKQRELVAAIHGQSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVQWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3298	Exemplary 02B11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVSWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3299	Exemplary 02B11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVSWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3300	Exemplary 01F10 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASSNIFSISPMGWYR QAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3301	Exemplary 02G08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3302	Exemplary 02G11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3303	Exemplary 02H06 TriTAC sequence	evqlvesgggLVQPGRSLTLSCAASTNIRSISPMGWYRQAP GKQRELVAAIHGSSTLYADSVKGRFTISRDNAKNSIYL QMNSLRPEDTALYYCNKVPWGDYHPRNVVWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLE WVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3304	Exemplary 01B02 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMGWY RQAPGKQRELVAAISGFSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNEVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3305	Exemplary 02H11 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSISPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3306	Exemplary 01F08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNITSVSPMGWY RQAPGKQRELVAAIHGPSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPTNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3307	Exemplary 01H01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIGSISPMGWY RQAPGKQRELVAAIHGQSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPQNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3308	Exemplary 01E10 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMGWY RQAPGKQRELVAAIHGKSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRRVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3309	Exemplary 01G01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIVSISPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRRVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3310	Exemplary 01G04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIDSISPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRMVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3311	Exemplary 01A04 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFMISPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3312	Exemplary 01F12 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFRISPMGWY RQAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3313	Exemplary 01B06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPMGWYR QAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGEYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3314	Exemplary 01C06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSISPMGWYR QAPGKQRELVAAIHGDSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGKYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3315	Exemplary 01B08 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMGWY RQAPGKQRELVAAIHGSSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3316	Exemplary 01C02 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIESISPMGWY RQAPGKQRELVAAIHGNSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3317	Exemplary 01C10 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMGWYR QAPGKQRELVAAIHGFSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGYYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3318	Exemplary 01F09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMGWYR QAPGKQRELVAAIHGHSTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3319	Exemplary 02D06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMGWYR QAPGKQRELVAAIHGFSTVYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3320	Exemplary 01A06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSIRPMGWY RQAPGKQRELVAAIHGFSTVYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3321	Exemplary 01C07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSIYPMGWY RQAPGKQRELVAAIHGFSTYYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGSYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3322	Exemplary 01G09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFNISPMGWY RQAPGKQRELVAAIHGFSTYYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3323	Exemplary 01F05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSSSPMGWY RQAPGKQRELVAAIHGFSTWYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3324	Exemplary 02B12 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNISSISPMGWYR QAPGKQRELVAAIHGFDTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3325	Exemplary 02G01 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSINPMGWY RQAPGKQRELVAAIHGFDTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRNVSWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3326	Exemplary 01A09 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMGWY RQAPGKQRELVAAIHGRSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGSYHPRNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3327	Exemplary 01H05 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMGWY RQAPGKQRELVAAIHGTSTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3328	Exemplary 02F06 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGRYHPRNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3329	Exemplary 02G07 TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPMGWY RQAPGKQRELVAAIHGESTLYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPRDVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY	BCMA TriTAC

		WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	
3330	Exemplary 01F07-M34Y TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPYGWY RQAPGKQRELVAAIHGFSTIYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3331	Exemplary 01F01-M34G TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSTSPGGWY RQAPGKQRELVAAIHGFSTIYADSVKGRFTISRDNAK NSIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGS GRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQA PGKGLEWVARIRSKYNNYATYYADQVKDRFTISRDD SKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3332	Exemplary 02G02-M34Y TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPYGWYR QAPGKQRELVAAIHGASTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC

3333	Exemplary 02G02-M34G TriTAC sequence	EVQLVESGGGLVQPGRSLTLSCAASTNIFSITPGGWYR QAPGKQRELVAAIHGASTLYADSVKGRFTISRDNAKN SIYLQMNSLRPEDTALYYCNKVPWGDYHPGNVYWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSG RDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAP GKGLEWVARIRSKYNNYATYYADQVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	BCMA TriTAC
3334	C00324 PSMA TriTAC CD3 high aff.	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYSMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLKPEDTAVYYCDGYGYRGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3335	C00339 PSMA TriTAC CD3 med. aff.	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYSMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLKPEDTAVYYCDGYGYRGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNNYAMNWVRQAPGKGLE WVARIRSGYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSYTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFNAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYANRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3336	C00325 PSMA TriTAC CD3 low aff.	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYSMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLKPEDTAVYYCDGYGYRGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFEFNKYAMNWVRQAPGKGLE WVARIRSKYNNYETYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSLISYWAYWGQ	PSMA TriTAC

		GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSSGAVTSGNYPNWVQQKPGQAPRGLI GGTKFGAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	
3337	C00236 Tool PSMA TriTAC	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYSMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLKPEDTAVYYCDGYGYRGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYAD SVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIG GSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLV QPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEW VARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQ MNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGT LVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGG TVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGG TKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYY CVLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3338	C00362 PSMA p8 TriTAC	EVQLVESGGGLVQPGGSLRLSCAASRFMISEYSMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLRAEDTAVYYCDGYGYRGQGTLVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3339	C00363 PSMA HDS TriTAC C363	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHW VRQAPGKGLEWVSDINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC

3340	C00364 PSMA HTS TriTAC C364	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLKPEDTAVYYCDSYGYRGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3341	C00298 PSMA BiTE	QVQLVESGGGLVKPGESLRLSCAASGFTFSDYYMYW VRQAPGKGLEWVAIISDGGYYTYYSDIIKGRFTISRDN AKNSLYLQMNSLKAEDTAVYYCARGFPLLRHGAMD YWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPS SLSASVGDRVTITCKASQNVDTNVAWYQQKPGQAPK SLIYSASYRYSDVPSRFSGSASGTDFTLTISSVQSEDFA TYYCQQYDSYPYTFGGGTKLEIKSGGGGSEVQLVESG GGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGK GLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKN TAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAY WGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3342	C00131EGF R TriTAC	QVKLEESGGGSVQTGGSLRLTCAASGRTSRSYGMGW FRQAPGKEREFVSGISWRGDSTGYADSVKGRFTISRD NAKNTVDLQMNSLKPEDTAIYYCAAAAGSAWYGTL YEYDYWGQGTQVTVSSGGGGSGGGSEVQLVESGGG LVQPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLE WVSSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYA MNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKD RFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNF GNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGG SQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKA ALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL HHHHHH	PSMA TriTAC
3343	C00457 PSMA PH1T TriTAC C480	QVQLVESGGGVVQAGRSLTLSCAYSGVTVNVYRMG WFRQAPGKEREFVANINWSGNNRDYADSVRGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCASEKPGRLGEY DYGSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV RQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS	PSMA TriTAC

		RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHH H	
3344	C00404 PSMA PH1 TriTAC C482	QVQLVESGGGVVQAGRSLRLSCAYSGVTVNVYRMG WFRQAPGKEREFVANINWSGNNRDYADSVRGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCASEKPGRLGEY DYGSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV RQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHH H	PSMA TriTAC
3345	C00410 PSMA Z2 TriTAC C481	EVQLVESGGGLVQPGGSLTLSCAASRFMISEYHMHW VRQAPGKGLEWVSTINPAGTTDYAESVKGRFTISRDN AKNTLYLQMNSLRAEDTAVYYCDSYGYRGQGTLVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	PSMA TriTAC
3346	3B4 TriTAC	QVQLVESGGGLVQAGGSLRLSCVASGSTSNINNMRW YRQAPGKERELVAVITRGGYAIYLDAVKGRFTISRDN ANNAIYLEMNSLKPEDTAVYVCNADRVEGTSGGPQL RDYFGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQ PGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSS ISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHH H	MSLN TriTAC

3347	4A2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTFGINAMGW YRQAPGKQRELVAVISRGGSTNYADSVKGRFTISRDN AENTVSLQMNTLKPEDTAVYFCNARTYTRHDYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3348	12D1 TriTAC	QVRLVESGGGLVQAGGSLRLSCAASISAFRLMSVRW YRQDPSKQREWVATIDQLGRTNYADSVKGRFAISKDS TRNTVYLQMNMLRPEDTAVYYCNAGGGPLGSRWLR GRHWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLV QPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWV SSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHH HHHH	MSLN TriTAC
3349	3G1 TriTAC	QVRLVESGGGLVQAGESLRLSCAASGRPFSINTMGW YRQAPGKQRELVASISSSGDFTYTDSVKGRFTISRDNA KNTVYLQMNSLKPEDTAVYYCNARRTYLPRRFGSWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3350	3G1 TriTAC	QVRLVESGGGLVQAGESLRLSCAASGRPFSINTMGW YRQAPGKQRELVASISSSGDFTYTDSVKGRFTISRDNA KNTVYLQMNSLKPEDTAVYYCNARRTYLPRRFGSWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS	MSLN TriTAC

		KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	
3351	2A1 TriTAC	QVQPVESGGGLVQPGGSLRLSCVVSGSDFTEDAMAW YRQASGKERESVAFVSKDGKRILYLDSVRGRFTISRDI DKKTVYLQMDNLKPEDTGVYYCNSAPGAARNYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3352	6F3 TriTAC	QVQPVESGGGLVQPGGSLRLSCVVSGSDFTEDAMAW YRQASGKERESVAFVSKDGKRILYLDSVRGRFTISRDI YKKTVYLQMDNLKPEDTGVYYCNSAPGAARNVWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3353	1H2 TriTAC	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAA SGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC

3354	1H2 TriTAC	EVQLVESGGGLVQPGNSLRLSCAASGFTFSSFGMSWV RQAPGKGLEWVSSISGSGSDTLYADSVKGRFTISRDN AKTTLYLQMNSLRPEDTAVYYCTIGGSLSRSSQGTLV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAA SGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3355	3F2 TriTAC	QVQIVESGGGLVQAGGSLRLSCVASGLTYSIVAVGW YRQAPGKEREMVADISPVGNTNYADSVKGRFTISKEN AKNTVYLQMNSLKPEDTAVYYCHIVRGWLDERPGPG PIVYWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLV QPGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWV SSISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMN WVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRF TISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGN SYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHH HHHH	MSLN TriTAC
3356	12C2 TriTAC	QVQLVESGGGLVQTGGSLRLSCAASGLTFGVYGMEW FRQAPGKQREWVASHTSTGYVYYRDSVKGRFTISRD NAKSTVYLQMNSLKPEDTAIYYCKANRGSYEYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3357	2D1 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASTTSSINSMSWYR QAQGKQREPVAVITDRGSTSYADSVKGRFTISRDNAK NTVYLQMNSLKPEDTAIYTCHVIADWRGYWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY	MSLN TriTAC

		LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	
3358	6H2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGRTLSRYAMG WFRQAPGKERQFVAAISRSGGTTRYSDSVKGRFTISR DNAANTFYLQMNNLRPDDTAVYYCNVRRRGWGRTL EYWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQP GNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSI SGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHH H	MSLN TriTAC
3359	5D2 TriTAC	QVQLGESGGGLVQAGGSLRLSCAASGSIFSPNAMIWH RQAPGKQREPVASINSSGSTNYGDSVKGRFTVSRDIV KNTMYLQMNSLKPEDTAVYYCSYSDFRRGTQYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3360	5D2 TriTAC	QVQLGESGGGLVQAGGSLRLSCAASGSIFSPNAMIWH RQAPGKQREPVASINSSGSTNYGDSVKGRFTVSRDIV KNTMYLQMNSLKPEDTAVYYCSYSDFRRGTQYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC

