TRISPECIFIC AND/OR TRIVALENT BINDING PROTEINS USING THE CROSS-OVER-DUAL-VARIABLE DOMAIN (CODV) FORMAT FOR TREATMENT OF HIV INFECTION

[0001] This application claims priority to U.S. Provisional Application No. 62/831,415, filed April 9, 2019, and EP Application No. EP19306312.0, filed October 8, 2019, the disclosures of each of which are incorporated herein by reference in their entirety.

SUBMISSION OF SEQUENCE LISTING ON ASCII TEXT FILE

[0002] The content of the following submission on ASCII text file is incorporated herein by reference in its entirety: a computer readable form (CRF) of the Sequence Listing (file name: 183952031940SEQLIST.TXT, date recorded: March 25, 2020, size: 580 KB).

FIELD

[0003] The disclosure relates to trispecific and/or trivalent binding proteins comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein a first pair of polypeptides forming the binding protein possess dual variable domains having a cross-over orientation. The disclosure also relates to methods for making trispecific and/or trivalent binding proteins and uses of such binding proteins for treating and/or preventing HIV/AIDS.

BACKGROUND

[0004] Anti-retroviral therapy (ART) has been the standard of care for HIV/AIDS patients in the past decades. ART drugs target internal proteins such as reverse transcriptase (RT), integrase (IN), and viral protease (PI) by inhibiting reverse transcription of HIV-1 genome, integration of HIV-1 genome, and proteolytic cleavage of protein precursors that are necessary for the production of infectious viral particles. Treatment using ART or combination of different classes of ART results in inhibition of HIV-1 replication and subsequent reduction of viremia, often to undetectable level (aviremic status). Although ART greatly helps HIV patients in controlling their disease progression, and containing the global HIV epidemic, it does require patients taking daily medicines often following a strict regimen. About 10% patients fail therapy each year due to drug toxicity, suboptimal adherence and emerging drug resistance. As more HIV patients can live a normal life span (over 80 years), chronic complications are of particular concern,

such as aging and drug-drug interaction, and cardiovascular/renal/bone toxicities. The economic burden treating HIV/AIDS has not subsided thus far.

[0005] HIV latently infects long-lived resting memory CD4+ T cells and others as a form of proviral DNA integrated into the host genome. The latently infected cells survive for decades and self-renew like stem cells via homeostatic proliferation, which is regarded as an HIV-1 reservoir. The HIV-1 reservoirs are neither affected by ART nor the host immune system as they do not express viral proteins. Yet, a small proportion of cells among the reservoirs are randomly reactivated by unknown mechanism(s), which are responsible for recurrence of viremia once ART is stopped.

[0006] Therefore, a need exists for developing HIV/AIDS treatments to target the HIV-1 reservoir(s), and ultimately eliminate them completely, achieving a cure, or long term remission of HIV without any further treatment. Any therapeutic strategy to eliminate the HIV-1 reservoir needs to activate the reservoir first, followed by elimination of the activated HIV-1 reservoir cells.

[0007] All references cited herein, including patent applications, patent publications, and UniProtKB/Swiss-Prot Accession numbers are herein incorporated by reference in their entirety, as if each individual reference were specifically and individually indicated to be incorporated by reference.

BRIEF SUMMARY

[0008] To meet these and other needs, provided herein are multispecific binding proteins (*e.g.*, antibodies) that form three antigen binding sites. In some embodiments, the binding proteins bind one or more HIV target proteins and a CD3 polypeptide. In some embodiments, the binding proteins bind an HIV target protein, a CD28 polypeptide, and a CD3 polypeptide. The trispecific anti-HIV/CD28xCD3 T cell engager (TCE) concept disclosed herein is thought to be an effective eliminator of the HIV-1 reservoir through activation by anti-CD3, co-activation by anti-CD28, and subsequent killing of activated HIV-1 reservoir cells through anti-HIV/anti-CD28 by engaging activated CD8 T cells, providing a potential strategy for attacking the HIV-1 reservoir. In addition, anti-CD3 binding sites are described with high affinity binding to human CD3 polypeptides and potential manufacturing liabilities (*e.g.*, deamidation sites) removed.

[0009] In some embodiments, provided herein are binding proteins comprising four polypeptide chains that form the three antigen binding sites that specifically bind one or

more HIV target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

$$V_{L2}\text{-}L_1\text{-}V_{L1}\text{-}L_2\text{-}C_L \quad [I]$$

and a second polypeptide chain comprises a structure represented by the formula:

$$V_{H1}\text{-}L_3\text{-}V_{H2}\text{-}L_4\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \quad [II]$$

and a third polypeptide chain comprises a structure represented by the formula:

$$V_{H3}\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \quad [III]$$

and a fourth polypeptide chain comprises a structure represented by the formula:

$$V_{L3}\text{-}C_L \quad [IV]$$

wherein:

V_{L1} is a first immunoglobulin light chain variable domain;

V_{L2} is a second immunoglobulin light chain variable domain;

V_{L3} is a third immunoglobulin light chain variable domain;

V_{H1} is a first immunoglobulin heavy chain variable domain;

V_{H2} is a second immunoglobulin heavy chain variable domain;

V_{H3} is a third immunoglobulin heavy chain variable domain;

C_L is an immunoglobulin light chain constant domain;

C_{H1} is an immunoglobulin C_{H1} heavy chain constant domain;

C_{H2} is an immunoglobulin C_{H2} heavy chain constant domain;

C_{H3} is an immunoglobulin C_{H3} heavy chain constant domain;

hinge is an immunoglobulin hinge region connecting the C_{H1} and C_{H2} domains; and

L_1, L_2, L_3 and L_4 are amino acid linkers;

wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair;

wherein V_{H1} and V_{L1} form a first antigen binding site;

wherein V_{H2} and V_{L2} form a second antigen binding site that binds a CD3 polypeptide, wherein the V_{H2} domain comprises a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22), and the V_{L2} domain comprises a CDR-L1 sequence comprising the amino acid sequence of $QSLVHX_1NX_2X_3TY$, wherein X_1 is E or Q, X_2 is A or L, and X_3 is Q, R, or F (SEQ ID NO:293), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30); and

wherein V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein.

[0010] In some embodiments, the first binding site binds a CD28 polypeptide (*e.g.*, a human CD28 polypeptide). In some embodiments, the V_{H1} domain comprises a CDR-H1 sequence comprising the amino acid sequence of GYTFTSYY (SEQ ID NO:31), a CDR-H2 sequence comprising the amino acid sequence of IYPGNVNT (SEQ ID NO:32), and a CDR-H3 sequence comprising the amino acid sequence of TRSHYGLDWNFDV (SEQ ID NO:33), and the V_{L1} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QNIYVW (SEQ ID NO:34), a CDR-L2 sequence comprising the amino acid sequence of KAS (SEQ ID NO:35), and a CDR-L3 sequence comprising the amino acid sequence of QQGQTYPY (SEQ ID NO:36). In some embodiments, the V_{H1} domain comprises the amino acid sequence of QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTAYMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSS (SEQ ID NO:59), and/or the V_{L1} domain comprises the amino acid sequence of DIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIK (SEQ ID NO:60).

[0011] In some embodiments, the CDR-L1 sequence of the V_{L2} domain comprises an amino acid sequence selected from the group consisting of QSLVHQNAQTY (SEQ ID NO:24), QSLVHENLQTY (SEQ ID NO:25), QSLVHENLFTY (SEQ ID NO:26), and QSLVHENLRTY (SEQ ID NO:27). In some embodiments, the V_{H2} domain comprises: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and the V_{L2} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QSLVHQNAQTY (SEQ ID NO:24), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, the V_{H2} domain comprises: a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of

RGVYYALSPFDY (SEQ ID NO:22); and the V_{L2} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLQTY (SEQ ID NO:25), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, the V_{H2} domain comprises: a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and the V_{L2} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLFTY (SEQ ID NO:26), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, the V_{H2} domain comprises: a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and the V_{L2} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLRTY (SEQ ID NO:27), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, the V_{H2} domain comprises the amino acid sequence of QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKD KSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPF DYWGQGTLVTVSS (SEQ ID NO:52), and/or the V_{L2} domain comprises an amino acid sequence selected from the group consisting of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVS NRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:54), DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVS NRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:55), DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVS NRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:56), and

DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLRTYLSWYLQKPGQSPQSLIYKVS NRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:57). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:54. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:55. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:56. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:57.

[0012] In some embodiments, the third antigen binding site binds an HIV target protein selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160. In some embodiments, the V_{H3} domain comprises a CDR-H1 sequence comprising the amino acid sequence of NCPIN (SEQ ID NO:1) a CDR-H2 sequence comprising the amino acid sequence of WMKPRHGAVSYARQLQG (SEQ ID NO:2), and a CDR-H3 sequence comprising the amino acid sequence of GKYCTARDYYNWDFEH (SEQ ID NO:3), and the V_{L3} domain comprises a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:4), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID NO:5), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:6). In some embodiments, the V_{H3} domain comprises a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAV (SEQ ID NO:8) or IKPQYGAT (SEQ ID NO:9), and a CDR-H3 sequence comprising the amino acid sequence of DRSYGDSSWALDA (SEQ ID NO:10), and the V_{L3} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a

CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13). In some embodiments, the V_{H3} domain comprises a CDR-H1 sequence comprising the amino acid sequence of DCTLN (SEQ ID NO:14) a CDR-H2 sequence comprising the amino acid sequence of WLKPRWGAVNYARPLQG (SEQ ID NO:15), and a CDR-H3 sequence comprising the amino acid sequence of GKNCDYNWDFEH (SEQ ID NO:16), and the V_{L3} domain comprises a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:17), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID NO:18), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:19). In some embodiments, the V_{H3} domain comprises the amino acid sequence of QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRH GAVSYARQLQGRVTMTRDMYSETAFLELRSLTSDDTAVYFCTRGKYCTARDYYN WDFEHWGQGTPVTVSS (SEQ ID NO:43), and/or the V_{L3} domain comprises the amino acid sequence of SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRF SGSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:45). In some embodiments, the V_{H3} domain comprises the amino acid sequence of QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRH GAVSYARQLQGRVTMTRQLSQDPDDPDWGTAFLELRSLTSDDTAVYFCTRGKYC TARDYYNWDFEHWGQGTPVTVSS (SEQ ID NO:44), and/or the V_{L3} domain comprises the amino acid sequence of SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRF SGSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:45). In some embodiments, the V_{H3} domain comprises the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQ YGAVNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWA LDAWGQGTTVVVSA (SEQ ID NO:46), and/or the V_{L3} domain comprises the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDG VPSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49). In some embodiments, the V_{H3} domain comprises the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQ YGATNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWA

LDAWGQGTTVVVSA (SEQ ID NO:47), and/or the V_{L3} domain comprises the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDG VPSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49). In some embodiments, the V_{H3} domain comprises the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQ YGAVNFGGGFRDRVTLTRQLSQDPDDPDWGIAYMDIRGLKPDDTAVYYCARDRS YGDSSWALDAWGQGTTVVVSA (SEQ ID NO:48), and/or the V_{L3} domain comprises the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDG VPSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49). In some embodiments, the V_{H3} domain comprises the amino acid sequence of QVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGKRPEWMGWLKPR WGAVNYARPLQGRVTMTRQLSQDPDDPDWGTAFLELRSLTVDDTAVYFCTRGKN CDYNWDFEHWGRGTPVIVSS (SEQ ID NO:50), and/or the V_{L3} domain comprises the amino acid sequence of LTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFS GSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:51).

[0013] In some embodiments that may be combined with any other embodiments described herein, at least one of L_1, L_2, L_3 or L_4 is independently 0 amino acids in length. In some embodiments, L_1, L_2, L_3 and L_4 each independently are zero amino acids in length or comprise a sequence selected from the group consisting of GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO: 41), S, RT, TKGPS (SEQ ID NO: 39), GQPKAAP (SEQ ID NO: 38), and GGSGSSGSGG (SEQ ID NO: 42). In some embodiments, L_1, L_2, L_3 and L_4 each independently comprise a sequence selected from the group consisting of GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO:41), S, RT, TKGPS (SEQ ID NO:39), GQPKAAP (SEQ ID NO: 38), and GGSGSSGSGG (SEQ ID NO:42). In some embodiments, L_1 comprises the sequence GQPKAAP (SEQ ID NO: 38), L_2 comprises the sequence TKGPS (SEQ ID NO:39), L_3 comprises the sequence S, and L_4 comprises the sequence RT. In some embodiments, at least one of L_1, L_2, L_3 or L_4 comprises the sequence DKTHT (SEQ ID NO:37). In some embodiments, L_1, L_2, L_3 and L_4 comprise the sequence DKTHT (SEQ ID NO:37).

[0014] In some embodiments that may be combined with any other embodiments described herein, the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG4 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 234 and 235 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A and L235A. In some embodiments, the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG4 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 233-236 of human IgG4 according to EU Index, wherein the amino acid substitutions are E233P, F234V, L235A, and a deletion at 236. In some embodiments, the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG4 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 228 and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P and R409K. In some embodiments, the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG1 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 234, 235, and 329 of human IgG1 according to EU Index, wherein the amino acid substitutions are L234A, L235A, and P329A. In some embodiments, the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG1 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 298, 299, and 300 of human IgG1 according to EU Index, wherein the amino acid substitutions are S298N, T299A, and Y300S. In some embodiments, the hinge-C_{H2}-C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the hinge-C_{H2}-C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are S354C and T366W. In some embodiments, the hinge-C_{H2}-C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the hinge-C_{H2}-C_{H3} domain of the third polypeptide chain comprises

amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0015] In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:61 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:61; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:62 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:62; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:63 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:63; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:64 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:64. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:65 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:65; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:66 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:66; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:67 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:67; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:68 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:68. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:69 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:69; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:70 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:70; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:71 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:71; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:72 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:72. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:73 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:73; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:74 or an amino acid sequence that is at least 95% identical to the

amino acid sequence of SEQ ID NO:74; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:75 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:75; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:76 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:76. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:77 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:77; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:78 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:78; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:79 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:79; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:80 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:80. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:81 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:81; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:82 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:82; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:83 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:83; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:84 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:84. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:85 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:85; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:86 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:86; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:87 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:87; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:88 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:88. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:89 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:89; the

second polypeptide chain comprises the amino acid sequence of SEQ ID NO:90 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:90; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:91 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:91; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:92 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:92. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:93 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:93; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:94 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:94; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:95 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:95; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:96 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:96. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:97 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:97; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:98 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:98; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:99 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:99; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:100 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:100. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:101 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:101; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:102 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:102; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:103 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:103; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:104 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:104. In some embodiments, the first polypeptide chain comprises

the amino acid sequence of SEQ ID NO:105 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:105; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:106 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:106; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:107 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:107; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:108 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:108. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:109 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:109; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:110 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:110; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:111 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:111; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:112 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:112. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:113 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:113; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:114 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:114; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:115 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:115; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:116 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:116. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:117 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:117; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:118 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:118; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:119 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:119; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:120 or an amino acid

sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:120. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:121 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:121; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:122 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:122; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:123 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:123; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:124 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:124. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:129 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:129; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:130 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:130; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:131 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:131; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:132 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:132. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:133 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:133; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:134 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:134; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:135 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:135; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:136 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:136. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:137 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:137; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:138 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:138; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:139 or an amino acid sequence that is at least 95% identical

to the amino acid sequence of SEQ ID NO:139; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:140 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:140. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:141 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:141; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:142 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:142; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:143 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:143; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:144 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:144. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:145 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:145; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:146 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:146; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:147 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:147; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:148 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:148. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:149 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:149; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:150 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:150; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:151 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:151; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:152 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:152. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:153 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:153; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:154 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID

NO:154; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:155 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:155; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:156 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:156. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:157 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:157; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:158 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:158; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:159 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:159; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:160 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:160. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:161 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:161; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:162 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:162; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:163 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:163; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:164 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:164. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:165 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:165; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:166 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:166; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:167 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:167; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:168 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:168. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:169 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:169; the second polypeptide chain

comprises the amino acid sequence of SEQ ID NO:170 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:170; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:171 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:171; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:172 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:172. In some embodiments, the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:173 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:173; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:174 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:174; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:175 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:175; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:176 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:176.

[0016] In some embodiments, provided herein are isolated nucleic acid molecules comprising a nucleotide sequence encoding the binding protein of any one of the above embodiments. In some embodiments, provided herein are expression vectors comprising the nucleic acid molecule of any one of the above embodiments. In some embodiments, provided herein are isolated host cells comprising the nucleic acid molecule of any one of the above embodiments or the expression vector of any one of the above embodiments. In some embodiments, the host cell is a mammalian or insect cell.

[0017] In some embodiments, provided herein are pharmaceutical compositions comprising the binding protein of any one of the above embodiments and a pharmaceutically acceptable carrier.

[0018] In some embodiments, provided herein are methods of preventing and/or treating HIV infection in a patient comprising administering to the patient a therapeutically effective amount of at least one binding protein of any one of the above embodiments or the pharmaceutical composition of any one of the above embodiments. In some embodiments, the binding protein is co-administered with standard anti-retroviral therapy. In some embodiments, administration of the at least one binding protein results in the elimination of one or more latently and/or chronically HIV-infected cells in the patient. In some embodiments, the patient is a human.

[0019] In some embodiments, the binding protein or pharmaceutical composition of any one of the above embodiments is provided for the prevention and/or treatment of HIV infection in a patient. In some embodiments, the binding protein is to be co-administered with standard anti-retroviral therapy. In some embodiments, the binding protein causes the elimination of one or more latently and/or chronically HIV-infected cells in the patient. In some embodiments, the patient is a human.

[0020] In some embodiments, the binding protein or pharmaceutical composition of any one of the above embodiments is provided for use in the manufacture of a medicament for the prevention and/or treatment of HIV infection in a patient. In some embodiments, the binding protein is to be co-administered with standard anti-retroviral therapy. In some embodiments, the binding protein causes the elimination of one or more latently and/or chronically HIV-infected cells in the patient. In some embodiments, the patient is a human.

[0021] In some embodiments, provided herein is a vector system comprising one or more vectors encoding a first, second, third, and fourth polypeptide chain of a binding protein of any one of the above embodiments. In some embodiments, the vector system comprises a first vector encoding the first polypeptide chain of the binding protein, a second vector encoding the second polypeptide chain of the binding protein, a third vector encoding the third polypeptide chain of the binding protein, and a fourth vector encoding the fourth polypeptide chain of the binding protein.

[0022] In some embodiments, provided herein are kits comprising one, two, three, or four polypeptide chains of a binding protein according to any one of the above embodiments. In some embodiments, the kits further comprise instructions for using the polypeptide chain or binding protein according to any of the methods or uses described herein, *e.g.*, *supra*.

[0023] In some embodiments, provided herein are kits comprising one, two, three, or four polynucleotides according to any one of the above embodiments. In some embodiments, provided herein are kits of polynucleotides comprising one, two, three, or four polynucleotides of a kit of polynucleotides comprising: (a) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:177, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:178, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:179, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:180; (b) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:181, a second polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:182, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:183, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:184; (c) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:185, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:186, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:187, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:188; (d) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:189, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:190, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:191, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:192; (e) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:193, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:194, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:195, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:196; (f) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:197, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:198, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:199, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:200; (g) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:201, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:202, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:203, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:204; (h) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:205, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:206, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:207, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:208; (i) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:209, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:210, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:211, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:212; (j) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:213, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:214, a third polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:215, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:216; (k) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:217, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:218, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:219, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:220; (l) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:221, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:222, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:223, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:224; (m) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:225, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:226, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:227, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:228; (n) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:229, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:230, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:231, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:232; (o) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:233, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:234, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:235, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:236; (p) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:237, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:238, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:239, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:240; (q) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:241, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:242, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:243, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:244; (r) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:245, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:246, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:247, and a fourth polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:248; (s) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:249, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:250, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:251, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:252; (t) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:253, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:254, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:255, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:256; (u) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:257, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:258, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:259, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:260; (v) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:261, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:262, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:263, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:264; (w) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:265, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:266, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:267, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:268; (x) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:269, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:270, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:271, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:272; (y) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:273, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:274, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:275, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:276; (z) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:277, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:278, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:279, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:280; (aa) a first polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:281, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:282, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:283, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:284; (bb) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:285, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:286, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:287, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:288; or (cc) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:289, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:290, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:291, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:292. In some embodiments, the first, second, third, and fourth polynucleotides are present on one or more expression vectors, *e.g.*, one, two, three, or four expression vectors.

[0024] It is to be understood that one, some, or all of the properties of the various embodiments described herein may be combined to form other embodiments of the present invention. These and other aspects of the invention will become apparent to one of skill in the art.

BRIEF DESCRIPTION OF THE DRAWINGS

[0025] **FIG. 1** provides a schematic representation of a trispecific binding protein comprising four polypeptide chains that form three antigen binding sites that binds three target proteins: CD28, CD3, and HIV Env. A first pair of polypeptides possess dual variable domains having a cross-over orientation (VH1-VH2 and VL2-VL1) forming two antigen binding sites (VH1 and VL1; VH2 and VL2) that recognize CD28 and CD3, resepectively, and a second pair of polypeptides possess a single variable domain (VH3 and VL3) forming a single antigen binding site that recognizes HIV Env. The trispecific binding protein shown in **FIG. 1** uses a constant region with a "knobs-into-holes" mutation, where the knob is on the second pair of polypeptides with a single variable domain.

[0026] **FIG. 2** shows a schematic representation of a trispecific T cell Engager (TCE) strategy for using the anti-HIV trispecific binding protein shown in **FIG. 1** to target and eliminate the HIV reservoir.

DETAILED DESCRIPTION

[0027] The present disclosure provides trispecific and/or trivalent binding proteins comprising four polypeptide chains that form three antigen binding sites that specifically bind to one or more human immunodeficiency virus (HIV) target proteins and/or one or more T-cell receptor target proteins, wherein a first pair of polypeptides forming the binding protein possess dual variable domains having a cross-over orientation, and wherein a second pair of polypeptides possess a single variable domain.

[0028] The following description sets forth exemplary methods, parameters, and the like. It should be recognized, however, that such description is not intended as a limitation on the scope of the present disclosure but is instead provided as a description of exemplary embodiments.

Definitions

[0029] As utilized in accordance with the present disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings. Unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

[0030] It is understood that aspects and embodiments of the disclosure described herein include "comprising," "consisting," and "consisting essentially of" aspects and embodiments.

[0031] The term "polynucleotide" as used herein refers to single-stranded or double-stranded nucleic acid polymers of at least 10 nucleotides in length. In certain embodiments, the nucleotides comprising the polynucleotide can be ribonucleotides or deoxyribonucleotides or a modified form of either type of nucleotide. Such modifications include base modifications such as bromuridine, ribose modifications such as arabinoside and 2',3'-dideoxyribose, and internucleotide linkage modifications such as phosphorothioate, phosphorodithioate, phosphoroselenoate, phosphorodiselenoate, phosphoroanilothioate, phoshoraniladate and phosphoroamidate. The term "polynucleotide" specifically includes single-stranded and double-stranded forms of DNA.

[0032] An "isolated polynucleotide" is a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, which: (1) is not associated with all or a portion of a polynucleotide in which the isolated polynucleotide is found in nature, (2) is linked to a polynucleotide to which it is not linked in nature, or (3) does not occur in nature as part of a larger sequence.

[0033] An "isolated polypeptide" is one that: (1) is free of at least some other polypeptides with which it would normally be found, (2) is essentially free of other polypeptides from the same source, *e.g.*, from the same species, (3) is expressed by a cell from a different species, (4) has been separated from at least about 50 percent of polynucleotides, lipids, carbohydrates, or other materials with which it is associated in nature, (5) is not associated (by covalent or noncovalent interaction) with portions of a polypeptide with which the "isolated polypeptide" is associated in nature, (6) is operably associated (by covalent or noncovalent interaction) with a polypeptide with which it is not associated in nature, or (7) does not occur in nature. Such an isolated polypeptide can be encoded by genomic DNA, cDNA, mRNA or other RNA, of synthetic origin, or any combination thereof. Preferably, the isolated polypeptide is substantially free from polypeptides or other contaminants that are found in its natural environment that would interfere with its use (therapeutic, diagnostic, prophylactic, research or otherwise).