3361	7C4 TriTAC	QVQLVESGGGLVPSGGSLRLSCAASGATSAITNLGWY RRAPGQVREMVARISVREDKEDYEDSVKGRFTISRDN TQNLVYLQMNNLQPHDTAIYYCGAQRWGRGPGTTW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGS GSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3362	5F2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTFRIRVMRW YRQAPGTERDLVAVISGSSTYYADSVKGRFTISRDNA KNTLYLQMNNLKPEDTAVYYCNADDSGIARDYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3363	2C2 TriTAC	QVQLVESGGGLVQAGESRRLSCAVSGDTSKFKAVGW YRQAPGAQRELLAWINNSGVGNTAESVKGRFTISRDN AKNTVYLQMNRLTPEDTDVYYCRFYRRFGINKNYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGS GSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3364	5G2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTFGNKPMGW YRQAPGKQRELVAVISSDGGSTRYAALVKGRFTISRD NAKNTVYLQMESLVAEDTAVYYCNALRTYYLNDPV VFSWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQ PGNSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSS ISGSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWV RQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYI	MSLN TriTAC

		SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHH H	
3365	9H2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYW YRQAPGKERELVAFISSGGSTNVRDSVKGRFSVSRDS AKNIVYLQMNSLTPEDTAVYYCNTYIPLRGTLHDYW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGS GSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3366	5D4 TriTAC	QVQLVESGGGLVQAGGSLRLSCVASGRTDRITTMGW YRQAPGKQRELVATISNRGTSNYANSVKGRFTISRDN AKNTVYLQMNSLKPEDTAVYYCNARKWGRNYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3367	2A4 TriTAC	QVQLVESGGGLVQARGSLRLSCTASGRTIGINDMAW YRQAPGNQRELVATITKGGTTDYADSVDGRFTISRDN AKNTVYLQMNSLKPEDTAVYYCNTKRREWAKDFEY WGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPG NSLRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSIS GSGSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPE DTAVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVR QAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYIS YWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHH H	MSLN TriTAC

3368	7F1 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASAIGSINSMSWYR QAPGKQREPVAVITDRGSTSYADSVKGRFTISRDNAK NTVYLQMNSLKPEDTAIYTCHVIADWRGYWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3369	5C2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYWF RQAPGEERELVATINRGGSTNVRDSVKGRFSVSRDSA KNIVYLQMNRLKPEDTAVYYCNTYIPYGGTLHDFWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3370	5C2 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYWF RQAPGEERELVATINRGGSTNVRDSVKGRFSVSRDSA KNIVYLQMNRLKPEDTAVYYCNTYIPYGGTLHDFWG QGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSL RLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSG SDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTA VYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLV ESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAP GKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDS KNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYW AYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQE PSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQ APRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQP EDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3371	2F4 TriTAC	QVQLVESGGGLVQAGGSLRLSCTTSTTFSINSMSWYR QAPGNQREPVAVITNRGTTSYADSVKGRFTISRDNAR NTVYLQMDSLKPEDTAIYTCHVIADWRGYWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ	MSLN TriTAC

		GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	
3372	2A2 TriTAC	QVQLVESGGGLVQAGGSLTLSCAASGSTFSIRAMRW YRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNA KNTLYLQMNNLKPEDTAVYYCNADTIGTARDYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3373	11F3 TriTAC	QVQLVESGGGLVQAGGSLRLSCVASGRTSTIDTMYW HRQAPGNERELVAYVTSRGTSNVADSVKGRFTISRDN AKNTAYLQMNSLKPEDTAVYYCSVRTTSYPVDFWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGS DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3374	10B3 TriTAC	QVQLVESGGGLVQAGGSLRLSCAASGSTSSINTMYW YRQAPGKERELVAFISSGGSTNVRDSVKGRFSVSRDS AKNIVYLQMNSLKPEDTAVYYCNTYIPYGGTLHDFW GQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNS LRLSCAASGFTFSSFGMSWVRQAPGKGLEWVSSISGS GSDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDT AVYYCTIGGSLSRSSQGTLVTVSSGGGGSGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQ APGKGLEWVARIRSKYNNYATYYADSVKDRFTISRD DSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISY WAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQ EPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPG QAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGV QPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC

3375	5H1 TriTAC	QVQLVESGGGLVQPGGSLRLSCAASGGDWSANFMY WYRQAPGKQRELVARISGRGVVDYVESVKGRFTISR DNAKNTVYLQMNSLKPEDTAVYYCAVASYWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSSFGMSWVRQAPGKGLEWVSSISGSGSDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSRSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLE WVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCVLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3376	MH6T TriTAC	QVQLVESGGGVVQAGGSLTLSCAASGSTFSIRAMRW YRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQ GTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRD TLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY YCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKN TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAY WGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3377	GFP TriTAC	QVQLVESGGALVQPGGSLRLSCAASGFPVNRYSMRW YRQAPGKEREWVAGMSSAGDRSSYEDSVKGRFTISR DDARNTVYLQMNSLKPEDTAVYYCNVNVGFEYWGQ GTQVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLR LSCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGR DTLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAV YYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPG KGLEWVARIRSKYNNYATYYADQVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWA YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQA PRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3378	TriTAC 74	QVQLVESGGGVVQAGGSLRLSCAASGSTFSIRAMRW YRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQ GTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRD TLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY YCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVES GGGLVQPGGSLKLSCAASGNTFNKYAMNWVRQAPG KGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSK NTAYLQMNNLKTEDTAVYYCVRHGNFGDSYISYWA	MSLN TriTAC

		YWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPS LTVSPGGTVTLTCGSSTGAVTHGNYPNWVQQKPGQA PRGLIGGTKVLAPGTPARFSGSLLGGKAALTLSGVQPE DEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH	
3379	TriTAC 75	QVQLVESGGGVVQAGGSLRLSCAASGSTFSIRAMRW YRQAPGTERDLVAVIYGSSTYYADAVKGRFTISRDNS KNTLYLQMNSLRAEDTAVYYCNADTIGTARDYWGQ GTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRD TLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY YCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKN TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAY WGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	MSLN TriTAC
3380	Exemplary EL1 TriTAC sequence	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDW YRQAPGKQRELVATSTRDGNVDYAESVKGRFTISRD NAKNTVYLQMNSLKPEDTAVYYCNADLRTAVDLIRA NYWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQ PGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVS SISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH**	EGFR TriTAC
3381	Exemplary EL104 TriTAC sequence	QVQLQESGGGLVQAGDSLRLSCVVSGRTDSWYVMG WFRQAPGKDREFVAGVSWSYGNTYYADSVKGRFTA SRDNAKNTAYLQMNSLNAEDTAVYYCAARVSREVIP TRWDLYNYWGQGTQVTVSSGGGGSGGGSEVQLVES GGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGK GLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGG GGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH ANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH**	EGFR TriTAC

3382	Exemplary EL106 TriTAC sequence	QVQLQESGGGSVQPGGSLRVSCVVSRTIISINAMTWY HQAPGKRRELVAIITSGGETNYADSVKGRFTISRDNA KNTAYLQMNNLKPEDTGVYYCNVVPPLGSWGQGTQ VTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCA ASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLY ADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCT IGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGG LVQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLE WVARIRSKYNNYATYYADQVKDRFTISRDDSKNTAY LQMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQ GTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSP GGTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLI GGTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAE YYCTLWYSNRWVFGGGTKLTVLHHHHHH**	EGFR TriTAC
3383	Exemplary EL113 TriTAC sequence	QVQLQESGGGRVQAGGSLRLSCSASARTLRLYAVGW FRQAPGKEREFVAGIGRSERTYYTDSVKGRFTLSRDN AKNTVFLEMNDLEPEDTAVYFCALTFQTTDMVDVPT TQHEYDYWGRGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH**	EGFR TriTAC
3384	Exemplary EL12 TriTAC sequence	QVQLQESGGGLVQAGGSLRLSCAASGSIAYIYTMDW YRQAPGKQRELVATSTHDGNTDYADSVKGRFTISRD NVKNTVYLQMNSLKPEDTAVYYCNADLRTAVDLIRA NYWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQ PGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVS SISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH**	EGFR TriTAC
3385	FLL101	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWY RQAPGKQREWVAQITRDSNSFYADSVKGRFAISRDNA KNTVYLQMNNLKPEDTAVYYCRVLSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA	FLT3 TriTAC

		RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	
3386	FLL103	QVQLQESGGGLVQAGGSLRLSCEASGPTFSINYIDWY RQAPGKQREWVAQITRDSNSFYADSVKGRFAVSRDN AKNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3387	FLL116	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWY RQAPGKQREWVAQITRDSNSFYADSVKGRFAISRDNA KNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3388	FLL125	QVQLQESGGGLVQAGGSLRLSCAASGSTFSRNYIDW YRQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDN AKNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC

3389	FLL129	QVQLQESGGGLVQAGGSLRLSCAASGVTFSASYIDW YRQAPGNEREWVAQITRGGDSFYADSVKGRFAISRD NAKNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAA SGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3390	FLL137	QVQLQESGGGLVQAGGSLRLSCAASGSTFNNYAMD WFRQAPGKQREWVAQITRDSSSFYADSVKGRFAISRD NAKNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAA SGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3391	FLL14	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWY RQAPGKQREWVAQITRDSNSFYADSVKGRFAISRDNA KNTVYLQMNSLKPEDTAVYYCRLLSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3392	FLL146	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWY RQAPGKQREWVAQITRDDTSFYADSVKGRFAISRDN AKNTVYLQMNNLRPEDTAVYYCRLLSFWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG	FLT3 TriTAC

		TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	
3393	FLL158	QVQLQESGGGLVQPGGSLRLSCAASGSTFGRNYIDW YRQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDN AKNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3394	FLL179	QVQLQESGGGLVQAGGSLRLSCKASGVTFSINYIDWY RQAPGKQREWVAQITRDGSSFYADSVKGRFAISRDNA KNTVYLQMNSLKPEDTAVYYCRILSDWGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGF TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3395	FLL181	QVQLQESGGGLVQAGDSLRLSCAASGVTFSASYIDW YRQAPGNEREWVAQITRGGDSFYADSVKGRFAISRD NAKNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQV TVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAA SGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC

3396	FLL187	QVQLQESGGGLVQPGGSLRLSCAASGVTFSINYIDWY RQAPGKQREWVAQITRDSNSFYADSVKGRFAISRENA KNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3397	FLL32	QVQLQESGGGLVQAGGSLRLSCQASGVTFNINYIDW YRQAPGRQREWVAQITRDSTRFYADSVKGRFAISRDN AKNMVYLQLNSLKPEDTAVYYCRILSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3398	FLL51	QVQLQESGGGLVQPGGSLRLSCAASGFDFSISYIDWY RQAPGNEREWVAQITRGGDSFYADSVKGRFAISRDN AKNTVYLQMNSLKPEDTAVYYCRILSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3399	FLL55	QVQLQESGGGLVQAGGSLRLSCAASGSTFSRNYIDW YRQAPGKQREWVAQITSAGNTHYEPSLKGRFTISRDN AKNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG	FLT3 TriTAC

		TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	
3400	FLL77	QVQLQESGGGLVQPGGSLRLSCAASGVTFSISYIDWY RQAPGNEREWVAQITRGGDSFYADSVKGRFAISRDN AKNTVYLQMNSLKPEDTAVYYCRILSYWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3401	FLL97	QVQLQESGGGLVQAGGSLRLSCAASGVTFSINYIDWY RQAPGKQREWVAQITRDSNSFYADSVKGRFAVSRDN AKNTVYLQMNSLKPEDTAVYYCRVLSYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3402	FLL21	QVQLQESGGGLVQPGGSLTLSCAASGSTFSRNYIDWY RQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNA KNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGF TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC

3403	FLL57	QVQLQESGGGLVQAGGSLRLSCAASGSTFSKNYIDW YRQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDN AKNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3404	FLL62	QVQLQESGGGLVQAGGSLRLSCAASGSTSSRNYIDW YRQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDN AKNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVT VSSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAAS GFTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYA DSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTI GGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEW VARIRSKYNNYATYYADQVKDRFTISRDDSKNTAYL QMNNLKTEDTAVYYCVRHANFGNSYISYWAYWGQG TLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPG GTVTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIG GTKFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEY YCTLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3405	FLL79	QVQLQESGGGLVQAGGSLRLSCSASGSTFSRNYIDWY RQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNA KNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGF TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3406	FLL86	QVQLQESGGGLVQPGDPLRLSCAASGSTFSRNYIDWY RQAPGKQREWVAQITSGGNTHYEPSLKGRFTISRDNA KNTAYLQMNSLKPEDTAVYYCRILDYWGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGF TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL	FLT3 TriTAC

		VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	
3407	FLL112	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWAGGRTHYEDSVKGRFTIHRD NAKNTVYLQMNSLKPEDTAVYYCAAQVSRAYDGIW YSGGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3408	FLL142	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWDGGRTHYADFVKGRFTISRD NAKNTVYLQMNSLKPEDTAVYYCAAQVARAYDSKW YSGGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3409	FLL143	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWVGGRTHYADSVKGRFTISRD NAKNTVYLQMNSLKPEDTAVYYCAAQVARAYDGN WYSGGDYWGQGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG	FLT3 TriTAC

		KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH	
3410	FLL154	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWSGGRTHYADSVKGRFTISRD NAKNTVYLQMNSLKPEDTAVYYCAGQVARAYDGN WYSRGDYWGQGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH	FLT3 TriTAC
3411	FLL168	QVQLQESGGGSVQAGGSLRLSCAFSGRTFSGFGTGWF RQAPEKEREFVAAISWDGGRTHYADSVKGRFTISRDN AKNTVYLQMDSLKPEDTAIYYCAAQVSRAYDGRWY SAVDYWGRGTQVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	FLT3 TriTAC
3412	FLL170	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRD NAKNTVYLQMNSLKPEDTAVYYCAGQVARAYDSSW YSRGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK	FLT3 TriTAC

		AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	
3413	FLL188	QVQLQESGGGLVQAGGSLGLSCAVSGRTFSGFGTGW FRQPPEKEREFVAAISWDGGRTHYADSVKGRFTISRD NAKNTVFLQMNSLKPEDTAVYYCAAQVARAYDSRW YSGGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3414	FLL40	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRD NAKNTVSLVYLQMNSLKPDDTAVYYCAGQVARAYD SSWYSRGDYLGQGTQVTVSSGGGGSGGGSEVQLVES GGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGK GLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGG GGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH ANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH	FLT3 TriTAC
3415	FLL6	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWDGGRTHYADSVKGRFTISRD NAANTVYLQMNSLKPEDTAVYYCAGQVSRAYDSMW YGRDDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK	FLT3 TriTAC

		AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	
3416	FLL75	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRD NAKNTVNLVYLQMNDLRPEDTAVYYCAGQVARAYD SNWYSRGDYWGQGTQVTVSSGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPG KGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTL YLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSG GGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTF NKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG NYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGT KLTVLHHHHHH	FLT3 TriTAC
3417	FLL83	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRD NAENTVYLEMNSLKPEDTAVYICAGQVSRAYDSNWY SRDDYWGQGTQVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	FLT3 TriTAC
3418	FLL94	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPEKEREFVAAISWDGGRTHYADSVKGRFTISRD NAKNTVYLQMNSLKPEDTAIYYCAGQVARAYDTRW YSRGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK	FLT3 TriTAC

		AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	
3419	FLL99	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWDGGRTHYADFVKGRFTISRD NAKNTVYLQMNSLKPEDTAVYYCAAQVARAYDSRW YSGGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3420	FLL38	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAVSWSGGTTEIADSVKGRFTISRD NAKNTVYLQMSSLKPGDTAVYYCAGQVARAYDSRW YSRGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3421	FLL53	QVQLQESGGGLVQAGDSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAVSQSGGTTHYADSVKGRFTISRD NAKNTETLVYLQMNSLKPEDTAVYYCAGQVARAYD SSWYARGDYWGQGTQVTVSSGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPG KGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTL YLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSG GGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTF NKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG NYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLL	FLT3 TriTAC

		GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGT KLTVLHHHHHH	
3422	FLL553	QVQLQESGGGLVQAGGSLRLSCAVSGRTFSGFGTGW FRQAPGKEREFVAAISWSGGTTHYADSVKGRFTISRD NAKNTVNLVYLQMNSLRPEDTAVYYCAGQVARAYD SNWYSRGDYWGQGTQVTVSSGGGGSGGGSEVQLVE SGGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPG KGLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTL YLQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSG GGGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTF NKYAINWVRQAPGKGLEWVARIRSKYNNYATYYAD QVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVR HANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGS GGGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSG NYPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLL GGKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGT KLTVLHHHHHH	FLT3 TriTAC
3423	FLL74	QVQLQESGGGLVQAGGSLRLSCRFSGRTFSGFGTGWF RQAPGKEREFVAAISWAGGRTHYEDSVKGRFTISRDN AKNTVYLQMNSLKPEDTAVYYCAVQVSRAYDGIWY SGGDYWGQGTQVTVSSGGGGSGGGSEVQLVESGGG LVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGS GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3424	FLL102	QVQLQESGGGLVQAGGSLMVSCAASGGTWSSYATG WFRQVPGKERKLIAGISRSGGRTYYAESVKGRFTISRD NAKNTVYLQMNTLKPDDTAVYYCAAARYFTSSVVY TSGNDYDYWGQGTQVTVSSGGGGSGGGSEVQLVES GGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGK GLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGG GGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH ANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG	FLT3 TriTAC

		GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH	
3425	FLL122	QVQLQESGGGLVQAGGSLMVSCAASGGTWSSYATG WFRQVPGKERELIAGISRSGGRTYYAESVKGRFTISRD NAKNTVYLQMNTLKPDDTAVYYCAAARYFTSSVVY TSGNDYDYWGQGTQVTVSSGGGGSGGGSEVQLVES GGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGK GLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGG GGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH ANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH	FLT3 TriTAC
3426	FLL134	QVQLQESGGGLVQPGGSLRLSCAASGGTFSSYATGW FRQVPGKEREFIAGISRNSGRTYAESVKGRFTISRDNA KNTVYLQMNTLRPDDTAVYYCAAARYFTRDAIYTSG DDYDYWGQGTQVTASSGGGGSGGGSEVQLVESGGG LVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGS GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3427	FLL153	QVQLQESGGGLVQVGGSLMVSCAASGGTFSSYATGW FRQVPGKEREFIAGVSRNSGRTYYAESVKGRFTISRDN AKNTVYLQMNTLKPDDTGVYYCAAARYFTRDAVYT SGDDYDYWGQGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG	FLT3 TriTAC

		KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH	
3428	FLL41	QVQLQESGGGLVQLGDSLMVSCAASGGTFSSYATGW FRQVPGREREFIAGISRSGGRTYYAESVKGRFTISRDN AKNTVYLQMNTLKPDDTAVYYCAAARYFTTSVVYTS GDDYDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3429	FLL67	QVQLQESGGGLVQLGDSLMVSCAASGGTFSSYATGW FRQVPGKEREFIAGISRSGGRTYYAESVKGRFTISRDN AKNTVYLQMNTLKPDDTAVYYCAAARYFTTSVVYTS GDDYDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3430	FLL92	QVQLQESGGGLVQAGGSLMVSCAASGGTWSSYATG WFRQVPGKERELIAGISRSGGRTYYAESVKGRFTISRD NAKNTVYLQMNTLKSDDTAVYYCAAARYFTSSVVY TSGNDYDYWGQGTQVTVSSGGGGSGGGSEVQLVES GGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGK GLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGG GGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH ANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG	FLT3 TriTAC

		GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH	
3431	FLL71	QVQLQESGGGLVQVGGSLMVSCAASGGTFSSYATGW FRQVPGKEREFIAGISRNSGRTYYAESVKGRFTISRDN AKNTVYLQMNTLKPDDTAVYYCAAARYFTRDAVYT SGDDYDYWGQGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH	FLT3 TriTAC
3432	FLL8	QVQLQESGGGLVQVGGSLMVSCAASGGTFSSYATGW FRQVPGKEREFIAGISRNSGRTYYAESVKGRFTISRDN AKNTVYLQMNTLKPDDTAVYYCAAARYFTRDVVYT SGDDYDYWGQGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH	FLT3 TriTAC
3433	FLL84	QVQLQESGGGLVQAGGSLMVSCAASGGTFSSYATGW FRQVPGKEREFIAGISRSGGRTYYAESVKGRFTISRDN AKNTVYLQMNTLKPDDTAVYYCAAARYFTTSVVYTS GDDYDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK	FLT3 TriTAC

		AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	
3434	FLL107	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYAMGW FRQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRD NAKNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTT TPVVKYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3435	FLL141	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYAMGW FRQAPGMEREFVAAISWSGYSTYYADSVKGRFTISRD DAKNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTT TPVVKYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3436	FLL34	QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYALGW FRQAPGKEREFVAAISWSGGNTYYADSVKGRFTISRD DAKNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTT TPVVKYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK	FLT3 TriTAC

		AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	
3437	FLL4	QVQLQESGGGLVQAGGSLRLSCAASERTFSSYTMGW FRQAPGKEREFVAAMSWSGGSTYYADSVKGRFTISR DNAKNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVT TTPVVKYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3438	FLL61	QVQLQESGGGLVQAGGSLRLSCAASERTFSSYAMGW FRQAPGKEREFVAAISWSGGSTYYADSVKGRFTISRD NAKNTVYLQMDSLKPEDTAVYYCAAGGSTRVVVTT TPIVKYWGQGTQVTVSSGGGGSGGGSEVQLVESGGG LVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGS GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3439	FLL78	QVQLQESGGGWVQAGGSLRLSCAASGRTFSSYAMG WFRQAPGKEREFVAAISWSGSSTYYADSVKGRFTISR DNAKNTVYLLMDSLKPEDTAVYYCAAGGSTRVVVT TTPVVKYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK	FLT3 TriTAC

		AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	
3440	FLL1	QVQLQESGGGLVQAGGSLRLSCAASGRTFSTLTVAW FRQAPGKEREFVVASIPSGSNTGYAESVKGRFTISRDI AKNTVYLQMNSLKPEDTAMYFCAARIYFGSSRGYDY WGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPG NSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSIS GSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPE DTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYIS YWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHH H	FLT3 TriTAC
3441	FLL26	QVQLQESGGGLVQAGGSLRLSCAASGRTFTTYTVAW FRQAPGKEREFLVASIPTGSNTAYAESVKGRFTISRGN AKNTVYLQMNSLKPEDTAMYYCAARTYFGSSRGYD YWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV RQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHH H	FLT3 TriTAC
3442	FLL160	QVQLQESGGGLVQAGDSLRLSCATSGRTFNLYRVGW FRQAPGKEREFVARITWSADITQYADSVKGRFTISRDN AKNTVYLQMNSLKPEDTAIYYCATTLRKSSGIYHVDD YDDWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLV QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWV SSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT	FLT3 TriTAC

		LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH	
3443	FLL173	QVQLQESGGGLVQAGGSLRLSCATSGRTFNLYRVGW FRQAPGKEREFVARITWSADITQYTDSVKGRFTISRDN AKNTVYLQMNSLKPEDTAIYYCATTLRKSSGIYHTDD YDYWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLV QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWV SSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH	FLT3 TriTAC
3444	FLL178	QVQLQESGGGLVQPGGSLRLSCAASGFTFSDYAMSW VRQAPGKGLEWVSGISSGGYKIGYTDSTKGRFTISRD NAKNTLYLQMNSLTAEDTAVYYCAKGTQWSWSLRD NTSRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQ PGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVS SISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH	FLT3 TriTAC
3445	FLL27	QVQLQESGGGLVQPGGSLRLSCKASGFTFSSYAMSW VRQAPGKGLEWVSGISSGGYKIGYTDSTKGRFTISRD NAKNTLYLQMNSLNAEDTAVYYCAKGTQWSWALR DSTSRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLV QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWV SSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT	FLT3 TriTAC

		LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH	
3446	FLL190	QVQLQESGGGLVQAGGSLTLSCTASGSTFSINHFSWY RQAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNDK NTAYLQMNGLKPEDTAVYYCYYRGFWGQGTQVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGF TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3447	FLL43	QVQLQESGGGLVQPGGSLTLSCTASGSTFSINHFAWY RQAPGKQRELVAFISSDGRSTDVESVKGRFTISGDND KNTAYLQMNGLKPEDTAVYYCYYRGSWGQGTQVTV SSGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASG FTFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3448	FLL15	QVQLQESGGGLVQAGGSLSLSCAASEGTISHAAMGW FRQAPGKERQFVAYDTWTGGSTNYADSVKDRFTITG DHAKNTVYLQMNSLKPEDTGVYYCAVRGRYSASYT YTNPASYKYWGQGTQVTVSSGGGGSGGGSEVQLVES GGGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGK GLEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLY LQMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGG GGSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFN KYAINWVRQAPGKGLEWVARIRSKYNNYATYYADQ VKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRH ANFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSG GGGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGN YPNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLG GKAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTK LTVLHHHHHH	FLT3 TriTAC

3449	FLL45	QVQLQESGGGLVQAGGSLRLSCAASGGTFSSSAMGW FRQAPGKEREFVATITQNDVPTYYTHSVKGRFTISRDN AKNTMYLQMNSLKPEDTAVYYCAQRVAQASGWRTT IKDYGYWGQGTQVTVSSGGGGSGGGSEVQLVESGGG LVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLE WVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQM NSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGS GGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3450	FLL39	QVQLQESGGGLVQAGGSLRLSCAASGLTSSTYRMAW FRQAPGKEREFAAGISYSADSGGSTNYADSVKGRFTIS RDNAKNTVYLQMSSLKPEDTAVYYCAAGRYSGTYNS PYSSSYVYWGQGTQVTVSSGGGGSGGGSEVQLVESG GGLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKG LEWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYL QMNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGG GSGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNK YAINWVRQAPGKGLEWVARIRSKYNNYATYYADQV KDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHA NFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGG GGSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNY PNWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGG KAALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLT VLHHHHHH	FLT3 TriTAC
3451	FLL177	QVQLQESGGGLVQTGGSLRLSCAASGSTFSRNTMGW FRQAPGKERVFVLGISWSGIRSYYLDSAKARFTISRDN AKNTVYLQMNSLRPEDTAVYYCAAQEGSSPGPYKY WGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQPG NSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSIS GSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRPE DTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEV QLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWVR QAPGKGLEWVARIRSKYNNYATYYADQVKDRFTISR DDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYIS YWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVT QEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQKP GQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHH H	FLT3 TriTAC

3452	FLL823	QVQLQESGGGVVQVGGSLRLSCAASGGTFGYYAVG WFRQAPGKEREFVAAVTWNGAYLYSDPVKGRFTISR DNAKNTVYLQMNSLKSEDTAVYYCGLDRWSAVVES TPSTRGQGTQVTVSSGGGGSGGGSEVQLVESGGGLV QPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWV SSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSL RPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGG SEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHH HHHH	FLT3 TriTAC
3453	FLL76	QVQLQESGGGLVQAGGSLRLSCAASGGAFSSYVMG WFRQAPGKEREFVAAVISWSGRITDYADSVKGRFSIS RDNAKSTVYLQMNNLKPEDTAVYYCAAKTGMYIDL RTSTFDYWGQGTQVTVSSGGGGSGGGSEVQLVESGG GLVQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGL EWVSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQ MNSLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGG SGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKY AINWVRQAPGKGLEWVARIRSKYNNYATYYADQVK DRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHAN FGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGG GSQTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYP NWVQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGK AALTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTV LHHHHHH	FLT3 TriTAC
3454	FLL822	QVQLQESGGGSVQAGGSLRLSCTASGRTFTDYTMGW FRQAPGKEREFMLGISSNGYRRYYTGSMKDRFTISRD NVKKTVYLQMNDLKPEDTAVYYCAASEDHGAPRYD YWGQGTQVTVSSGGGGSGGGSEVQLVESGGGLVQP GNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEWVSSI SGSGRDTLYADSVKGRFTISRDNAKTTLYLQMNSLRP EDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSGGGSE VQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINWV RQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTIS RDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNSYI SYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVV TQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALTLSG VQPEDEAEYYCTLWYSNRWVFGGGTKLTVLHHHHH H	FLT3 TriTAC

3455	FLH107	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWF RQAPGKEREFVAAISWSGSNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	FLT3 TriTAC
3456	FLH141	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWF RQAPGMEREFVAAISWSGYSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	FLT3 TriTAC
3457	FLH19C	EVQLVESGGGLVQPGGSLTLSCAASGSTFSINHFSWY RQAPGKQRELVAFISSDGVSIDVESVKGRFTISGDNSK NTAYLQMNSLRAEDTAVYYCYYRGFWGQGTLVTVS SGGGGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGF TFSKFGMSWVRQAPGKGLEWVSSISGSGRDTLYADS VKGRFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGG SLSVSSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQ PGGSLKLSCAASGFTFNKYAINWVRQAPGKGLEWVA RIRSKYNNYATYYADQVKDRFTISRDDSKNTAYLQM NNLKTEDTAVYYCVRHANFGNSYISYWAYWGQGTL VTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGT VTLTCASSTGAVTSGNYPNWVQQKPGQAPRGLIGGT KFLVPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYC TLWYSNRWVFGGGTKLTVLHHHHHH	FLT3 TriTAC
3458	FLH34	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYALGWF RQAPGKEREFVAAISWSGGNTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI	FLT3 TriTAC

		NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	
3459	FLH4	EVQLLESGGGLVQPGGSLTLSCAASERTFSSYTMGWF RQAPGKEREFVAAMSWSGGSTYYADSVKGRFTISRD NSKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTT PVVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	FLT3 TriTAC
3460	FLH78	EVQLLESGGGLVQPGGSLTLSCAASGRTFSSYAMGWF RQAPGKEREFVAAISWSGSSTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAAGGSTRVVVTTTP VVKYWGQGTLVTVSSGGGGSGGGSEVQLVESGGGL VQPGNSLRLSCAASGFTFSKFGMSWVRQAPGKGLEW VSSISGSGRDTLYADSVKGRFTISRDNAKTTLYLQMN SLRPEDTAVYYCTIGGSLSVSSQGTLVTVSSGGGGSG GGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAI NWVRQAPGKGLEWVARIRSKYNNYATYYADQVKDR FTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFG NSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGS QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNW VQQKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAA LTLSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLH HHHHH	FLT3 TriTAC
3461	Exemplary anti-DLL3 trispecific protein (anti-CD3:anti-ALB:anti-DLL3 configuration)(CAT)	EVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAINW VRQAPGKGLEWVARIRSKYNNYATYYADQVKDRFTI SRDDSKNTAYLQMNNLKTEDTAVYYCVRHANFGNS YISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQT VVTQEPSLTVSPGGTVTLTCASSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLVPGTPARFSGSLLGGKAALT LSGVQPEDEAEYYCTLWYSNRWVFGGGTKLTVLGG GGSGGGSEVQLVESGGGLVQPGNSLRLSCAASGFTFS KFGMSWVRQAPGKGLEWVSSISGSGRDTLYADSVKG RFTISRDNAKTTLYLQMNSLRPEDTAVYYCTIGGSLSV SSQGTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGGS LTLSCAASSSSVSLLSLAWYRQAPGKKRELVAGISDD GSIVYMDSVKGRFTISRDNAKNSVYLQMNSLRAEDT AVYYCYAYSWITRSPYWGQGTLVTVSSHHHHHH	DLL3 TriTAC

3462	Exemplary anti-DLL3 trispecific protein (anti-DLL3:anti-ALB:anti-CD3 configuration)(TAC)	EVQLVESGGGLVQPGGSLTLSCAASSSSVSLLSLAWY RQAPGKKRELVAGISDDGSIVYMDSVKGRFTISRDNA KNSVYLQMNSLRAEDTAVYYCYAYSWITRSPYWGQ GTLVTVSSGGGGSGGGSEVQLVESGGGLVQPGNSLRL SCAASGFTFSKFGMSWVRQAPGKGLEWVSSISGSGRD TLYADSVKGRFTISRDNAKTTLYLQMNSLRPEDTAVY YCTIGGSLSVSSQGTLVTVSSGGGGSGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAINWVRQAPGK GLEWVARIRSKYNNYATYYADQVKDRFTISRDDSKN TAYLQMNNLKTEDTAVYYCVRHANFGNSYISYWAY WGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSL TVSPGGTVTLTCASSTGAVTSGNYPNWVQQKPGQAP RGLIGGTKFLVPGTPARFSGSLLGGKAALTLSGVQPED EAEYYCTLWYSNRWVFGGGTKLTVLHHHHHH	DLL3 TriTAC

Table 23. Masking peptide sequences

SEQ ID NO:	**Sequence**
3663	QDGNEE
3664	LDGNEE
3665	PDGNEE
3666	DDGNEE
3667	EDGNEE
3668	NDGNEE
3669	QEGNEE
3670	QNGNEE
3671	QQGNEE
3672	QDANEE
3673	QDSNEE
3674	QDGQEE
3675	QDGDEE
3676	QDGEEE
3677	QDGNDE
3678	QDGNQE
3679	QDGNNE
3680	QDGNED
3681	QDGNEQ
3682	QDGNEN

Table 24. CD19 sequences

SEQ ID NO	Sequence
3771	ENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAPRLLIYDASNRAS GVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKLEIKGGGGS GGGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMGVGWIRQPPGK ALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFLTMTNMDPVDTATYYCA RMELWSYYFDYWGQGTTVTVSS