[0034] Naturally occurring antibodies typically comprise a tetramer. Each such tetramer is typically composed of two identical pairs of polypeptide chains, each pair having one full-length "light" chain (typically having a molecular weight of about 25 kDa) and one full-length "heavy" chain (typically having a molecular weight of about 50-70 kDa). The terms "heavy chain" and "light chain" as used herein refer to any immunoglobulin polypeptide having sufficient variable domain sequence to confer specificity for a target antigen. The amino-terminal portion of each light and heavy chain typically includes a variable domain of about 100 to 110 or more amino acids that typically is responsible for antigen recognition. The carboxy-terminal portion of each chain typically defines a constant domain responsible for effector function. Thus, in a naturally occurring antibody, a full-length heavy chain immunoglobulin polypeptide includes a variable domain (V_H) and three constant domains (C_{H1}, C_{H2}, and C_{H3}), wherein the V_H domain is at the amino-terminus of the polypeptide and the C_{H3} domain is at the carboxyl-terminus, and a full-length light chain immunoglobulin polypeptide includes a variable domain (V_L) and a constant domain (C_L), wherein the V_L domain is at the amino-terminus of the polypeptide and the C_L domain is at the carboxyl-terminus.

[0035] Human light chains are typically classified as kappa and lambda light chains, and human heavy chains are typically classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subclasses, including, but not limited to, IgG1, IgG2, IgG3, and IgG4. IgM has subclasses

including, but not limited to, IgM1 and IgM2. IgA is similarly subdivided into subclasses including, but not limited to, IgA1 and IgA2. Within full-length light and heavy chains, the variable and constant domains typically are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. *See*, *e.g.*, FUNDAMENTAL IMMUNOLOGY (Paul, W., ed., Raven Press, 2nd ed., 1989), which is incorporated by reference in its entirety for all purposes. The variable regions of each light/heavy chain pair typically form an antigen binding site. The variable domains of naturally occurring antibodies typically exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, also called complementarity determining regions or CDRs. The CDRs from the two chains of each pair typically are aligned by the framework regions, which may enable binding to a specific epitope. From the amino-terminus to the carboxyl-terminus, both light and heavy chain variable domains typically comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3, and FR4.

[0036] The term "CDR set" refers to a group of three CDRs that occur in a single variable region capable of binding the antigen. The exact boundaries of these CDRs have been defined differently according to different systems. The system described by Kabat (Kabat *et al.*, SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST (National Institutes of Health, Bethesda, Md. (1987) and (1991)) not only provides an unambiguous residue numbering system applicable to any variable region of an antibody, but also provides precise residue boundaries defining the three CDRs. These CDRs may be referred to as Kabat CDRs. Chothia and coworkers (Chothia and Lesk, 1987, *J. Mol. Biol.* 196: 901-17; Chothia *et al.*, 1989, *Nature* 342: 877-83) found that certain sub-portions within Kabat CDRs adopt nearly identical peptide backbone conformations, despite having great diversity at the level of amino acid sequence. These sub-portions were designated as L1, L2, and L3 or H1, H2, and H3 where the "L" and the "H" designates the light chain and the heavy chain regions, respectively. These regions may be referred to as Chothia CDRs, which have boundaries that overlap with Kabat CDRs. Other boundaries defining CDRs overlapping with the Kabat CDRs have been described by Padlan, 1995, *FASEB J.* 9: 133-39; MacCallum, 1996, *J. Mol. Biol.* 262(5): 732-45; and Lefranc, 2003, *Dev. Comp. Immunol.* 27: 55-77. Still other CDR boundary definitions may not strictly follow one of the herein systems, but will nonetheless overlap with the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular

residues or groups of residues or even entire CDRs do not significantly impact antigen binding. The methods used herein may utilize CDRs defined according to any of these systems, although certain embodiments use Kabat or Chothia defined CDRs. Identification of predicted CDRs using the amino acid sequence is well known in the field, such as in Martin, A.C. "Protein sequence and structure analysis of antibody variable domains," *In Antibody Engineering*, Vol. 2. Kontermann R., Dübel S., eds. Springer-Verlag, Berlin, p. 33–51 (2010). The amino acid sequence of the heavy and/or light chain variable domain may be also inspected to identify the sequences of the CDRs by other conventional methods, *e.g.*, by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. The numbered sequences may be aligned by eye, or by employing an alignment program such as one of the CLUSTAL suite of programs, as described in Thompson, 1994, *Nucleic Acids Res.* 22: 4673-80. Molecular models are conventionally used to correctly delineate framework and CDR regions and thus correct the sequence-based assignments.

[0037] The term "Fc" as used herein refers to a molecule comprising the sequence of a non-antigen-binding fragment resulting from digestion of an antibody or produced by other means, whether in monomeric or multimeric form, and can contain the hinge region. The original immunoglobulin source of the native Fc is preferably of human origin and can be any of the immunoglobulins, although IgG1 and IgG2 are preferred. Fc molecules are made up of monomeric polypeptides that can be linked into dimeric or multimeric forms by covalent (*i.e.*, disulfide bonds) and non-covalent association. The number of intermolecular disulfide bonds between monomeric subunits of native Fc molecules ranges from 1 to 4 depending on class (*e.g.*, IgG, IgA, and IgE) or subclass (*e.g.*, IgG1, IgG2, IgG3, IgA1, and IgGA2). One example of a Fc is a disulfide-bonded dimer resulting from papain digestion of an IgG. The term " Fc" as used herein is generic to the monomeric, dimeric, and multimeric forms.

[0038] A F(ab) fragment typically includes one light chain and the V_H and C_{H1} domains of one heavy chain, wherein the V_H-C_{H1} heavy chain portion of the F(ab) fragment cannot form a disulfide bond with another heavy chain polypeptide. As used herein, a F(ab) fragment can also include one light chain containing two variable domains separated by an amino acid linker and one heavy chain containing two variable domains separated by an amino acid linker and a C_{H1} domain.

[0039] A F(ab') fragment typically includes one light chain and a portion of one heavy chain that contains more of the constant region (between the C_{H1} and C_{H2} domains), such that an interchain disulfide bond can be formed between two heavy chains to form a $F(ab')_2$ molecule.

[0040] The term "binding protein" as used herein refers to a non-naturally occurring (or recombinant or engineered) molecule that specifically binds to at least one target antigen. A trispecific binding protein of the present disclosure, unless otherwise specified, typically comprises four polypeptide chains that form at least three antigen binding sites, wherein a first polypeptide chain has a structure represented by the formula:

$$V_{L2}\text{-}\ L_1\text{-}V_{L1}\text{-}\ L_2\text{-}C_L \qquad [I]$$

and a second polypeptide chain has a structure represented by the formula:

$$V_{H1}\text{-}L_3\text{-}V_{H2}\text{-}L_4\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \qquad [II]$$

and a third polypeptide chain has a structure represented by the formula:

$$V_{H3}\text{-}C_{H1} \qquad [III]$$

and a fourth polypeptide chain has a structure represented by the formula:

$$V_{L3}\text{-}C_L \qquad [IV]$$

wherein:

V_{L1} is a first immunoglobulin light chain variable domain;

V_{L2} is a second immunoglobulin light chain variable domain;

V_{L3} is a third immunoglobulin light chain variable domain;

V_{H1} is a first immunoglobulin heavy chain variable domain;

V_{H2} is a second immunoglobulin heavy chain variable domain;

V_{H3} is a third immunoglobulin heavy chain variable domain;

C_L is an immunoglobulin light chain constant domain;

C_{H1} is the immunoglobulin C_{H1} heavy chain constant domain; and

hinge is an immunoglobulin hinge region connecting the C_{H1} and C_{H2} domains;

L_1, L_2, L_3 and L_4 are amino acid linkers;

and wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair.

[0041] A "recombinant" molecule is one that has been prepared, expressed, created, or isolated by recombinant means.

[0042] One embodiment of the disclosure provides binding proteins having biological and immunological specificity to between one and three target antigens. Another

embodiment of the disclosure provides nucleic acid molecules comprising nucleotide sequences encoding polypeptide chains that form such binding proteins. Another embodiment of the disclosure provides expression vectors comprising nucleic acid molecules comprising nucleotide sequences encoding polypeptide chains that form such binding proteins. Yet another embodiment of the disclosure provides host cells that express such binding proteins (*i.e.*, comprising nucleic acid molecules or vectors encoding polypeptide chains that form such binding proteins).

[0043] The term "swapability" as used herein refers to the interchangeability of variable domains within the binding protein format and with retention of folding and ultimate binding affinity. "Full swapability" refers to the ability to swap the order of both V_{H1} and V_{H2} domains, and therefore the order of V_{L1} and V_{L2} domains, in the polypeptide chain of formula I or the polypeptide chain of formula II (*i.e.*, to reverse the order) while maintaining full functionality of the binding protein as evidenced by the retention of binding affinity. Furthermore, it should be noted that the designations V_H and V_L refer only to the domain's location on a particular protein chain in the final format. For example, V_{H1} and V_{H2} could be derived from V_{L1} and V_{L2} domains in parent antibodies and placed into the V_{H1} and V_{H2} positions in the binding protein. Likewise, V_{L1} and V_{L2} could be derived from V_{H1} and V_{H2} domains in parent antibodies and placed in the V_{H1} and V_{H2} positions in the binding protein. Thus, the V_H and V_L designations refer to the present location and not the original location in a parent antibody. V_H and V_L domains are therefore "swappable."

[0044] The term "antigen" or "target antigen" or "antigen target" as used herein refers to a molecule or a portion of a molecule that is capable of being bound by a binding protein, and additionally is capable of being used in an animal to produce antibodies capable of binding to an epitope of that antigen. A target antigen may have one or more epitopes. With respect to each target antigen recognized by a binding protein, the binding protein is capable of competing with an intact antibody that recognizes the target antigen.

[0045] The term "HIV" as used herein means Human Immunodeficiency Virus. As used herein, the term “HIV infection” generally encompasses infection of a host, particularly a human host, by the human immunodeficiency virus (HIV) family of retroviruses including, but not limited to, HIV I, HIV II, HIV III (also known as HTLV-II, LAV-1, LAV-2). HIV can be used herein to refer to any strains, forms, subtypes, clades and variations in the HIV family. Thus, treating HIV infection will encompass the treatment of a person who is a carrier of any of the HIV family of retroviruses or a person who is

diagnosed with active AIDS, as well as the treatment or prophylaxis of the AIDS-related conditions in such persons.

[0046] The term "AIDS" as used herein means Acquired Immunodeficiency Syndrome. AIDS is caused by HIV.

[0047] The terms "CD4bs" or "CD4 binding site" refer to the binding site for CD4 (cluster of differentiation 4), which is a glycoprotein found on the surface of immune cells such as T helper cells, monocytes, macrophages, and dendritic cells.

[0048] The term "CD3" is cluster of differentiation factor 3 polypeptide and is a T-cell surface protein that is typically part of the T cell receptor (TCR) complex.

[0049] "CD28" is cluster of differentiation 28 polypeptide and is a T-cell surface protein that provides co-stimulatory signals for T-cell activation and survival.

[0050] The term "glycoprotein 160" or "gp160 protein" refers to the envelope glycoprotein complex of HIV and which is a homotrimer that is cleaved into gp120 and gp41 subunits.

[0051] The term "MPER" refers to the membrane-proximal external region of glycoprotein 41 (gp41), which is a subunit of the envelope protein complex of retroviruses, including HIV.

[0052] The term "glycan" refers to the carbohydrate portion of a glycoconjugate, such as a glycoprotein, glycolipid, or a proteoglycan. In the disclosed binding proteins, glycan refers to the HIV-1 envelope glycoprotein gp120.

[0053] The term "T-cell engager" refers to binding proteins directed to a host's immune system, more specifically the T cells' cytotoxic activity as well as directed to a HIV target protein.

[0054] The term "trimer apex" refers to apex of HIV-1 envelope glycoprotein gp120.

[0055] The term "monospecific binding protein" refers to a binding protein that specifically binds to one antigen target.

[0056] The term "monovalent binding protein" refers to a binding protein that has one antigen binding site.

[0057] The term "bispecific binding protein" refers to a binding protein that specifically binds to two different antigen targets.

[0058] The term "bivalent binding protein" refers to a binding protein that has two binding sites.

[0059] The term "trispecific binding protein" refers to a binding protein that specifically binds to three different antigen targets.

[0060] The term "trivalent binding protein" refers to a binding protein that has three binding sites. In particular embodiments the trivalent binding protein can bind to one antigen target. In other embodiments, the trivalent binding protein can bind to two antigen targets. In other embodiments, the trivalent binding protein can bind to three antigen targets.

[0061] An "isolated" binding protein is one that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the binding protein, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In some embodiments, the binding protein will be purified: (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated binding proteins include the binding protein *in situ* within recombinant cells since at least one component of the binding protein's natural environment will not be present.

[0062] The terms "substantially pure" or "substantially purified" as used herein refer to a compound or species that is the predominant species present (*i.e.*, on a molar basis it is more abundant than any other individual species in the composition). In some embodiments, a substantially purified fraction is a composition wherein the species comprises at least about 50% (on a molar basis) of all macromolecular species present. In other embodiments, a substantially pure composition will comprise more than about 80%, 85%, 90%, 95%, or 99% of all macromolar species present in the composition. In still other embodiments, the species is purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

[0063] A "neutralizing" binding protein as used herein refers to a molecule that is able to block or substantially reduce an effector function of a target antigen to which it binds. As used herein, "substantially reduce" means at least about 60%, preferably at least about 70%, more preferably at least about 75%, even more preferably at least about 80%, still

more preferably at least about 85%, most preferably at least about 90% reduction of an effector function of the target antigen.

[0064] The term "epitope" includes any determinant, preferably a polypeptide determinant, capable of specifically binding to an immunoglobulin or T-cell receptor. In certain embodiments, epitope determinants include chemically active surface groupings of molecules such as amino acids, sugar side chains, phosphoryl groups, or sulfonyl groups, and, in certain embodiments, may have specific three-dimensional structural characteristics and/or specific charge characteristics. An epitope is a region of an antigen that is bound by an antibody or binding protein. In certain embodiments, a binding protein is said to specifically bind an antigen when it preferentially recognizes its target antigen in a complex mixture of proteins and/or macromolecules. In some embodiments, a binding protein is said to specifically bind an antigen when the equilibrium dissociation constant is $\leq 10^{-8}$ M, more preferably when the equilibrium dissociation constant is $\leq 10^{-9}$ M, and most preferably when the dissociation constant is $\leq 10^{-10}$ M.

[0065] The dissociation constant (K_D) of a binding protein can be determined, for example, by surface plasmon resonance. Generally, surface plasmon resonance analysis measures real-time binding interactions between ligand (a target antigen on a biosensor matrix) and analyte (a binding protein in solution) by surface plasmon resonance (SPR) using the BIAcore system (Pharmacia Biosensor; Piscataway, NJ). Surface plasmon analysis can also be performed by immobilizing the analyte (binding protein on a biosensor matrix) and presenting the ligand (target antigen). The term "K_D," as used herein refers to the dissociation constant of the interaction between a particular binding protein and a target antigen.

[0066] The term "specifically binds" as used herein refers to the ability of a binding protein or an antigen-binding fragment thereof to bind to an antigen containing an epitope with an Kd of at least about 1×10^{-6} M, 1×10^{-7} M, 1×10^{-8} M, 1×10^{-9} M, 1×10^{-10} M, 1×10^{-11} M, 1×10^{-12} M, or more, and/or to bind to an epitope with an affinity that is at least two-fold greater than its affinity for a nonspecific antigen.

[0067] The term "linker" as used herein refers to one or more amino acid residues inserted between immunoglobulin domains to provide sufficient mobility for the domains of the light and heavy chains to fold into cross over dual variable region immunoglobulins. A linker is inserted at the transition between variable domains or between variable and constant domains, respectively, at the sequence level. The transition between domains can

be identified because the approximate size of the immunoglobulin domains are well understood. The precise location of a domain transition can be determined by locating peptide stretches that do not form secondary structural elements such as beta-sheets or alpha-helices as demonstrated by experimental data or as can be assumed by techniques of modeling or secondary structure prediction. The linkers described herein are referred to as L_1, which is located on the light chain between the C-terminus of the V_{L2} and the N-terminus of the V_{L1} domain; and L_2, which is located on the light chain between the C-terminus of the V_{L1} and the N-terminus of the C_L domain. The heavy chain linkers are known as L_3, which is located between the C-terminus of the V_{H1} and the N-terminus of the V_{H2} domain; and L_4, which is located between the C-terminus of the V_{H2} and the N-terminus of the C_{H1} domain.

[0068] The term "vector" as used herein refers to any molecule (*e.g.*, nucleic acid, plasmid, or virus) that is used to transfer coding information to a host cell. The term "vector" includes a nucleic acid molecule that is capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double-stranded DNA molecule into which additional DNA segments may be inserted. Another type of vector is a viral vector, wherein additional DNA segments may be inserted into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell and thereby are replicated along with the host genome. In addition, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors"). In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. The terms "plasmid" and "vector" may be used interchangeably herein, as a plasmid is the most commonly used form of vector. However, the disclosure is intended to include other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses, and adeno-associated viruses), which serve equivalent functions.

[0069] The phrase "recombinant host cell" (or "host cell") as used herein refers to a cell into which a recombinant expression vector has been introduced. A recombinant host cell or host cell is intended to refer not only to the particular subject cell, but also to the progeny

of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but such cells are still included within the scope of the term "host cell" as used herein. A wide variety of host cell expression systems can be used to express the binding proteins, including bacterial, yeast, baculoviral, and mammalian expression systems (as well as phage display expression systems). An example of a suitable bacterial expression vector is pUC19. To express a binding protein recombinantly, a host cell is transformed or transfected with one or more recombinant expression vectors carrying DNA fragments encoding the polypeptide chains of the binding protein such that the polypeptide chains are expressed in the host cell and, preferably, secreted into the medium in which the host cells are cultured, from which medium the binding protein can be recovered.

[0070] The term "transformation" as used herein refers to a change in a cell's genetic characteristics, and a cell has been transformed when it has been modified to contain a new DNA. For example, a cell is transformed where it is genetically modified from its native state. Following transformation, the transforming DNA may recombine with that of the cell by physically integrating into a chromosome of the cell, or may be maintained transiently as an episomal element without being replicated, or may replicate independently as a plasmid. A cell is considered to have been stably transformed when the DNA is replicated with the division of the cell. The term "transfection" as used herein refers to the uptake of foreign or exogenous DNA by a cell, and a cell has been "transfected" when the exogenous DNA has been introduced inside the cell membrane. A number of transfection techniques are well known in the art. Such techniques can be used to introduce one or more exogenous DNA molecules into suitable host cells.

[0071] The term "naturally occurring" as used herein and applied to an object refers to the fact that the object can be found in nature and has not been manipulated by man. For example, a polynucleotide or polypeptide that is present in an organism (including viruses) that can be isolated from a source in nature and that has not been intentionally modified by man is naturally-occurring. Similarly, "non-naturally occurring" as used herein refers to an object that is not found in nature or that has been structurally modified or synthesized by man.

[0072] As used herein, the twenty conventional amino acids and their abbreviations follow conventional usage. Stereoisomers (*e.g.*, D-amino acids) of the twenty conventional amino acids; unnatural amino acids and analogs such as α-, α-disubstituted amino acids, N-

alkyl amino acids, lactic acid, and other unconventional amino acids may also be suitable components for the polypeptide chains of the binding proteins. Examples of unconventional amino acids include: 4-hydroxyproline, γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, σ-N-methylarginine, and other similar amino acids and imino acids (*e.g.*, 4-hydroxyproline). In the polypeptide notation used herein, the left-hand direction is the amino terminal direction and the right-hand direction is the carboxyl-terminal direction, in accordance with standard usage and convention.

[0073] Naturally occurring residues may be divided into classes based on common side chain properties:

(1) hydrophobic: Met, Ala, Val, Leu, Ile, Phe, Trp, Tyr, Pro;

(2) polar hydrophilic: Arg, Asn, Asp, Gln, Glu, His, Lys, Ser, Thr ;

(3) aliphatic: Ala, Gly, Ile, Leu, Val, Pro;

(4) aliphatic hydrophobic: Ala, Ile, Leu, Val, Pro;

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

(6) acidic: Asp, Glu;

(7) basic: His, Lys, Arg;

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

(9) aromatic: His, Trp, Tyr, Phe; and

(10) aromatic hydrophobic: Phe, Trp, Tyr.

[0074] Conservative amino acid substitutions may involve exchange of a member of one of these classes with another member of the same class. Non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class.

[0075] A skilled artisan will be able to determine suitable variants of the polypeptide chains of the binding proteins using well-known techniques. For example, one skilled in the art may identify suitable areas of a polypeptide chain that may be changed without destroying activity by targeting regions not believed to be important for activity. Alternatively, one skilled in the art can identify residues and portions of the molecules that are conserved among similar polypeptides. In addition, even areas that may be important for biological activity or for structure may be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the polypeptide structure.

[0076] The term "patient" as used herein includes human and animal subjects.

[0077] The terms "treatment" or "treat" as used herein refer to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those having the disorder as well as those prone to have a disorder or those in which the disorder is to be prevented. In particular embodiments, binding proteins can be used to treat humans infected with HIV, or humans susceptible to HIV infection, or ameliorate HIV infection in a human subject infected with HIV. The binding proteins can also be used to prevent HIV in a human patient.

[0078] It should be understood as that treating humans infected with HIV include those subjects who are at any one of the several stages of HIV infection progression, which, for example, include acute primary infection syndrome (which can be asymptomatic or associated with an influenza-like illness with fevers, malaise, diarrhea and neurologic symptoms such as headache), asymptomatic infection (which is the long latent period with a gradual decline in the number of circulating $CD4^+$T cells), and AIDS (which is defined by more serious AIDS-defining illnesses and/or a decline in the circulating CD4 cell count to below a level that is compatible with effective immune function). In addition, treating or preventing HIV infection will also encompass treating suspected infection by HIV after suspected past exposure to HIV by e.g., contact with HIV-contaminated blood, blood transfusion, exchange of body fluids, “unsafe” sex with an infected person, accidental needle stick, receiving a tattoo or acupuncture with contaminated instruments, or transmission of the virus from a mother to a baby during pregnancy, delivery or shortly thereafter.

[0079] The terms "pharmaceutical composition" or "therapeutic composition" as used herein refer to a compound or composition capable of inducing a desired therapeutic effect when properly administered to a patient.

[0080] The term "pharmaceutically acceptable carrier" or "physiologically acceptable carrier" as used herein refers to one or more formulation materials suitable for accomplishing or enhancing the delivery of a binding protein.

[0081] The terms "effective amount" and "therapeutically effective amount" when used in reference to a pharmaceutical composition comprising one or more binding proteins refer to an amount or dosage sufficient to produce a desired therapeutic result. More specifically, a therapeutically effective amount is an amount of a binding protein sufficient to inhibit, for some period of time, one or more of the clinically defined pathological processes associated

with the condition being treated. The effective amount may vary depending on the specific binding protein that is being used, and also depends on a variety of factors and conditions related to the patient being treated and the severity of the disorder. For example, if the binding protein is to be administered *in vivo*, factors such as the age, weight, and health of the patient as well as dose response curves and toxicity data obtained in preclinical animal work would be among those factors considered. The determination of an effective amount or therapeutically effective amount of a given pharmaceutical composition is well within the ability of those skilled in the art.

[0082] One embodiment of the disclosure provides a pharmaceutical composition comprising a pharmaceutically acceptable carrier and a therapeutically effective amount of a binding protein.

Trispecific and/or Trivalent Binding Proteins

[0083] Certain aspects of the present disclosure relate to trispecific and/or trivalent binding proteins. Any of the CDRs or variable domains of any of the antigen binding proteins described herein may find use in a trispecific binding protein of the present disclosure. Trispecific binding proteins of various formats are contemplated. In some embodiments, the binding protein of the disclosure is a trispecific and/or trivalent binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

$$V_{L2}\text{-}L_1\text{-}V_{L1}\text{-}L_2\text{-}C_L \qquad [I]$$

and a second polypeptide chain comprises a structure represented by the formula:

$$V_{H1}\text{-}L_3\text{-}V_{H2}\text{-}L_4\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \qquad [II]$$

and a third polypeptide chain comprises a structure represented by the formula:

$$V_{H3}\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \qquad [III]$$

and a fourth polypeptide chain comprises a structure represented by the formula:

$$V_{L3}\text{-}C_L \qquad [IV]$$

wherein:

V_{L1} is a first immunoglobulin light chain variable domain;

V_{L2} is a second immunoglobulin light chain variable domain;

V_{L3} is a third immunoglobulin light chain variable domain;

V_{H1} is a first immunoglobulin heavy chain variable domain;

V_{H2} is a second immunoglobulin heavy chain variable domain;

V_{H3} is a third immunoglobulin heavy chain variable domain;
C_L is an immunoglobulin light chain constant domain;
C_{H1} is an immunoglobulin C_{H1} heavy chain constant domain;
C_{H2} is an immunoglobulin C_{H2} heavy chain constant domain;
C_{H3} is an immunoglobulin C_{H3} heavy chain constant domain;
hinge is an immunoglobulin hinge region connecting the C_{H1} and C_{H2} domains; and
L_1, L_2, L_3 and L_4 are amino acid linkers;
and wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair.