3772	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYIMHWVRQAPGQGLEWMGYINP YNDGSKYTEKFQGRVTMTSDTSISTAYMELSRLRSDDTAVYYCARGTYYYGPQLF DYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMTQTPLSLSVTPGQPASISCKSSQ SLETSTGTTYLNWYLQKPGQSPQLLIYRVSKRFSGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCLQLLEDPYTFGQGTKLEIK
3773	QVQLQESGPGLVKPSQTLSLTCTVSGGSISTSGMGVGWIRQHPGKGLEWIGHIWW DDDKRYNPALKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARMELWSYYFDY WGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPATLSLSPGERATLSCSASSSVS YMHWYQQKPGQAPRLLIYDTSKLASGIPARFSGSGSGTDFTLTISSLEPEDFAVYY CFQGSVYPFTFGQGTKLEIKR
3774	QTVVTQEPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNNKRP SGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAGVFGTGTKLTVLGS RGGGGSGGGGSGGGGSLEMAQVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAM SWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARYYYSRLDYWGQGTLVTVSS
3775	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYRQLPGTAPKLLIYENNKRPS GIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLRAGVFGTGTKVTVLGSR GGGGSGGGGSGGGGSLEMAQVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMS WVRQAPGKGLEWVSGISASGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARYYLSQIDSWGQGTLVTVSS
3776	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGHVVFGGGTKLTVLG SRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGATVKISCKVSGYTFTDYY MHWVQQAPGKGLEWMGLVDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLR SEDTAVYYCATGIYSRPLGYWGQGTLVTVSS
3777	SYVLTQPPSASGTPGQRVTISCSGSSSNIGSHTVNWYQQLPGTAPKLLIYSNNQRPS GVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGYVFGTGTKVTVLGS RGGGGSGGGGSGGGGSLEMAEVQLVETGGGLVQPGGSLRLSCAASGFTFSSYAM SWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE DTAVYYCARSDGKHFWQQYDAWGQGTLVTVSS
3778	DIQLTQSPSSLSAYVGDRVTITCRASQGITNSLAWYQQKPGKAPKLLLHAASRLES GVPSRFSGSGFGTDFTLTISSLQPEDFAVYYCQHYLGTPYSFGQGTKVEIKRSRGGG GSGGGGSGGGGSLEMAEVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMSWVR QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAV YYCARMNIDYWGQGTLVTVSS
3779	EIVLTQSPSSLSASVGDRVTISCRASQSVSRFLNWYQQKPGKAPKLLIYGVSTLERG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQESYIIPLTFGGGTKLEIKRSRGGGGS GGGGSGGGGSLEMAEVQLVQSGAEVKRPGESLTISCKGSEYSFASYWITWVRQM PGKGLEWMGRIDPSDSYTNYSPSFQGHVTISADKSISTAYLQWSSLKASDTAIYYC ARPFQYDYGGYSDAFDIWGQGTMVTVSS
3780	EIVMTQSPLSLSVTPGEPASISCRSSQSLLDSNGFNSLDWYLQKPGQSPQLLIHLGSD RASGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQSLQIPTFGQGTKVEIKRSRG GGGSGGGGSGGGGSLEMAQMQLVQSGAEVKKAGSSVKVSCETSGGTFSSSSVNW VRQAPGQGLEWMGGIIPIVGTPNYAQKFQDRVTITAVESTFTAYMELSGLRSEDTA VYYCARGGYRDYMDVWGRGTTVTVSS
3781	SYELTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYRNNQRPS GVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGYVFGTGTKVTVLGS RGGGGSGGGGSGGGGSLEMAEVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMS WVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAED TA VYYCARGGFGAEFDYWGQGTLVTVSS

3782	SYVLTQPPSVSVSPGQTASITCSGDKLGDKYASWYQQKPGQSPVLVIYQDNKRPS GIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTEDVFGPGTKVTVLGSR GGGGSGGGGSGGGGSLEMAEVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMS WVRQAPGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAED TA VYYCARGGISDDYYGSGSYDNWGQGTLVTVSS
3783	DIQLTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSG VPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPFTFGGGTKVEIKRSRGGGG SGGGGSGGGGSLEMAEVQLVESGGGLVQPGGSLRLSCAASGFTVSSNYMSWVRQ APGKGLEWVSVIYSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYY CARERGMGYAFDIWGQGTMVTVSS
3784	DIQMTQSPSSLSASVGDRVTITCRASQGIGSYLAWYQQKPGKAPKLLIYPASTLQS GVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSLFGQGTRLEIKRSRGGGGSG GGGSGGGGSLEMAQLQLQESGPGLVKPSETLSLTCSVSGVSMSENYWSWIRQPPG KRLEWIGCAHYTGDTHYNPSLKGRVTISLDTSMNQFSLRLNSVTAADTAVYYCAS YHPFNYWGQGTLVTVSS
3785	QAVLTQPPSASGTPGQRVTISCSGSSSNIGTKTVNWYQVLPGTAPKLLIYSNYRRPS GVPDRFSGSKSGTSASLAISGLQSDDEADYYCALWDDSLDGYVFGTGTKVTVLGS RGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVRRPGATVKISCKVSGYTFNDFYL HWVRQAPGKGLEWMGRIDPEDGKTRYAEKFQGRLTITADTSTDTLYMQLGGLTS DDTAVYYCTTDWGYSSSLREEDIWYDCWGQGTLVTVSS
3786	SYELTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSG IPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHYVFGTGTKVTVLGSR GGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAIS WVRQAPGQGLEWMGGIIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDT AVYYCARDYGYGDYGDAFDIWGQGTMVTVSS
3787	SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQRPGQAPVLVVYDDSDRPS GIPERFSGSNSGNTATLTISRVEAGDEADYSCQVWDSSSDHYVFGPGTKVTVLGSR GGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIG WVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYYCARVVGTIYSMQYDVWGQGTLVTVSS
3788	LPVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPS GIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDYVVFGGGTKLTVLGS RGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIG WVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASD TAMYYCARQVWGWQGGMYPRSNWWYNMDSWGQGTLVTVSS
3789	QAVLTQPPSVSEAPRQRVTISCSGSSSNVGNNAVNWYQQVPGKAPKLLIYYDDLL SSGVSDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGPVFGGGTKLTVL GSRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGESLKISCKGSGYSFTSY WIGWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLK ASDTAMYYCARWSSTWDSMYMDYWGQGTLVTVSS
3790	QPVLTQPPSVSVAPGKTARITCGGNNIGSESVHWYQQKPGQAPMVVIYYDSNRPS GIPERFSGSNSGNTATLTVSRVEAEDEADYYCQVWNSSSDHRGVFGGGTKLTVLG SRGGGGSGGGGSGGGGSLEMAEVQLVQSGAEVKKPGESLRISCKGSGYSFTSYWI GWVRQMPGKGLEWMGIIYPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKAS DTAMYYCARVTYSMDSYYFDSWGQGTLVTVSS
3791	EVKLQESGPGLVAPSQSLSVTCTVSGVSLPDYGVSWIRQPPRKGLEWLGVIWGSET TYYNSALKSRLTIIKDNSKSQVFLKMNSLQTDDTAIYYCAKHYYYGGSYAMDYW GQGTSVTVSS
3792	DIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQKPDGTVKLLIYHTSRLHS GVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPYTFGGGTKLEIT

Table 25. CD20 sequences

SEQ ID NO	Sequence
3793	ENVLTQSPATLSVTPGEKATITCRASQSVSYMHWYQQKPGQAPRLLIYDAS NRASGVPSRFSGSGSGTDHTLTISSLEAEDAATYYCFQGSVYPFTFGQGTKL EIKGGGGSGGGGSGGGGSQVTLRESGPALVKPTQTLTLTCTFSGFSLSTSG MGVGWIRQPPGKALEWLAHIWWDDDKRYNPALKSRLTISKDTSKNQVFL TMTNMDPVDTATYYCARMELWSYYFDYWGQGTTVTVSS
3794	EVQLQASGGGLVQVGGSLRLSCTASGSTESIKHHGWYRRAPGNQREWVA GISSENITNVAEAVEGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSIEPKTPK
3795	DVQLQASGGGLVQAGGSLRLSCAASGSTESIKHHGWYRRAPGNQREWVA GINSENITNVAGAVKGRFTISRDNAKNITYLQMNSLKVEDTAVYFCYAQDN DYRFLHRFWGQGTQVITSLEPKTPK
3796	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GINSENITNVAGAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYFCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3797	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GINSENITNVAGAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYFCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3798	DVQLQASGGGLVQAEGSLRLSCAASGSTEGIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNITYLQMNSLKVEDTAVYYCYAQDN NYRFLHRFWGQGTQVITSLEPKTPK
3799	DVQLQASGGGLVQAGGSLRLSCAASGSTESIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNITYLQMNSLKVEDTAVYYCYAQDN DYRFLHRFWGQGTQVITSLEPKTPK
3800	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3801	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3802	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3803	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3804	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3805	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3806	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3807	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK

3808	DVQLQASGGGLVQAGGSLRLSCAASGSTFSIKHHGWYRRAPGNQREWVA GISSENITNVAEAVKGRFTISRDNAKNTVYLQMNSLKVEDTAVYYCYAQD NDYRFLHRFWGQGTQVTVSLEPKTPK
3880	EVQLLESGGGLVQPGGSLTLSCAASGRTFSNYNMGWFRQAPGKEREFVAA IDWSGGSPYYAASVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAAPL SYGSTWLADYWGQGTLVTVSS

Table 26. CD33 sequences

SEQ ID NO	Sequence
3809	EVQLAESGGGLVQAGGSLRLSCTASGFTFDDYVMGWFRQAPGKEREGVS CISWSGDTTYYADSVKGRFTASRDNAKNTLYLQMNSLKPEDTAMYYCAA DQGKCSLASAEPDDMDYWGRGT LVTVSS
3810	EVQLAESGGGSVQAGGSLRLSCAASGVTFSSTSVAWFRQAPGKEREGVAY IYTGDSSTYYADSVKGRFTIAQDNAKNAVYLQMNSLKPEDTAMYYCAAD GFLLNHRSYQYWGQGTQVTVSS
3811	EVQLVESGGGSVQAGGSLRLSCAASGYTYSINCMGWFRQAPGKEREGVA VISTGGGRTDYRDSVKGRFTISQDNAKNTVYLQMNSLKPEDTAMYYCAGK TTYPGYGCGLGRSAYNYWGQGTQVTVSS
3812	QIQLVESGGGSVQAGGSLRLSCVASGYIGGHYYMGWFRQAPGKEREGVA AIDIDSDGRTRYAGSVQGRFTISQDNAKNTLHLQMSSLKPEDTGMYYCAV GVGWVPARLTPQAVSYWGKGTLVTVSS
3813	EVQLVESGGGSVQAGGSLRLSCVASGYTYGINCMGWFRQAPGKEREGIAA ISTGGGTTGVADSVKGRFTISQDNAKNTVYLQMNSLKPEDTAMYYCAARS TYSGYACVYSEVNGYNYRGQ GTQVTVSS
3814	EVQLVESGGGSVQAGGSLRLSCVASGYTWCRYDMSWYRQAPGKEREFVS GFDNDGTTSYADSVKGRFTISQDNDKNTVYLQMNSLKPEDTAMYYCKED RSRGSLDGRVCPLSYDNWGQGTQVTVSS
3815	EVQLVESGGGLVQAGGSLRLSCTASGFTFDDYVMGWFRQAPGKEREGVS CISWSGDTTYYADSVKGRFTVSRDNAKNTLYLQMNSLKPEDTAMYYCAA DQSLCSLAPPYNYAYWGQGTQVTVSS
3816	QVQLVESGGGLVQAGGSLRLSCTASGFTFDNYVMGWFRQAPGKEREGVS CIGWSGGSTYYADSVKGRFTISRDNAKNTLYLQMNSLKPEDTAMYYCAA DQGKCSLGSAGADDMDYWGRGTLVTVSS
3817	EVQLVESGGGSVQAGGSLRLSCAAPGYTYCTYDMMWYRQALGKEREFVS AVYTDGSTLYADSVKGRFTISQDNAKNTLYLQMNSLKPEDTAMYYCKTET AVTYDKPCDFWGQGTQVTVSS
3818	QVQLVESGGGLVQPGGSLRLSCAASGSIFSITAMGWYRQAPGKQRELVAT VTSGGSTKYVESVKGRFTISNDNAKNTVYLQMNSLKPEDTAVYYCWADIV ARWNSDYNVYDDYWGQGTQVTVSS
3819	QVKLEESGGGLVQEGGSLRLSCAASGTIYTDSTIYWYRQAPGKQRELVASI TRGGDTKYVDSVKGRFAISSDNAKNTVYLQMNSLKPEDTAVYYCNLYYR TGPSSYYRNDWGQGTQVTVSS
3820	AVQLVESGGGLVQPGGSLRLSCAVSGIYYSINLMGWYRQAPGKPRELAASI TDSGITNYADSVKGRFTISRDNAKNTVHLQMNNLKPEDTAVYYCKPMGV NWGQGIQVTVSS
3821	AVQLVESGGGLVQAGGSLRLSCTASGSILRTYEMGWYRQAPGSQRELVAS ITSDGDTNYVDSVKGRFTISRDNGKNMVYLQMNSLKPDDTAVYYCNAVIL SPSYSMRTSHWGQGTQVTVSS

3822	QVQLVESGGGLVQAGGSLRLSCAASGNVFRFNIMGWYRQAPGNQRELVA SIDDGGDRSYADSVEGRFTISRENGKKIMYLQMNSLKPEDTAVYYCAAGL GTYLNGRVSMATNYWGQGTQVTVSS
3823	EVQLVESGGGLVQAGGSLRLSCAASGDTFSFAAMGWYRQAPGKQRELVA SISFSGGESTVYANSVRGRFTISGDNAKNRVSLEMNNLKPEDTAVYYCTAK RGPYLPGPEYWGQGTQVTVSS

CLAIMS

WHAT IS CLAIMED IS:

1. A pharmaceutical composition comprising an extended-release binding protein which comprises a half-life extended immune cell engaging protein, a masking peptide, and a cleavable linker,

wherein the masking peptide is covalently linked to the N-terminus or the C-terminus of the half-life-extended immune cell engaging protein through the cleavable linker, and

wherein the cleavable linker is significantly cleaved in systemic circulation.