[0084] In some embodiments, the first polypeptide chain and the second polypeptide chain have a cross-over orientation that forms two distinct antigen binding sites. In some embodiments, the V_{H1} and V_{L1} form a binding pair and form the first antigen binding site. In some embodiments, the V_{H2} and V_{L2} form a binding pair and form the second antigen binding site. In some embodiments, the third polypeptide and the fourth polypeptide form a third antigen binding site. In some embodiments, the V_{H3} and V_{L3} form a binding pair and form the third antigen binding site.

[0085] In some embodiments, one or more of the antigen binding sites binds an HIV target protein. In some embodiments, V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein. In some embodiments, V_{H1} and V_{L1} form a first antigen binding site that binds a T cell target protein, V_{H2} and V_{L2} form a second antigen binding site that binds a T cell target protein, and V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein. In some embodiments, V_{H1} and V_{L1} form a first antigen binding site that binds a T cell target protein, V_{H2} and V_{L2} form a second antigen binding site that binds a CD3 polypeptide, and V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein. In some embodiments, V_{H1} and V_{L1} form a first antigen binding site that binds a CD28 polypeptide, V_{H2} and V_{L2} form a second antigen binding site that binds a CD3 polypeptide, and V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein.

[0086] In some embodiments, the binding proteins specifically bind to one or more HIV target proteins (*e.g.*, as described *infra*) and one or more target proteins on a T-cell including T cell receptor complex. These T-cell engager binding proteins are capable of recruiting T cells transiently to target cells and, at the same time, activating the cytolytic activity of the T cells. The T-cell engager trispecific antibodies can be used to activate HIV-

1 reservoirs and redirect/activate T cells to lyse latently infected HIV-1$^+$ T cells. Examples of target proteins on T cells include but are not limited to CD3 and CD28, among others. In some embodiments, the trispecific binding proteins may be generated by combining the antigen binding domains of two or more monospecific antibodies (parent antibodies) into one antibody. *See* International Publication Nos. WO 2011/038290 A2, WO 2013/086533 A1, WO 2013/070776 A1, WO 2012/154312 A1, and WO 2013/163427 A1. The binding proteins of the disclosure may be prepared using domains or sequences obtained or derived from any human or non-human antibody, including, for example, human, murine, or humanized antibodies.

[0087] In some embodiments of the disclosure, the trivalent binding protein is capable of binding three different antigen targets. In one embodiment, the binding protein is trispecific and one light chain-heavy chain pair is capable of binding two different antigen targets or epitopes and one light chain-heavy chain pair is capable of binding one antigen target or epitope.

[0088] In some embodiments, a binding protein of the present disclosure binds one or more HIV target proteins and one or more T cell target proteins. In some embodiments, the binding protein is capable of specifically binding one HIV target protein and two different epitopes on a single T cell target protein. In some embodiments, the binding protein is capable of specifically binding one HIV target protein and two different T cell target proteins (e.g., CD28 and CD3). In some embodiments, the first and second polypeptide chains of the binding protein form two antigen binding sites that specifically target two T cell target proteins, and the third and fourth polypeptide chains of the binding protein form an antigen binding site that specifically binds an HIV target protein. In some embodiments, the one or more HIV target proteins are one or more of glycoprotein 120, glycoprotein 41, and glycoprotein 160. In some embodiments, the one or more T cell target proteins are one or more of CD3 and CD28.

[0089] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:61 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:61; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:62 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:62; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:63 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:63; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:64 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:64.

[0090] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:65 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:65; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:66 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:66; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:67 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:67; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:68 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:68.

[0091] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:69 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:69; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:70 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:70; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:71 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:71; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:72 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:72.

[0092] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:73 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:73; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:74 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:74; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:75 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:75; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:76 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:76.

[0093] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:77 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:77; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:78 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:78; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:79 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:79; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:80 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:80.

[0094] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:81 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:81; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:82 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:82; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:83 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:83; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:84 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:84.

[0095] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:85 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:85; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:86 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:86; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:87 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:87; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:88 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:88.

[0096] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:89 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:89; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:90 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:90; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:91 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:91; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:92 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:92.

[0097] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:93 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:93; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:94 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:94; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:95 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:95; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:96 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:96.

[0098] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:97 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:97; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:98 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:98; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:99 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:99; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:100 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:100.

[0099] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:101 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:101; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:102 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:102; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:103 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:103; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:104 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:104.

[0100] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:105 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:105; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:106 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:106; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:107 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:107; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:108 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:108.

[0101] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:109 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:109; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:110 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:110; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:111 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:111; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:112 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:112.

[0102] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:113 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:113; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:114 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:114; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:115 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:115; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:116 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:116.

[0103] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:117 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:117; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:118 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:118; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:119 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:119; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:120 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:120.

[0104] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:121 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:121; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:122 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:122; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:123 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:123; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:124 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:124.

[0105] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:129 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:129; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:130 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:130; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:131 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:131; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:132 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:132.

[0106] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:133 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:133; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:134 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:134; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:135 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:135; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:136 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:136.

[0107] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:137 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:137; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:138 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:138; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:139 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:139; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:140 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:140.

[0108] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:141 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:141; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:142 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:142; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:143 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:143; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:144 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:144.

[0109] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:145 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:145; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:146 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:146; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:147 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:147; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:148 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:148.

[0110] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:149 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:149; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:150 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:150; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:151 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:151; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:152 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:152.

[0111] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:153 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:153; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:154 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:154; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:155 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:155; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:156 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:156.

[0112] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:157 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:157; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:158 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:158; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:159 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:159; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:160 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:160.

[0113] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:161 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:161; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:162 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:162; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:163 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:163; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:164 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:164.

[0114] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:165 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:165; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:166 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:166; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:167 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:167; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:168 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:168.

[0115] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:169 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:169; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:170 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:170; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:171 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:171; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:172 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:172.

[0116] In some embodiments, a binding protein of the present disclosure comprises four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:173 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:173; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:174 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:174; the third polypeptide chain comprises the amino

acid sequence of SEQ ID NO:175 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:175; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:176 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:176.

Exemplary and non-limiting polypeptides that may find use in any of the trispecific binding proteins described herein are provided in Table 4.

Anti-HIV Binding Sites

[0117] Certain aspects of the present disclosure relate to binding proteins that comprise an antigen binding site that binds an HIV target protein or polypeptide.

[0118] In some embodiments, the HIV target protein is glycoprotein 120, glycoprotein 41, or glycoprotein 160. In some embodiments, a binding protein binds one or more of: glycoprotein 120, glycoprotein 41, and glycoprotein 160. Exemplary HIV target proteins include, without limitation, MPER of the HIV-1 gp41 protein, a CD4 binding site of the HIV-1 gp120 protein, a glycan in the V3 loop of the HIV-1 gp120 protein, or a trimer apex of the HIV-1 gp120 protein or gp160. For example, in some embodiments, a binding protein of the present disclosure comprises an antigen binding site that binds a CD4 binding site of the HIV-1 gp120 protein. Exemplary antigen binding sites that bind HIV target proteins contemplated for use herein include, without limitation, those described in International Publication No. WO2017/074878, such as those from antibodies CD4BS “a”, CD4BS “b”, MPER, MPER_100W, V1/V2 “a”, V1/V2 “b”, or V3.

[0119] In some embodiments, a binding protein comprising an antigen binding site that binds an HIV target protein is monospecific and/or monovalent, bispecific and/or bivalent, trispecific and/or trivalent, or multispecific and/or multivalent. In some embodiments, a binding protein that comprises an antigen binding site that binds an HIV target protein is a trispecific binding protein comprising four polypeptides that form three antigen binding sites.

[0120] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of NCPIN (SEQ ID NO:1) a CDR-H2 sequence comprising the amino acid sequence of WMKPRHGAVSYARQLQG (SEQ ID NO:2), and a CDR-H3 sequence comprising the amino acid sequence of GKYCTARDYYNWDFEH (SEQ ID NO:3); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:4), a CDR-L2 sequence comprising the amino acid sequence of

SGSTRAA (SEQ ID NO:5), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:6). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of NCPIN (SEQ ID NO:1) a CDR-H2 sequence comprising the amino acid sequence of WMKPRHGAVSYARQLQG (SEQ ID NO:2), and a CDR-H3 sequence comprising the amino acid sequence of GKYCTARDYYNWDFEH (SEQ ID NO:3); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:4), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID NO:5), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:6).

[0121] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAV (SEQ ID NO:8) or IKPQYGAT (SEQ ID NO:9); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAV (SEQ ID NO:8) or IKPQYGAT (SEQ ID NO:9); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAV (SEQ ID NO:8); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the

amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAV (SEQ ID NO:8); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAT (SEQ ID NO:9); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAT (SEQ ID NO:9); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13).

[0122] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of DCTLN (SEQ ID NO:14) a CDR-H2 sequence comprising the amino acid sequence of WLKPRWGAVNYARPLQG (SEQ ID NO:15), and a CDR-H3 sequence comprising the amino acid sequence of GKNCDYNWDFEH (SEQ ID NO:16); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:17), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID

NO:18), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:19). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of DCTLN (SEQ ID NO:14) a CDR-H2 sequence comprising the amino acid sequence of WLKPRWGAVNYARPLQG (SEQ ID NO:15), and a CDR-H3 sequence comprising the amino acid sequence of GKNCDYNWDFEH (SEQ ID NO:16); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:17), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID NO:18), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:19).

[0123] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site with a VH domain comprising an extended heavy chain FR3 loop of antibody VRC03, *e.g.*, as described in Liu, Q. *et al.* (2019) *Nat. Commun.* 10:721.

[0124] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHG AVSYARQLQGRVTMTRDMYSETAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWD FEHWGQGTPVTVSS (SEQ ID NO:43), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFS GSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:45). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:43, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:45. In some embodiments, a binding protein of the

present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:43, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:45.

[0125] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHG AVSYARQLQGRVTMTRQLSQDPDDPDWGTAFLELRSLTSDDTAVYFCTRGKYCTA RDYYNWDFEHWGQGTPVTVSS (SEQ ID NO:44), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFS GSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:45). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:44, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:45. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:44, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:45.

[0126] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of

RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQY GAVNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALD AWGQGTTVVVSA (SEQ ID NO:46), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGV PSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:46, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:49. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:46, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:49.

[0127] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQY GATNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALD AWGQGTTVVVSA (SEQ ID NO:47), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGV PSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49). In some embodiments, a binding protein of the present disclosure comprises an antigen binding

site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:47, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:49. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:47, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:49.

[0128] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQY GAVNFGGGFRDRVTLTRQLSQDPDDPDWGIAYMDIRGLKPDDTAVYYCARDRSYG DSSWALDAWGQGTTVVVSA (SEQ ID NO:48), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGV PSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:48, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:49. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:48, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:49.

[0129] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least

89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of QVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGKRPEWMGWLKPRW GAVNYARPLQGRVTMTRQLSQDPDDPDWGTAFLELRSLTVDDTAVYFCTRGKNCD YNWDFEHWGRGTPVIVSS (SEQ ID NO:50), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of LTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSG SRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:51). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:50, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:51. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:50, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:51.

[0130] In some embodiments of any of the above embodiments, the binding protein is a trispecific binding protein. In some embodiments, the trispecific binding protein comprising an antigen binding site that binds an HIV target protein, an antigen binding site that binds a CD28 polypeptide, and an antigen binding site that binds a CD3 polypeptide. In some embodiments, the binding protein is a trispecific binding protein comprising four polypeptides comprising three antigen binding sites, wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair (*e.g.*, as described herein). In some embodiments, the VH and VL domains of any of the anti-CD38 antigen binding sites described above represent V_{H3} and V_{L3} and form a third antigen binding site that binds an HIV target protein. In some embodiments, V_{H1} and V_{L1} form a first antigen binding site that binds a CD28 polypeptide, V_{H2} and V_{L2} form a second antigen binding site that binds a CD3 polypeptide, and the VH and VL domains of any of the anti-HIV antigen

binding sites described above and/or in Table 1 represent V_{H3} and V_{L3} and form a third antigen binding site that binds an HIV target protein.

[0131] Sequences of exemplary anti-HIV antigen binding sites are provided in Table 1. In some embodiments, a binding protein comprising an anti-HIV antigen binding site of the present disclosure comprises 1, 2, 3, 4, 5, or all 6 CDR sequences of an anti-HIV antibody described in Table 1. In some embodiments, a binding protein comprising an anti-HIV antigen binding site of the present disclosure comprises a VH domain sequence and/or VL domain sequence of an anti-HIV antibody described in Table 1.

Table 1. Anti-HIV binding protein sequences.

Sequence Type	*Molecule*	*Description*	*SEQ ID NO*	*Sequence*
CDR	VRC07_523 (anti-Env gp120 CD4bs)	CDR-H1	1	NCPIN
		CDR-H2	2	WMKPRHGAVSYARQLQG
		CDR-H3	3	GKYCTARDYYNWDFEH
		CDR-L1	4	RTSQYGSLA
		CDR-L2	5	SGSTRAA
		CDR-L3	6	QQYEF
	N6 (anti-Env gp120 CD4bs)	CDR-H1	7	GYTFTAHI
		CDR-H2 Original	8	IKPQYGAV
		CDR-H2 rw52	9	IKPQYGAT
		CDR-H3	10	DRSYGDSSWALDA
		CDR-L1	11	QGVGSD
		CDR-L2	12	HTS
		CDR-L3	13	CQVLQF
	VRC01.23	CDR-H1	14	DCTLN
		CDR-H2	15	WLKPRWGAVNYARPLQG
		CDR-H3	16	GKNCDYNWDFEH
		CDR-L1	17	RTSQYGSLA
		CDR-L2	18	SGSTRAA
		CDR-L3	19	QQYEF
Variable domain	VRC07_523	VH	43	QVRLSQSGGQMKKPGDSMRISCRASG YEFINCPINWIRLAPGKRPEWMGWM KPRHGAVSYARQLQGRVTMTRDMYS ETAFLELRSLTSDDTAVYFCTRGKYC TARDYYNWDFEHWGQGTPVTVSS
		FR3-03 VH	44	QVRLSQSGGQMKKPGDSMRISCRASG YEFINCPINWIRLAPGKRPEWMGWM KPRHGAVSYARQLQGRVTMTRQLSQ DPDDPDWGTAFLELRSLTSDDTAVYF CTRGKYCTARDYYNWDFEHWGQGT PVTVSS

		VL	45	SLTQSPGTLSLSPGETAIISCRTSQYGS LAWYQQRPGQAPRLVIYSGSTRAAGI PDRFSGSRWGPDYNLTISNLESGDFG VYYCQQYEFFGQGTKVQVDIK
	N6	VH	46	RAHLVQSGTAMKKPGASVRVSCQTS GYTFTAHILFWFRQAPGRGLEWVGWI KPQYGAVNFGGGFRDRVTLTRDVYR EIAYMDIRGLKPDDTAVYYCARDRSY GDSSWALDAWGQGTTVVVSA
		rw52 VH	47	RAHLVQSGTAMKKPGASVRVSCQTS GYTFTAHILFWFRQAPGRGLEWVGWI KPQYGATNFGGGFRDRVTLTRDVYR EIAYMDIRGLKPDDTAVYYCARDRSY GDSSWALDAWGQGTTVVVSA
		FR3-03 VH	48	RAHLVQSGTAMKKPGASVRVSCQTS GYTFTAHILFWFRQAPGRGLEWVGWI KPQYGAVNFGGGFRDRVTLTRQLSQ DPDDPDWGIAYMDIRGLKPDDTAVY YCARDRSYGDSSWALDAWGQGTTV VVSA
		VL	49	YIHVTQSPSSLSVSIGDRVTINCQTSQG VGSDLHWYQHKPGRAPKLLIHHTSSV EDGVPSRFSGSGFHTSFNLTISDLQAD DIATYYCQVLQFFGRGSRLHIK
	VRC01.23	VH	50	QVQLVQSGGQMKKPGESMRISCRAS GYEFIDCTLNWIRLAPGKRPEWMGW LKPRWGAVNYARPLQGRVTMTRQLS QDPDDPDWGTAFLELRSLTVDDTAV YFCTRGKNCDYNWDFEHWGRGTPVI VSS
		VL	51	LTQSPGTLSLSPGETAIISCRTSQYGSL AWYQQRPGQAPRLVIYSGSTRAAGIP DRFSGSRWGPDYNLTISNLESGDFGV YYCQQYEFFGQGTKVQVDIK

Anti-CD28 Binding Sites

[0132] Certain aspects of the present disclosure relate to binding proteins that comprise an antigen binding site that binds a CD28 polypeptide. In some embodiments, the CD28 polypeptide is a human CD28 polypeptide, also known as Tp44. Human CD28 polypeptides are known in the art and include, without limitation, the polypeptides represented by NCBI Accession Numbers XP_011510499.1, XP_011510497.1, XP_011510496.1, NP_001230007.1, NP_001230006.1, or NP_006130.1, or a polypeptide produced from NCBI Gene ID Number 940. In some embodiments, a binding protein comprising an antigen binding site that binds a CD28 polypeptide is monospecific and/or monovalent, bispecific and/or bivalent, trispecific and/or trivalent, or multispecific and/or multivalent. In some embodiments, a binding protein that comprises an antigen binding site that binds a CD28

polypeptide is a trispecific binding protein comprising four polypeptides that form three antigen binding sites. In some embodiments, a binding protein that comprises an antigen binding site that binds a CD28 polypeptide is a trispecific binding protein comprising four polypeptides that form three antigen binding sites, one of which binds a CD28 polypeptide, and one of which binds a CD3 polypeptide. In some embodiments, a binding protein that comprises an antigen binding site that binds a CD28 polypeptide is a trispecific binding protein comprising four polypeptides that form three antigen binding sites, one of which binds a CD28 polypeptide, one of which binds a CD3 polypeptide, and one of which binds an HIV target protein.

[0133] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTSYY (SEQ ID NO:31), a CDR-H2 sequence comprising the amino acid sequence of IYPGNVNT (SEQ ID NO:32), and a CDR-H3 sequence comprising the amino acid sequence of TRSHYGLDWNFDV (SEQ ID NO:33); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QNIYVW (SEQ ID NO:34), a CDR-L2 sequence comprising the amino acid sequence of KAS (SEQ ID NO:35), and a CDR-L3 sequence comprising the amino acid sequence of QQGQTYPY (SEQ ID NO:36). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GYTFTSYY (SEQ ID NO:31), a CDR-H2 sequence comprising the amino acid sequence of IYPGNVNT (SEQ ID NO:32), and a CDR-H3 sequence comprising the amino acid sequence of TRSHYGLDWNFDV (SEQ ID NO:33); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QNIYVW (SEQ ID NO:34), a CDR-L2 sequence comprising the amino acid sequence of KAS (SEQ ID NO:35), and a CDR-L3 sequence comprising the amino acid sequence of QQGQTYPY (SEQ ID NO:36).

[0134] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of

QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNV NTNYAQKFQGRATLTVDTSISTAYMELSRLRSDDTAVYYCTRSHYGLDWNFDVWG KGTTVTVSS (SEQ ID NO:59), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of DIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPKLLIYKASNLHTG VPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIK (SEQ ID NO:60). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:59, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:60. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:59, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:60.

[0135] In some embodiments of any of the above embodiments, the binding protein is a trispecific binding protein. In some embodiments, the trispecific binding protein comprising an antigen binding site that binds an HIV target protein, an antigen binding site that binds a CD28 polypeptide, and an antigen binding site that binds a CD3 polypeptide. In some embodiments, the binding protein is a trispecific binding protein comprising four polypeptides comprising three antigen binding sites, wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair (*e.g.*, as described herein). In some embodiments, the VH and VL domains of any of the anti-CD28 antigen binding sites described above represent V_{H1} and V_{L1} and form a first antigen binding site that binds a CD28 polypeptide. In some embodiments, the VH and VL domains of any of the anti-CD28 antigen binding sites described above represent V_{H1} and V_{L1} and form a first antigen binding site that binds a CD28 polypeptide, V_{H2} and V_{L2} form a second antigen binding site that binds a CD3 polypeptide, and V_{H3} and V_{L3} and form a third antigen binding site that binds an HIV target protein.

[0136] Sequences of exemplary anti-CD28 antigen binding sites are provided in Table 2. In some embodiments, a binding protein comprising an anti-CD28 antigen binding site of the

present disclosure comprises 1, 2, 3, 4, 5, or all 6 CDR sequences of an anti-CD28 antibody described in Table 2. In some embodiments, a binding protein comprising an anti-CD28 antigen binding site of the present disclosure comprises a VH domain sequence and/or VL domain sequence of an anti-CD28 antibody described in Table 2.

Table 2. Anti-CD28 binding protein sequences.

Sequence Type	*Molecule*	*Description*	*SEQ ID NO*	*Sequence*
CDR	Anti-CD28 (sup)	CDR-H1	31	GYTFTSYY
		CDR-H2	32	IYPGNVNT
		CDR-H3	33	TRSHYGLDWNFDV
		CDR-L1	34	QNIYVW
		CDR-L2	35	KAS
		CDR-L3	36	QQGQTYPY
Variable Domain	Anti-CD28 (sup)	VH	59	QVQLVQSGAEVVKPGASVKVSCKAS GYTFTSYYIHWVRQAPGQGLEWIGSI YPGNVNTNYAQKFQGRATLTVDTSIS TAYMELSRLRSDDTAVYYCTRSHYG LDWNFDVWGKGTTVTVSS
		VL	60	DIQMTQSPSSLSASVGDRVTITCQASQ NIYVWLNWYQQKPGKAPKLLIYKAS NLHTGVPSRFSGSGSGTDFTLTISSLQP EDIATYYCQQGQTYPYTFGQGTKLEI K

Anti-CD3 Binding Sites

[0137] Certain aspects of the present disclosure relate to binding proteins that comprise an antigen binding site that binds a CD3 polypeptide. In some embodiments, the CD3 polypeptide is a human CD3 polypeptide, including CD3-delta (also known as T3D, IMD19, and CD3-DELTA), CD3-epsilon (also known as T3E, IMD18, and TCRE), and CD3-gamma (also known as T3G, IMD17, and CD3-GAMMA). Human CD3 polypeptides are known in the art and include, without limitation, the polypeptides represented by NCBI Accession Numbers XP_006510029.1 or NP_031674.1, or a polypeptide produced from NCBI Gene ID Numbers 915, 916, or 917. In some embodiments, a binding protein comprising an antigen binding site that binds a CD3 polypeptide is monospecific and/or monovalent, bispecific and/or bivalent, trispecific and/or trivalent, or multispecific and/or multivalent. In some embodiments, a binding protein that comprises an antigen binding site that binds a CD3 polypeptide is a trispecific binding protein comprising four polypeptides that form three antigen binding sites. In some embodiments, a binding protein that comprises an antigen binding site that binds a CD3 polypeptide is a trispecific binding protein comprising four polypeptides that form three antigen binding sites, one of which binds a CD28 polypeptide,

and one of which binds a CD3 polypeptide. In some embodiments, a binding protein that comprises an antigen binding site that binds a CD3 polypeptide is a trispecific binding protein comprising four polypeptides that form three antigen binding sites, one of which binds a CD28 polypeptide, one of which binds a CD3 polypeptide, and one of which binds an HIV target protein.

[0138] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHX$_1$NX$_2$X$_3$TY, wherein X$_1$ is E or Q, X$_2$ is A or L, and X$_3$ is Q, R, or F (SEQ ID NO:293), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, the CDR-L1 sequence of the V$_{L2}$ domain comprises an amino acid sequence selected from the group consisting of QSLVHQNAQTY (SEQ ID NO:24), QSLVHENLQTY (SEQ ID NO:25), QSLVHENLFTY (SEQ ID NO:26), and QSLVHENLRTY (SEQ ID NO:27).

[0139] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHQNAQTY (SEQ ID NO:24), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence

comprising the amino acid sequence of QSLVHQNAQTY (SEQ ID NO:24), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30).

[0140] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLQTY (SEQ ID NO:25), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLQTY (SEQ ID NO:25), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30).

[0141] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLFTY (SEQ ID NO:26), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-

H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLFTY (SEQ ID NO:26), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30).

[0142] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and/or an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLRTY (SEQ ID NO:27), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22); and an antibody light chain variable (VL) domain comprising a CDR-L1 sequence comprising the amino acid sequence of QSLVHENLRTY (SEQ ID NO:27), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30).