2. The pharmaceutical composition of claim 1, wherein the extended-release binding protein has a higher therapeutic index than a corresponding half-life-extended immune cell engaging protein without the masking peptide.

3. The pharmaceutical composition of claim 1, wherein administration of the extended-release binding protein results in a lower Cmax/Cmin ratio of an active version of the extended-release binding protein in systemic circulation than the Cmax/Cmin ratio when a corresponding half-life extended immune cell engaging protein without the masking peptide is administered.

4. The pharmaceutical composition of claim 1, wherein multiple administration of the extended-release binding protein results in a more gradual increase of a level of an active version of the extended-release binding protein in systemic circulation than when a corresponding half-life-extended immune cell engaging protein without the masking peptide is administered.

5. The pharmaceutical composition of claim 1, wherein administration of the extended-release binding protein results in a lower Cytokine release syndrome (CRS) level than the CRS observed when a corresponding half-life extended immune cell engaging protein without the masking peptide is administered.

6. The pharmaceutical composition of any one of claims 1-5, wherein the half-life extended immune cell engaging protein comprises an immune cell engaging domain.

7. The pharmaceutical composition of claim 6, wherein the immune cell engaging domain comprises a natural killer (NK) cell engaging domain, a T cell engaging domain, a NK-T cell engaging domain, a B cell engaging domain, a dendritic cell engaging domain, a macrophage cell engaging domain, or a combination thereof.

8. The pharmaceutical composition of claim 7, wherein the immune cell engaging domain comprises the T cell engaging domain.

9. The pharmaceutical composition of claim 8, wherein the T cell engaging domain binds a CD3 molecule.

10. The pharmaceutical composition of claim 9, wherein the CD3 molecule is at least one of: a CD3γ molecule, a CD3δ molecule, or a CD3ε molecule.

11. The pharmaceutical composition of any one of claims 1-10, wherein the half-life extended immune cell engaging protein comprises a first domain (A), a second domain (B), and a third domain (C), wherein

(i) the first domain (A) is the T cell engaging domain and specifically binds to human CD3,

(ii) the second domain (B) specifically binds to human serum albumin (HSA), and

(iii) the third domain (C) specifically binds to a target antigen; and

wherein the domains are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(B)-(A)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, H_2N-(B)-(C)-(A)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(B)-L1-(A)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH, H_2N-(B)-L1-(C)-L2-(A)-COOH.

12. The pharmaceutical composition of claim 11, wherein the third domain comprises a single domain antibody (sdAb), a single-chain variable fragment (scFv), a variable heavy domain (VH), a variable light domain (VL), antigen-binding fragment (Fab), a DARPin or a peptide.

13. The pharmaceutical composition of claim 11, wherein the masking peptide inhibits or reduces the binding of the first domain (A) to the human CD3.

14. The pharmaceutical composition of claim 13, wherein the masking peptide inhibits or reduces the binding of the first domain (A) to the N-terminus of human CD3ε.

15. The pharmaceutical composition of claim 14, wherein the masking peptide comprises an amino acid sequence having at least 80% homology to QDGNEE (SEQ ID NO: 3633).

16. The pharmaceutical composition of claim 14, wherein the masking peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 3633-3652.

17. The pharmaceutical composition of claim 11, wherein the masking peptide inhibits or reduces the binding of the third domain (C) to the target antigen.

18. The pharmaceutical composition of any one of claims 1-17, wherein the cleavable linker comprises a cleavage site.

19. The pharmaceutical composition of claim 18, wherein the cleavable site is recognized by a protease.

20. The pharmaceutical composition of claim 19, wherein the protease is selected from the group consisting of a serine protease, a cysteine protease, an aspartate protease, a threonine

protease, a glutamic acid protease, a metalloproteinase, a gelatinase, and an asparagine peptide lyase.

21. The pharmaceutical composition of claim 19, wherein the protease is present in blood circulation.

22. The pharmaceutical composition of claim 19, wherein the protease is selected from the group consisting of a Cathepsin, a Cathepsin B, a Cathepsin C, a Cathepsin D, a Cathepsin E, a Cathepsin H, a Cathepsin S, a Cathepsin K, a Cathepsin L, a kallikrein, a hK1, a hK10, a hK15, a plasmin, a collagenase, a Type IV collagenase, a stromelysin, a Factor Xa, a chymotrypsin-like protease, a trypsin-like protease, a elastase-like protease, a subtilisin-like protease, an actinidain, a bromelain, a calpain, a caspase, a caspase-3, a Mir1-CP, a papain, a HIV-1 protease, a HSV protease, a CMV protease, a chymosin, a renin, a pepsin, a matriptase, a legumain, a plasmepsin, a nepenthesin, a metalloexopeptidase, a metalloendopeptidase, a matrix metalloprotease (MMP), a MMP1, a MMP2, a MMP3, a MMP7, a MMP8, a MMP9, a MMP10, a MMP11, a MMP12, a MMP13, a MMP14, an ADAM10, an ADAM12, an urokinase plasminogen activator (uPA), an enterokinase, a prostate-specific target (PSA, hK3), an interleukin-1β converting enzyme, a thrombin, a FAP (FAP-α), a type II transmembrane serine protease (TTSP), a neutrophil elastase, a cathepsin G, a proteinase 3, a neutrophil serine protease 4, a mast cell chymase, a mast cell tryptase, a dipeptidyl peptidase, and a dipeptidyl peptidase IV (DPPIV/CD26).

23. The pharmaceutical composition of any one of claims 1-22, wherein the cleavable linker comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3688-3770 and SEQ ID No: 3878.

24. The pharmaceutical composition of claim 23, wherein the cleavable linker comprises an amino acid sequence of SEQ ID Nos: 3688-3770 and SEQ ID No: 3878.

25. The pharmaceutical composition of any one of claims 12-24, wherein the target antigen is a tumor antigen.

26. The pharmaceutical composition of claim 25, wherein the third domain specifically binds to a target antigen selected from the group consisting of: CD19 (B-lymphocyte antigen CD19, B-Lymphocyte Surface Antigen B4, T-Cell Surface Antigen Leu-12, CVID3), PSMA (prostate specific membrane antigen), MSLN (mesothelin), BCMA (B-cell maturation antigen), DLL3 (Delta-like ligand 3), FLT3 (FMS-like tyrosine kinase 3), CD20 (B-lymphocyte antigen CD20, MS4A1, B1, Bp35, CVID5, LEU-16, MS4A2, S7, membrane spanning 4-domains A1), CD22 (SIGLEC-2, SIGLEC2), CD25 (IL2RA, interleukin-2 receptor alpha chain), CD27 (S152, S152. LPFS2, T14, TNFRSF7, Tp55), CD30 (TNFRSF8), CD33 (Siglec-3, sialic acid binding Ig-like lectin 3, SIGLEC3, SIGLEC-3, gp67, p67), CD37 (GP52-40, TSPAN26), CD38 (cyclic

ADP ribose hydrolase, ADPRC1, ADPRC 1), CD40 (Bp50, CDW40, TNFRSF5, p50), CD44 (HCAM, homing cell adhesion molecule), Pgp-1 (phagocytic glycoprotein-1), Hermes antigen, lymphocyte homing receptor, ECM-III, and HUTCH-1), CD48 (BLAST-1, B-lymphocyte activation marker, SLAMF2, signaling lymphocytic activation molecule 2), CD52 (CAMPATH-1 antigen), CD70, CD73 (NT5E, ecto-5'-nucleotidase), CD39 (ENTPD1, Ectonucleoside triphosphate diphosphohydrolase-1), CD74 (HLA class II histocompatibility antigen gamma chain, HLA-DR antigens-associated invariant chain), CD79b (immunoglobulin-associated beta), CD80 (B7-1), CD86 (B7-2), CD123 (IL3RA, interleukin-3 receptor), CD133 (PROM1), CD137 (TNFRSF9, tumor necrosis factor receptor superfamily member 9, 4-1BB, ILA, induced by lymphocyte activation), CD138 (SDC1), alpha fetoprotein (AFP), c-Met; c-Kit; CD371 (CLEC12A, C-type lectin domain family 12 member A, CLL1)); CD370 (CLEC9A, C-type lectin domain containing 9A); cadherin 3 (CDH3, p-cadherin, PCAD); carbonic anhydrase 6 (CA6); carbonic anhydrase 9 (CA9, CAIX); carcinoembryonic antigen related cell adhesion molecule 3 (CEACAM3); carcinoembryonic antigen related cell adhesion molecule 5 (CEACAM5); CD66c (CEACAM6, carcinoembryonic antigen related cell adhesion molecule 6); chorionic somatomammotropin hormone 1 (CSH1, CS1); coagulation factor III, tissue factor (F3, TF); collectin subfamily member 10 (COLEC10); delta like canonical Notch ligand 3 (DLL3); ectonucleotide pyrophosphatase/ phosphodiesterase 3 (ENPP3); ephrin A1 (EFNA1); epidermal growth factor receptor (EGFR); EGFR variant III (EGFRvIII); EPH receptor A2 (EPHA2); epithelial cell adhesion molecule (EPCAM); erb-b2 receptor tyrosine kinase 2 (ERBB2, HER2); fibroblast activation protein alpha (FAP); fibroblast growth factor receptor 2 (FGFR2); fibroblast growth factor receptor 3 (FGFR3); folate hydrolase 1 (FOLH1, PSMA); folate receptor 1 (FOLR1, FRa); GD2 ganglioside; glycoprotein NMB (GPNMB, osteoactivin); guanylate cyclase 2C (GUCY2C, GCC); human papillomavirus (HPV) E6; HPV E7; major histocompatibility complex (MHC) class I-presented neoantigens, major histocompatibility complex (MHC) class II-presented neoantigens, major histocompatibility complex, class I, E (HLA-E); major histocompatibility complex, class I, F (HLA-F); major histocompatibility complex, class I, G (HLA-G, MHC-G); integrin subunit beta 7 (ITGB7); leukocyte immunoglobulin like receptor B1 (LILRB1, ILT2); leukocyte immunoglobulin like receptor B2 (LILRB2, ILT4); LY6/PLAUR domain containing 3 (LYPD3, C4.4A); glypican 3 (GPC3); KRAS proto-oncogene, GTPase (KRAS); MAGE family member A1 (MAGEA1); MAGE family member A3 (MAGEA3); MAGE family member A4 (MAGEA4); MAGE family member A11 (MAGEA11); MAGE family member C1 (MAGEC1); MAGE family member C2 (MAGEC2); MAGE family member D1 (MAGED1); MAGE family member D2 (MAGED2); mesothelin (MSLN); mucin 1 (MUC1) and splice variants thereof (*e.g.*, MUC1/C, D, and Z);

mucin 16 (MUC16); necdin (NDN); nectin cell adhesion molecule 4 (NECTIN4); SLIT and NTRK like family member 6 (SLITRK6); promyelocytic leukemia (PML, TRIM19); protein tyrosine kinase 7 (inactive) (PTK7); CD352 (SLAMF6, SLAM family member 6); CD319 (SLAMF7, SLAM family member 7, 19A, CRACC, CS1); sialic acid binding Ig like lectin 7 (SIGLEC7); sialic acid binding Ig like lectin 9 (SIGLEC9); solute carrier family 34 (sodium phosphate), member 2 (SLC34A2); solute carrier family 39 member 6 (SLC39A6, LIV1); STEAP family member 1 (STEAP1); STEAP family member 2 (STEAP2); CD134 (TNFRSF4, TNF receptor superfamily member 4, OX40); CD137L (TNFSF9, TNF superfamily member 9, 4-1BB-L); CD261 (TNFRSF10A, TNF receptor superfamily member 10a, DR4, TRAILR1); CD262 (TNFRSF10B, TNF receptor superfamily member 10b, DR5, TRAILR2); CD267 (TNFRSF13B, TNF receptor superfamily member 13B, TACI, IGAD2); CD269 (TNFRSF17, TNF receptor superfamily member 17, BCMA,); CD357 (TNFRSF18, TNF receptor superfamily member 18 GITR); transferrin (TF); transforming growth factor beta 1 (TGFB1); trophoblast glycoprotein (TPBG, 5T4); trophinin (TRO, MAGED3); tumor associated calcium signal transducer 2 (TACSTD2, TROP2, EGP1); Fucosyl GM1; sialyl Lewis adhesion molecule (sLe); ROR1; CD30; and Lewis Y antigen.

27. The pharmaceutical composition of claim 26, wherein the third domain specifically binds to CD19.

28. The pharmaceutical composition of claim 27, wherein the third domain comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3771-3792.

29. The pharmaceutical composition of claim 28, wherein the third domain comprises an amino acid sequence having at least 90% homology to SEQ ID Nos: 3771-3792.

30. The pharmaceutical composition of claim 29, wherein the third domain comprises an amino acid sequence of SEQ ID Nos: 3771-3792.

31. The pharmaceutical composition of claim 30, wherein the third domain comprises an amino acid sequence of SEQ ID No: 3771.

32. The pharmaceutical composition of any one of claims 27-31, wherein the domains of the half-life extended immune cell engaging protein are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(C)-(A)-(B)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2-(A)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH.

33. The pharmaceutical composition of claim 32, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3839-3843.

34. The pharmaceutical composition of claim 33, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3839-3843.

35. The pharmaceutical composition of claim 26, wherein the third domain specifically binds to CD20.

36. The pharmaceutical composition of claim 35, wherein the third domain comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3793-3808, 3880.

37. The pharmaceutical composition of claim 36, wherein the third domain comprises an amino acid sequence having at least 90% homology to SEQ ID Nos: 3793-3808, 3880.

38. The pharmaceutical composition of claim 37, wherein the third domain comprises an amino acid sequence of SEQ ID Nos: 3793-3808, 3880.

39. The pharmaceutical composition of claim 38, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3882.

40. The pharmaceutical composition of any one of claims 35-39, wherein the domains of the half-life extended immune cell engaging protein are linked in the following order: H_2N-(A)-(B)-(C)-COOH, or by linkers L1 and L2 in the following order: H_2N-(A)-L1-(B)-L2-(C)-COOH.

41. The pharmaceutical composition of claim 26, wherein the third domain specifically binds to CD33.

42. The pharmaceutical composition of claim 41, wherein the third domain comprises an amino acid sequence having at least 80% homology to SEQ ID Nos: 3809-3823.

43. The pharmaceutical composition of claim 42, wherein the third domain comprises an amino acid sequence having at least 90% homology to SEQ ID Nos: 3809-3823.

44. The pharmaceutical composition of claim 43, wherein the third domain comprises an amino acid sequence of SEQ ID Nos: 3809-3823.

45. The pharmaceutical composition of claim 44, wherein the third domain comprises an amino acid sequence of SEQ ID No: 3809.

46. The pharmaceutical composition of any one of claims 42-45, wherein the domains of the half-life extended immune cell engaging protein are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH.

47. The pharmaceutical composition of claim 46, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3833-3837.

48. The pharmaceutical composition of claim 49, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3834-3837.

49. The pharmaceutical composition of claim 26, wherein the third domain specifically binds to FLT3.

50. The pharmaceutical composition of claim 49, wherein the third domain is a single domain antibody that specifically binds to FLT3.

51. The pharmaceutical composition of claim 50, wherein the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1080-1155 and 3497-3498, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1156-1231, and 3499-3500, a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1232-1307, and 3501-3502.

52. The pharmaceutical composition of claim 51, wherein the CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1150, 1152, 3497, and 3498; the CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1226, 1228, 3499, and 3500; the CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1302, 1304, 3501, and 3502.

53. The pharmaceutical composition of claim 51 or 52, wherein the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1004-1079 and 3495-3496.

54. The combination of any one of claims 49-53, wherein the third domain comprises an amino acid sequence selected from the group consisting of: SEQ ID Nos: 1074, 1076, 3495, and 3496.

55. The pharmaceutical composition of claim 54, wherein the third domain comprises an amino acid sequence of SEQ ID No: 1074.

56. The pharmaceutical composition of claim 55, wherein the domains of the half-life extended immune cell engaging protein are linked in one of the following orders: H_2N-(C)-(B)-(A)-COOH, H_2N-(A)-(B)-(C)-COOH, H_2N-(C)-(A)-(B)-COOH, H_2N-(A)-(C)-(B)-COOH, or by linkers L1 and L2 in one of the following orders: H_2N-(C)-L1-(B)-L2(A)-COOH, H_2N-(A)-L1-(B)-L2-(C)-COOH, H_2N-(C)-L1-(A)-L2-(B)-COOH, H_2N-(A)-L1-(C)-L2(B)-COOH.

57. The pharmaceutical composition of claim 54, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3844-3849.

58. The pharmaceutical composition of claim 57, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3846-3849.

59. The pharmaceutical composition of claim 54, wherein the third domain comprises an amino acid sequence of SEQ ID No: 1076.

60. The pharmaceutical composition of claim 59, wherein the domains of the half-life extended immune cell engaging protein are linked in the following order: H_2N-(C)-(B)-(A)-COOH, or by linkers L1 and L2 in the following order: H_2N-(C)-L1-(B)-L2(A)-COOH.

61. The pharmaceutical composition of claim 60, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID Nos: 3850-3855.

62. The pharmaceutical composition of claim 61, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID No: 3854.

63. The pharmaceutical composition of claim 26, wherein the third domain is a single domain antibody that specifically binds to PSMA.

64. The pharmaceutical composition of claim 63, wherein the third domain comprises a CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 462-465, a CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 466-472, and a CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 474-475.

65. The pharmaceutical composition of claim 64, wherein the CDR1 comprises the amino acid sequence of SEQ ID No: 462, the CDR2 comprises the amino acid of SEQ ID No: 473, the CDR3 comprises the amino acid sequence of SEQ ID No: 474.

66. The pharmaceutical composition of any one of claims 63-65, wherein the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 476-489.

67. The pharmaceutical composition of any one of claims 63-66, wherein the third domain comprises the amino acid sequence of SEQ ID Nos: 489.

68. The pharmaceutical composition of claim 63, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID No: 3824-3831.

69. The pharmaceutical composition of claim 26, wherein the third domain is a single domain antibody that specifically binds to MSLN.

70. The pharmaceutical composition of claim 69, wherein the third domain comprises a CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID Nos: 490-528, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 529-567, and a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 568-606.

71. The pharmaceutical composition of claim 70, wherein the CDR1 comprises the amino acid sequence of SEQ ID No: 523, the CDR2 comprises the amino acid of SEQ ID No: 562, the CDR3 comprises the amino acid sequence of SEQ ID No: 601.

72. The pharmaceutical composition of any one of claims 69-71, wherein the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 607-650.

73. The pharmaceutical composition of any one of claims 69-72, wherein the third domain comprises the amino acid sequence of SEQ ID No: 647.

74. The pharmaceutical composition of claim 69, wherein the half-life extended immune cell engaging protein comprises an amino acid sequence of SEQ ID No: 3856-3858.

75. The pharmaceutical composition of claim 26, wherein the third domain is a single domain antibody that specifically binds to BCMA.

76. The pharmaceutical composition of claim 75, wherein the third domain CDR1 comprises comprising an amino acid selected from the group consisting of SEQ ID Nos: 1-115, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 116-230, and a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 231-345.

77. The pharmaceutical composition of claim 76, wherein the CDR1 comprises the amino acid sequence of SEQ ID No: 73, the CDR2 comprises the amino acid of SEQ ID No: 188, the CDR3 comprises the amino acid sequence of SEQ ID No: 303.

78. The pharmaceutical composition of any one of claims 75-77, wherein the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 346-461.

79. The pharmaceutical composition of any one of claims 75-78, wherein the third domain comprises the amino acid sequence of SEQ ID No: 383.

80. The pharmaceutical composition of claim 26, wherein the third domain is a single domain antibody that specifically binds to DLL3.

81. The pharmaceutical composition of claim 80, wherein the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 1751-2193, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 2194-2636, and a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 2637-3080.

82. The pharmaceutical composition of claim 81, wherein the CDR1 comprises the amino acid sequence of SEQ ID No: 2182, the CDR2 comprises the amino acid of SEQ ID No: 2625, the CDR3 comprises the amino acid sequence of SEQ ID No: 3069.

83. The pharmaceutical composition of any one of claims 80-82, wherein the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 1308-1750.

84. The pharmaceutical composition of any one of claims 80-83, wherein the third domain comprises the amino acid sequence of SEQ ID No: 1739.

85. The pharmaceutical composition of claim 26, wherein the third domain is a single domain antibody that specifically binds to EGFR.

86. The pharmaceutical composition of claim 85, wherein the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 651-699, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 700-748, a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 479-797.

87. The pharmaceutical composition of claim 86, wherein the third domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 798-846.

88. The pharmaceutical composition of claim 26, wherein the third domain is a single domain antibody that specifically binds to EpCAM.

89. The pharmaceutical composition of claim 88, wherein the third domain comprises a CDR1 comprising an amino acid selected from the group consisting of SEQ ID Nos: 847-884, a CDR2 comprising an amino acid selected from the group consisting of SEQ ID Nos: 885-922, a CDR3 comprising an amino acid selected from the group consisting of SEQ ID Nos: 923-960.

90. The pharmaceutical composition of claim 89, wherein the CDR1 comprises the amino acid sequence of SEQ ID No: 874 or 863, the CDR2 comprises the amino acid of SEQ ID No: 885 or 901, the CDR3 comprises the amino acid sequence of SEQ ID No: 923 or 939.

91. The pharmaceutical composition of any one of claims 88-90, wherein the third domain comprises an sequence selected from the group consisting of SEQ ID Nos: 961-1003.

92. The pharmaceutical composition of any one of claims 88-91, wherein the third domain comprises the amino acid sequence of SEQ ID No: 999 or 1003.

93. The pharmaceutical composition of claims 11-92, wherein the first domain comprises a single-chain variable fragment (scFv) specific to human CD3.

94. The pharmaceutical composition of claim 93, wherein the scFv specific to human CD3 comprises a variable heavy chain region (VH), a variable light chain region (VL), and a linker, wherein VH comprises complementarity determining regions HC CDR1, HC CDR2, and HC CDR3, and wherein VL comprises complementarity determining regions LC CDR1, LC CDR2, and LC CDR3.