[0143] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of

QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKDKS NSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDY WGQGTLVTVSS (SEQ ID NO:52), and/or an antibody light chain variable (VL) domain

comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to an amino acid sequence selected from the group consisting of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:54), DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:55), DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNR FSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:56), and DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLRTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:57). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising an amino acid sequence selected from the group consisting of SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, and SEQ ID NO:57. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and an antibody light chain variable (VL) domain comprising an amino acid sequence selected from the group consisting of SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, and SEQ ID NO:57.

[0144] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKDKS NSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDY

WGQGTLVTVSS (SEQ ID NO:52), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:54). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:54. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:54.

[0145] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKDKS NSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDY WGQGTLVTVSS (SEQ ID NO:52), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:55). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL)

domain comprising the amino acid sequence of SEQ ID NO:55. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:55.

[0146] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKDKS NSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDY WGQGTLVTVSS (SEQ ID NO:52), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNR FSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:56). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:56. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:56.

[0147] In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence

of QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKDKS NSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDY WGQGTLVTVSS (SEQ ID NO:52), and/or an antibody light chain variable (VL) domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to the amino acid sequence of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLRTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:57). In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and/or an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:57. In some embodiments, a binding protein of the present disclosure comprises an antigen binding site comprising: an antibody heavy chain variable (VH) domain comprising the amino acid sequence of SEQ ID NO:52, and an antibody light chain variable (VL) domain comprising the amino acid sequence of SEQ ID NO:57.

[0148] Advantageously, anti-CD3 binding sites are described herein with high affinity binding to human CD3 polypeptides and potential manufacturing liabilities (*e.g.*, deamidation sites) removed.

[0149] In some embodiments of any of the above embodiments, the binding protein is a trispecific binding protein. In some embodiments, the trispecific binding protein comprising an antigen binding site that binds an HIV target protein, an antigen binding site that binds a CD28 polypeptide, and an antigen binding site that binds a CD3 polypeptide. In some embodiments, the binding protein is a trispecific binding protein comprising four polypeptides comprising three antigen binding sites, wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair (*e.g.*, as described herein). In some embodiments, the VH and VL domains of any of the anti-CD3 antigen binding sites described above represent V_{H2} and $V_{L2}$and form a second antigen binding site that binds a CD3 polypeptide. In some embodiments, V_{H1} and V_{L1} form a first antigen binding site that binds a CD28 polypeptide, the VH and VL domains of any of the anti-CD3 antigen binding sites described above and/or in Table 3 represent V_{H2} and V_{L2} and

form a second antigen binding site that binds a CD3 polypeptide, and V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein.

[0150] Sequences of exemplary anti-CD3 antigen binding sites are provided in Table 3. In some embodiments, a binding protein comprising an anti-CD3 antigen binding site of the present disclosure comprises 1, 2, 3, 4, 5, or all 6 CDR sequences of an anti-CD3 antibody described in Table 3. In some embodiments, a binding protein comprising an anti-CD3 antigen binding site of the present disclosure comprises a VH domain sequence and/or VL domain sequence of an anti-CD3 antibody described in Table 3.

Table 3. Anti-CD3 binding protein sequences.

Sequence Type	*Molecule*	*Description*	*SEQ ID NO*	*Sequence*
CDR	Anti-CD3 (mid)	CDR-H1 original	20	GFTFTKAW
		CDR-H2 original	21	IKDKSNSYAT
		CDR-H3 original	22	RGVYYALSPFDY
		CDR-L1 original	23	QSLVHNNANTY
		CDR-L1 QQ	24	QSLVHQNAQTY
		CDR-L1 ENLQ	25	QSLVHENLQTY
		CDR-L1 ENLF	26	QSLVHENLFTY
		CDR-L1 ENLR	27	QSLVHENLRTY
		CDR-L1 DNAQ	28	QSLVHDNAQTY
		CDR-L2 original	29	KVS
		CDR-L3 Original	30	GQGTQYPFT
		consensus CDR-L1	293	QSLVHX$_1$NX$_2$X$_3$TY, wherein X$_1$ is E or Q, X$_2$ is A or L, and X$_3$ is Q, R, or F
Variable domain	Anti-CD3 (mid)	VH	52	QVQLVESGGGVVQPGRSLRLSCAASG FTFTKAWMHWVRQAPGKQLEWVAQ IKDKSNSYATYYADSVKGRFTISRDDS KNTLYLQMNSLRAEDTAVYYCRGVY YALSPFDYWGQGTLVTVSS
		VL Original	53	DIVMTQTPLSLSVTPGQPASISCKSSQS LVHNNANTYLSWYLQKPGQSPQSLIY KVSNRFSGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCGQGTQYPFTFGSG TKVEIK

		VL 32/35 QQ	54	DIVMTQTPLSLSVTPGQPASISCKSSQS LVHQNAQTYLSWYLQKPGQSPQSLIY KVSNRFSGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCGQGTQYPFTFGSG TKVEIK
		VL ENLQ	55	DIVMTQTPLSLSVTPGQPASISCKSSQS LVHENLQTYLSWYLQKPGQSPQSLIY KVSNRFSGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCGQGTQYPFTFGSG TKVEIK
		VL ENLF	56	DIVMTQTPLSLSVTPGQPASISCKSSQS LVHENLFTYLSWYLQKPGQSPQSLIY KVSNRFSGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCGQGTQYPFTFGSG TKVEIK
		VL ENLR	57	DIVMTQTPLSLSVTPGQPASISCKSSQS LVHENLRTYLSWYLQKPGQSPQSLIY KVSNRFSGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCGQGTQYPFTFGSG TKVEIK
		VL DNAQ	58	DIVMTQTPLSLSVTPGQPASISCKSSQS LVHDNAQTYLSWYLQKPGQSPQSLIY KVSNRFSGVPDRFSGSGSGTDFTLKIS RVEAEDVGVYYCGQGTQYPFTFGSG TKVEIK

Linkers

[0151] In some embodiments, the linkers L_1, L_2, L_3, and L_4 range from no amino acids (length=0) to about 100 amino acids long, or less than 100, 50, 40, 30, 20, or 15 amino acids or less. The linkers can also be 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acids long. L_1, L_2, L_3, and L_4 in one binding protein may all have the same amino acid sequence or may all have different amino acid sequences.

[0152] Examples of suitable linkers include, for example, GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO: 41), S, RT, TKGPS (SEQ ID NO: 39), GQPKAAP (SEQ ID NO: 38), GGSGSSGSGG (SEQ ID NO: 42), and DKTHT (SEQ ID NO:37), as well as those disclosed in International Publication Nos. WO2017/074878 and WO2017/180913. The examples listed above are not intended to limit the scope of the disclosure in any way, and linkers comprising randomly selected amino acids selected from the group consisting of valine, leucine, isoleucine, serine, threonine, lysine, arginine, histidine, aspartate, glutamate, asparagine, glutamine, glycine, and proline have been shown to be suitable in the binding proteins.

[0153] The identity and sequence of amino acid residues in the linker may vary depending on the type of secondary structural element necessary to achieve in the linker. For example, glycine, serine, and alanine are best for linkers having maximum flexibility. Some combination of glycine, proline, threonine, and serine are useful if a more rigid and extended linker is necessary. Any amino acid residue may be considered as a linker in combination with other amino acid residues to construct larger peptide linkers as necessary depending on the desired properties.

[0154] In some embodiments, the length of L_1 is at least twice the length of L_3. In some embodiments, the length of L_2 is at least twice the length of L_4. In some embodiments, the length of L_1 is at least twice the length of L_3, and the length of L_2 is at least twice the length of L_4. In some embodiments, L_1 is 3 to 12 amino acid residues in length, L_2 is 3 to 14 amino acid residues in length, L_3 is 1 to 8 amino acid residues in length, and L_4 is 1 to 3 amino acid residues in length. In some embodiments, L_1 is 5 to 10 amino acid residues in length, L_2 is 5 to 8 amino acid residues in length, L_3 is 1 to 5 amino acid residues in length, and L_4 is 1 to 2 amino acid residues in length. In some embodiments, L_1 is 7 amino acid residues in length, L_2 is 5 amino acid residues in length, L_3 is 1 amino acid residue in length, and L_4 is 2 amino acid residues in length.

[0155] In some embodiments, L_1, L_2, L_3 and L_4 each independently are zero amino acids in length or comprise a sequence selected from the group consisting of GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO: 41), S, RT, TKGPS (SEQ ID NO: 39), GQPKAAP (SEQ ID NO: 38), and GGSGSSGSGG (SEQ ID NO: 42). In some embodiments, L_1, L_2, L_3 and L_4 each independently comprise a sequence selected from the group consisting of GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO:41), S, RT, TKGPS (SEQ ID NO:39), GQPKAAP (SEQ ID NO: 38), and GGSGSSGSGG (SEQ ID NO:42). In some embodiments, L_1 comprises the sequence GQPKAAP (SEQ ID NO: 38), L_2 comprises the sequence TKGPS (SEQ ID NO:39), L_3 comprises the sequence S, and L_4 comprises the sequence RT.

[0156] In some embodiments, at least one of L_1, L_2, L_3 or L_4 comprises the sequence DKTHT (SEQ ID NO:37). In some embodiments, L_1, L_2, L_3 and L_4 comprise the sequence DKTHT (SEQ ID NO:37).

Fc regions and constant domains

[0157] In some embodiments, a binding protein of the present disclosure comprises a second polypeptide chain further comprising an Fc region linked to C_{H1}, the Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains. In some embodiments, a binding protein of the present disclosure comprises a third polypeptide chain further comprising an Fc region linked to C_{H1}, the Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains. In some embodiments, a binding protein of the present disclosure comprises a second polypeptide chain further comprising an Fc region linked to C_{H1}, the Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains, and a third polypeptide chain further comprising an Fc region linked to C_{H1}, the Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains.

[0158] In some embodiments, a binding protein of the present disclosure comprises a full-length antibody heavy chain or a polypeptide chain comprising an Fc region. In some embodiments, the Fc region is a human Fc region, *e.g.*, a human IgG1, IgG2, IgG3, or IgG4 Fc region. In some embodiments, the Fc region includes an antibody hinge, C_{H1}, C_{H2}, C_{H3}, and optionally C_{H4} domains. In some embodiments, the Fc region is a human IgG1 Fc region. In some embodiments, the Fc region is a human IgG4 Fc region. In some embodiments, the Fc region includes one or more of the mutations described *infra*. In some embodiments, the Fc region is an Fc region of one of the heavy chain polypeptides (*e.g.*, polypeptide 2 or 3) of a binding protein shown in Table 4. In some embodiments, the heavy chain constant region is a constant region of one of the heavy chain polypeptides (*e.g.*, polypeptide 2 or 3) of a binding protein shown in Table 4. In some embodiments, the light chain constant region is a constant region of one of the light chain polypeptides (*e.g.*, polypeptide 1 or 4) of a binding protein shown in Table 4.

[0159] In some embodiments, a binding protein of the present disclosure includes one or two Fc variants. The term "Fc variant" as used herein refers to a molecule or sequence that is modified from a native Fc but still comprises a binding site for the salvage receptor, FcRn (neonatal Fc receptor). Exemplary Fc variants, and their interaction with the salvage receptor, are known in the art. Thus, the term "Fc variant" can comprise a molecule or sequence that is humanized from a non-human native Fc. Furthermore, a native Fc comprises regions that can be removed because they provide structural features or biological activity that are not

required for the antibody-like binding proteins of the invention. Thus, the term "Fc variant" comprises a molecule or sequence that lacks one or more native Fc sites or residues, or in which one or more Fc sites or residues has be modified, that affect or are involved in: (1) disulfide bond formation, (2) incompatibility with a selected host cell, (3) N-terminal heterogeneity upon expression in a selected host cell, (4) glycosylation, (5) interaction with complement, (6) binding to an Fc receptor other than a salvage receptor, or (7) antibody-dependent cellular cytotoxicity (ADCC).