95. The pharmaceutical composition of claim 94, wherein the HC CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3081, and 3087-3098, the HC CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3082, and 3099-3109, the HC CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3083, and 3110-3119.

96. The pharmaceutical composition of claim 95, wherein the HC CDR1 comprises the amino acid sequence of SEQ ID No: 3097, the HC CDR2 comprises the amino acid sequence of SEQ ID No: 3108, the HC CDR3 comprises the amino acid sequence of SEQ ID No: 3110.

97. The pharmaceutical composition of claims 94-96, wherein the LC CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3084, and 3120-3132, the LC CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3085, and 3099-3109, the LC CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3086, and 3146-3152.

98. The pharmaceutical composition of claim 97, wherein the LC CDR1 comprises the amino acid sequence of SEQ ID No: 3120, the LC CDR2 comprises the amino acid sequence of SEQ ID No: 3145, the LC CDR3 comprises the amino acid sequence of SEQ ID No: 3146.

99. The pharmaceutical composition of any one of claims 11-94, wherein the first domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3153-3169.

100. The pharmaceutical composition of any one of claims 11-94, wherein the first domain comprises the amino acid sequence of SEQ ID No: 3153.

101. The pharmaceutical composition of any one of claims 94-100, wherein the linker comprises an amino acid sequence GGGGSGGGGSGGGGS (SEQ ID NO: 3868).

102. The pharmaceutical composition of any one of claims 11-101, wherein the second domain comprises a single domain antibody (sdAb) which specifically binds to HSA.

103. The pharmaceutical composition of claim 102, wherein the sdAb which specifically binds to HSA comprises complementarity determining regions CDR1, CDR2, and CDR3, wherein the CDR1 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3170, and 3173-3175, the CDR2 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3171, and 3176-3181, the CDR3 comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3172, and 8182-3183.

104. The pharmaceutical composition of claim 103, wherein the CDR1 comprises an amino acid sequence of SEQ ID No: 3174, the CDR2 comprises an amino acid of SEQ ID No: 3178, the CDR3 comprises an amino acid sequence of SEQ ID No: 3183.

105. The pharmaceutical composition of any one of claims 11-103, wherein the second domain comprises an amino acid sequence selected from the group consisting of SEQ ID Nos: 3184-3193.

106. The pharmaceutical composition of claim 105, wherein the second domain comprises the amino acid sequence of SEQ ID No: 3190.

107. The pharmaceutical composition of any one of claims 11-106, wherein linkers L1 and L2 are each independently selected from $(GS)_n$ (SEQ ID No. 3859), $(GGS)_n$ (SEQ ID No. 3860), $(GGGS)_n$ (SEQ ID No. 3861), $(GGSG)_n$ (SEQ ID No. 3862), $(GGSGG)_n$ (SEQ ID No. 3863), $(GGGGS)_n$ (SEQ ID No. 3864), $(GGGGG)_n$ (SEQ ID No. 3865), or $(GGG)_n$ (SEQ ID No. 3866), wherein n is 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10, (GGGGSGGGGSGGGGSGGGGS)(SEQ ID No. 3867), (GGGGSGGGGSGGGGS) (SEQ ID No. 3868), LPETG (SEQ ID NO. 3869), (GGGGSGGGS) (SEQ ID No. 3871) or SGGG (SEQ ID NO. 3872).

108. The pharmaceutical composition of any one of claims 11-106, wherein linkers L1 and L2 are each independently GGGGSGGGS (SEQ ID NO: 3871).

109. A method for the treatment or amelioration of a disease comprising administrating to a subject in need thereof a pharmaceutical composition according to any one of claims 1-108.

110. The method of claim 106, wherein the disease is a cancer.

111. A method for increasing survival in a subject suffering from a cancer, the method comprising administering to the subject a pharmaceutical composition according to any one of claims 1-108.

112. A method of reducing tumor size, the method comprising administering to a subject from a cancer a pharmaceutical composition according to any one of claims 1-108.

113. The method of any one of claims 109-112, wherein the cancer is selected from the group consisting of: mesothelioma, a prostate cancer, a breast cancer, a brain cancer, a bladder cancer, a pancreatic carcinoma, a renal cancer, a solid tumor, a liver cancer, a leiomyosarcoma, an endometrium cancer, a breast cancer, a female reproductive system cancer, an ovarian carcinoma, a soft tissue sarcoma, a gastric cancer, a digestive/gastrointestinal cancer, a colorectal cancer, a glioblastoma multiforme, a head and neck cancer, a squamous cell carcinoma, a colon cancer, a gastric cancer, a rhabdomyosarcoma, an adrenal cancer, a lung cancer, an esophageal cancer, a colon cancer, a lung cancer, a non-small cell lung carcinoma (NSCLC), a neuroblastoma, a melanoma, glioblastoma multiforme, an ovarian cancer, an endocrine cancer, a respiratory/thoracic cancer, an anal cancer, a gastro-esophageal cancer, a thyroid cancer, a cervical cancer, an endometrial cancer, a hematological cancer, a leukemia, a lymphocytic leukemia, a multiple myeloma, a lymphoma, a Hodgkin's lymphoma, a non-Hodgkin's lymphoma, a lymphocytic leukemia, an anaplastic large-cell lymphoma (ALCL), or a myeloid leukemia.

114. The method of claim 113, wherein the cancer is the prostate cancer.

115. The method of claim 113, wherein the cancer is the ovarian carcinoma.

116. The method of claim 113, wherein the cancer is the pancreatic carcinoma.

117. The method of claim 113, wherein the cancer is the mesothelioma.

118. The method of claim 113, wherein the cancer is the lung cancer.

119. A pharmaceutical composition comprising an extended-release binding protein which comprises an antigen binding protein, a masking peptide, and a cleavable linker,
wherein upon administering to a subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation.

120. The pharmaceutical composition of claim 119, wherein the antigen binding protein comprises an antigen binding domain binds to a target antigen.

121. The pharmaceutical composition of claim 120, wherein the masking peptide inhibits or reduces the binding of the antigen binding protein to the target antigen.

122. The pharmaceutical composition of claim 119, wherein the antigen binding protein comprises an immune cell engaging domain.

123. The pharmaceutical composition of claim 122, wherein the immune cell engaging domain comprises a T cell engaging domain.

124. The pharmaceutical composition of claim 123, wherein the T cell engaging domain binds a CD3 molecule.

125. The pharmaceutical composition of claim 124, wherein the masking peptide inhibits or reduces the binding of the antigen binding protein to the CD3 molecule.

126. The pharmaceutical composition of any one of claims 119-125, wherein the antigen binding protein comprises a half-life extension domain.

127. The pharmaceutical composition of claim 126, wherein the half-life extension domain binds a human serum albumin (HSA).

128. The pharmaceutical composition of any one of claims 119-127, wherein the cleavable linker comprises a cleavage site.

129. The pharmaceutical composition of claim 128, wherein the cleavable site is recognized by a protease.

130. The pharmaceutical composition of any one of claims 119-129, wherein the masking peptide is covalently linked to the N-terminus or the C-terminus of the antigen binding protein through the cleavable linker.

131. A method of making an extended-release binding protein comprising adding a cleavable linker and a masking peptide to an antigen binding protein,
wherein upon administering to a subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation.

132. The pharmaceutical composition of claim 131, wherein the antigen binding protein comprises an antigen binding domain binds to a target antigen.

133. The pharmaceutical composition of claim 132, wherein the masking peptide inhibits or reduces the binding of the antigen binding protein to the target antigen.

134. The pharmaceutical composition of claim 131, wherein the antigen binding protein comprises an immune cell engaging domain.

135. The pharmaceutical composition of claim 134, wherein the immune cell engaging domain comprises a T cell engaging domain.

136. The pharmaceutical composition of claim 135, wherein the T cell engaging domain binds a CD3 molecule.

137. The pharmaceutical composition of claim 136, wherein the masking peptide inhibits or reduces the binding of the antigen binding protein to the CD3 molecule.

138. The pharmaceutical composition of any one of claims 131-137, wherein the antigen binding protein comprises a half-life extension domain.

139. The pharmaceutical composition of claim 138, wherein the half-life extension domain binds a human serum albumin (HSA).

140. The pharmaceutical composition of any one of claims 131-139, wherein the cleavable linker comprises a cleavage site.

141. The pharmaceutical composition of claim 140, wherein the cleavable site is recognized by a protease.

142. The pharmaceutical composition of any one of claims 131-141, wherein the masking peptide is covalently linked to the N-terminus or the C-terminus of the antigen binding protein through the cleavable linker.

143. A method of treating or ameliorating a disease comprising administrating to a subject in need thereof a pharmaceutical composition according to any one of claims 119-130.

144. A method of increasing the therapeutic index of an antigen binding protein, comprising adding a cleavable linker and a masking peptide to the antigen binding protein to form an extended-release binding protein,

wherein upon administering to a subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation.

145. A method of decreasing the CRS level in a subject, comprising adding a cleavable linker and a masking peptide to an antigen binding protein to form an extended-release binding protein,

wherein upon administering to the subject, the extended-release binding protein gradually releases an active version of the extended-release binding protein when the cleavable linker is cleaved in systemic circulation.

146. A method of gradually increase an active drug's concentration in a subject's systemic circulation comprising administering an extended-release binding protein to the subject, wherein the extended-release binding protein comprises an antigen binding protein, a masking peptide, and a cleavable linker, wherein the extended-release binding protein releases the active drug upon cleavage of the cleavable linker in systemic circulation.

147. A pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker,

wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, and

wherein the cleavable linker is significantly cleaved in systemic circulation.

148. A pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker,

wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, and

wherein a half-life of the protein in systemic circulation is longer than a comparable protein without the masking peptide.

149. A pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker,

wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker, and

wherein a comparable protein without the masking peptide has a nonlinear pharmacokinetics (PK) across a dose range evaluated, and

wherein the protein has an improved linearity of PK across the dose range evaluated compared to the comparable protein.

150. A pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker,

wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker,

wherein the binding moiety specifically binds to a target in a subject, and

wherein a molar amount of the protein's binding moiety bound to the target when administered to the subject is lower compared to a molar amount of a binding moiety of a

comparable protein without the masking peptide when administered to the subject at a same dose level.

151. A pharmaceutical composition comprising a protein which comprises a binding moiety, a masking peptide, and a cleavable linker,

wherein the masking peptide is covalently linked to the binding moiety through the cleavable linker,

wherein the binding moiety specifically binds to a target in a subject, and

wherein a first binding rate between the protein's binding moiety and the target when administered to the subject is lower compared to a second binding rate between a binding moiety of a comparable protein without the masking peptide and the target.

152. The pharmaceutical composition of any one of claims 147-151, wherein the binding moiety specifically binds to ICOS (inducible T cell co-stimulator, CD278), OX40 (CD134, TNFRSF4, tumor necrosis factor receptor superfamily member 4), CD40 (TNFRSF5, tumor necrosis factor receptor superfamily member 5), DR5 (death receptor 5, TRAIL receptor 2), GITR (glucocorticoid-induced TNFR-related protein, TNFRSF18, tumor necrosis factor receptor superfamily member 18), 4-1BB (CD137, TNFRSF9, tumor necrosis factor receptor superfamily member 9) or any combinations thereof.

153. The pharmaceutical composition of claim 152, wherein the protein comprises an antibody selected from the group consisting of GSK3359609, PF-8600, JNJ-64457107, CP-870,893, SGN-40 (Dacetuzumab), MEDI3039, ABBV-621, MEDI1873, AMG 228, PF-05082566 (Utomilumab), and urelumab.

154. A method of treating or ameliorating a disease comprising administrating to a subject in need thereof a pharmaceutical composition according to any one of claims 147-153.