[0160] In some embodiments, a binding protein of the present disclosure (*e.g.*, a trispecific binding protein) comprises a “knob” mutation on the second polypeptide chain and a “hole” mutation on the third polypeptide chain. In some embodiments, a binding protein of the present disclosure comprises a “knob” mutation on the third polypeptide chain and a “hole” mutation on the second polypeptide chain. In some embodiments, the “knob” mutation comprises substitution(s) at positions corresponding to positions 354 and/or 366 of human IgG1 or IgG4 according to EU Index. In some embodiments, the amino acid substitutions are S354C, T366W, T366Y, S354C and T366W, or S354C and T366Y. In some embodiments, the “knob” mutation comprises substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index. In some embodiments, the amino acid substitutions are S354C and T366W. In some embodiments, the “hole” mutation comprises substitution(s) at positions corresponding to positions 407 and, optionally, 349, 366, and/or 368 and of human IgG1 or IgG4 according to EU Index. In some embodiments, the amino acid substitutions are Y407V or Y407T and optionally Y349C, T366S, and/or L368A. In some embodiments, the “hole” mutation comprises substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index. In some embodiments, the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

[0161] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, the first Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitution(s) at positions corresponding to positions 366 and optionally 354 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are T366W or T366Y and optionally S354C; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, the second Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitution(s) at positions

corresponding to positions 407 and optionally 349, 366, and/or 368 and of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y407V or Y407T and optionally Y349C, T366S, and/or L368A.

[0162] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, the first Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitution(s) at positions corresponding to positions 407 and optionally 349, 366, and/or 368 and of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y407V or Y407T and optionally Y349C, T366S, and/or L368A; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, the second Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitution(s) at positions corresponding to positions 366 and optionally 354 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are T366W or T366Y and optionally S354C.

[0163] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, the first Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitution at position corresponding to position 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitution is T366W; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, the second Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitution(s) at positions corresponding to positions 366, 368, and/or 407 and of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are T366S, L368A, and/or Y407V.

[0164] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, the first Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitution(s) at positions corresponding to positions 366, 368, and/or 407 and of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are T366S, L368A, and/or Y407V; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, the second Fc region comprising an immunoglobulin hinge

region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitution at position corresponding to position 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitution is T366W.

[0165] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, the first Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, the second Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V. In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, the first Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, the second Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are S354C and T366W. In some embodiments, the first and/or second Fc regions are human IgG1 Fc regions. In some embodiments, the first and/or second Fc regions are human IgG4 Fc regions.

[0166] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, wherein the first Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 228, 354, 366, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, S354C, T366W, and R409K; and wherein

the third polypeptide chain further comprises a second Fc region linked to CH1, wherein the second Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 228, 349, 366, 368, 407, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, Y349C, T366S, L368A, Y407V, and R409K. In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, wherein the first Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 228, 349, 366, 368, 407, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, Y349C, T366S, L368A, Y407V, and R409K; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, wherein the second Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 228, 354, 366, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, S354C, T366W, and R409K.

[0167] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, wherein the first Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 234, 235, 354, and 366 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A, L235A, S354C, and T366W; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, wherein the second Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 234, 235, 349, 366, 368, and 407 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A, L235A, Y349C, T366S, L368A, and Y407V. In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, wherein the first Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region

comprises amino acid substitutions at positions corresponding to positions 234, 235, 349, 366, 368, and 407 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A, L235A, Y349C, T366S, L368A, and Y407V; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, wherein the second Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 234, 235, 354, and 366 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A, L235A, S354C, and T366W.

[0168] In some embodiments, a binding protein of the present disclosure comprises one or more mutations to reduce effector function, *e.g.*, Fc receptor-mediated antibody-dependent cellular phagocytosis (ADCP), complement-dependent cytotoxicity (CDC), and/or antibody-dependent cellular cytotoxicity (ADCC). In some embodiments, the second polypeptide chain further comprises a first Fc region linked to C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains; wherein the third polypeptide chain further comprises a second Fc region linked to C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains; wherein the first and second Fc regions are human IgG1 Fc regions; and wherein the first and the second Fc regions each comprise amino acid substitutions at positions corresponding to positions 234 and 235 of human IgG1 according to EU Index, wherein the amino acid substitutions are L234A and L235A. In some embodiments, the Fc regions of the second and the third polypeptide chains are human IgG1 Fc regions, and wherein the Fc regions each comprise amino acid substitutions at positions corresponding to positions 234 and 235 of human IgG1 according to EU Index, wherein the amino acid substitutions are L234A and L235A. In some embodiments, the second polypeptide chain further comprises a first Fc region linked to C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains; wherein the third polypeptide chain further comprises a second Fc region linked to C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains; wherein the first and second Fc regions are human IgG1 Fc regions; and wherein the first and the second Fc regions each comprise amino acid substitutions at positions corresponding to positions 234, 235, and 329 of human IgG1 according to EU Index, wherein the amino acid substitutions are L234A, L235A, and

P329A. In some embodiments, the Fc regions of the second and the third polypeptide chains are human IgG1 Fc regions, and wherein the Fc regions each comprise amino acid substitutions at positions corresponding to positions 234, 235, and 329 of human IgG1 according to EU Index, wherein the amino acid substitutions are L234A, L235A, and P329A. In some embodiments, the Fc regions of the second and the third polypeptide chains are human IgG4 Fc regions, and the Fc regions each comprise amino acid substitutions at positions corresponding to positions 234 and 235 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A and L235A. In some embodiments, the binding protein comprises a second polypeptide chain further comprising a first Fc region linked to C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains, and a third polypeptide chain further comprising a second Fc region linked to C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains; and wherein the first and the second Fc regions each comprise amino acid substitutions at positions corresponding to positions 234 and 235 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A and L235A.

[0169] In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, wherein the first Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 228, 234, 235, 354, 366, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, F234A, L235A, S354C, T366W, and R409K; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, wherein the second Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 228, 234, 235, 349, 366, 368, 407, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, F234A, L235A, Y349C, T366S, L368A, Y407V, and R409K. In some embodiments, the second polypeptide chain further comprises a first Fc region linked to CH1, wherein the first Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the first Fc region comprises amino acid substitutions at positions corresponding to positions 228, 234, 235, 349, 366, 368, 407,

and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, F234A, L235A, Y349C, T366S, L368A, Y407V, and R409K; and wherein the third polypeptide chain further comprises a second Fc region linked to CH1, wherein the second Fc region is a human IgG4 Fc region comprising an immunoglobulin hinge region and CH2 and CH3 immunoglobulin heavy chain constant domains, wherein the second Fc region comprises amino acid substitutions at positions corresponding to positions 228, 234, 235, 354, 366, and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P, F234A, L235A, S354C, T366W, and R409K.

[0170] In some embodiments, the Fc region is a human IgG4 Fc region comprising one or more mutations that reduce or eliminate FcγI and/or FcγII binding. In some embodiments, the Fc region is a human IgG4 Fc region comprising one or more mutations that reduce or eliminate FcγI and/or FcγII binding but do not affect FcRn binding. In some embodiments, the Fc region is a human IgG4 Fc region comprising amino acid substitutions at positions corresponding to positions 228 and/or 409 of human IgG4 according to EU Index. In some embodiments, the amino acid substitutions are S228P and /or R409K. In some embodiments, the Fc region is a human IgG4 Fc region comprising amino acid substitutions at positions corresponding to positions 234 and/or 235 of human IgG4 according to EU Index. In some embodiments, the amino acid substitutions are F234A and/or L235A. In some embodiments, the Fc region is a human IgG4 Fc region comprising amino acid substitutions at positions corresponding to positions 228, 234, 235, and/or 409 of human IgG4 according to EU Index. In some embodiments, the amino acid substitutions are S228P, F234A, L235A, and /or R409K. In some embodiments, the Fc region is a human IgG4 Fc region comprising amino acid substitutions at positions corresponding to positions 233-236 of human IgG4 according to EU Index. In some embodiments, the amino acid substitutions are E233P, F234V, L235A, and a deletion at 236. In some embodiments, the Fc region is a human IgG4 Fc region comprising amino acid mutations at substitutions corresponding to positions 228, 233-236, and/or 409 of human IgG4 according to EU Index. In some embodiments, the amino acid mutations are S228P; E233P, F234V, L235A, and a deletion at 236; and /or R409K.

[0171] In some embodiments, the Fc region comprises one or more mutations that reduce or eliminate Fc receptor binding and/or effector function of the Fc region (*e.g.*, Fc receptor-mediated antibody-dependent cellular phagocytosis (ADCP), complement-dependent cytotoxicity (CDC), and/or antibody-dependent cellular cytotoxicity (ADCC)).

[0172] In some embodiments, the Fc region is a human IgG1 Fc region comprising one or more amino acid substitutions at positions corresponding to positions 234, 235, and/or 329 of human IgG1 according to EU Index. In some embodiments, the amino acid substitutions are L234A, L235A, and/or P329A. In some embodiments, the Fc region is a human IgG1 Fc region comprising amino acid substitutions at positions corresponding to positions 298, 299, and/or 300 of human IgG1 according to EU Index. In some embodiments, the amino acid substitutions are S298N, T299A, and/or Y300S.

[0173] In some embodiments, a binding protein of the present disclosure comprises one or more mutations to improve stability, *e.g.*, of the hinge region and/or dimer interface of IgG4 (*See e.g.*, Spiess, C. *et al.* (2013) *J. Biol. Chem.* 288:26583-26593). In some embodiments, the mutation comprises substitutions at positions corresponding to positions 228 and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P and R409K. In some embodiments, the binding protein comprises a second polypeptide chain further comprising a first Fc region linked to C_{H1}, the first Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains, and a third polypeptide chain further comprising a second Fc region linked to C_{H1}, the second Fc region comprising an immunoglobulin hinge region and C_{H2} and C_{H3} immunoglobulin heavy chain constant domains; wherein the first and second Fc regions are human IgG4 Fc regions; and wherein the first and the second Fc regions each comprise amino acid substitutions at positions corresponding to positions 228 and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P and R409K. In some embodiments, a binding protein of the present disclosure comprises knob and hole mutations and one or more mutations to improve stability. In some embodiments, the first and/or second Fc regions are human IgG4 Fc regions.

[0174] In some embodiments, the Fc region is a human IgG1 Fc region comprising one or more amino acid substitutions at positions corresponding to positions 234, 235, and/or 329 of human IgG1 according to EU Index. In some embodiments, the amino acid substitutions are L234A, L235A, and/or P329A. In some embodiments, the Fc region is a human IgG1 Fc region comprising amino acid substitutions at positions corresponding to positions 298, 299, and/or 300 of human IgG1 according to EU Index. In some embodiments, the amino acid substitutions are S298N, T299A, and/or Y300S.

Nucleic acids

[0175] Other aspects of the present disclosure relate to isolated nucleic acid molecules comprising a nucleotide sequence encoding any of the binding proteins described herein. Exemplary and non-limiting nucleic acid sequences are provided in Table 5.

[0176] Other aspects of the present disclosure relate to kits of polynucleotides, *e.g.*, that encode one or more polypeptides of a binding protein as described herein. In some embodiments, a kit of polynucleotides of the present disclosure comprises one, two, three, or four polynucleotides of a kit of polynucleotides comprising: (a) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:177, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:178, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:179, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:180; (b) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:181, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:182, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:183, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:184; (c) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:185, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:186, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:187, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:188; (d) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:189, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:190, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:191, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:192; (e) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:193, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:194, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:195, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:196; (f) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:197, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:198, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:199, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:200; (g) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:201, a second polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:202, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:203, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:204; (h) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:205, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:206, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:207, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:208; (i) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:209, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:210, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:211, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:212; (j) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:213, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:214, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:215, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:216; (k) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:217, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:218, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:219, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:220; (l) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:221, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:222, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:223, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:224; (m) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:225, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:226, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:227, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:228; (n) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:229, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:230, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:231, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:232; (o) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:233, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:234, a third polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:235, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:236; (p) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:237, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:238, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:239, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:240; (q) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:241, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:242, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:243, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:244; (r) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:245, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:246, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:247, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:248; (s) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:249, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:250, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:251, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:252; (t) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:253, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:254, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:255, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:256; (u) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:257, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:258, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:259, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:260; (v) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:261, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:262, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:263, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:264; (w) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:265, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:266, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:267, and a fourth polynucleotide

comprising the polynucleotide sequence of SEQ ID NO:268; (x) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:269, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:270, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:271, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:272; (y) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:273, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:274, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:275, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:276; (z) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:277, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:278, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:279, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:280; (aa) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:281, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:282, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:283, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:284; (bb) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:285, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:286, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:287, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:288; or (cc) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:289, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:290, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:291, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:292.

[0177] Other aspects of the present disclosure relate to a vector system comprising one or more vectors encoding a first, second, third, and fourth polypeptide chain of any of the binding proteins described herein. In some embodiments, the vector system comprises a first vector encoding the first polypeptide chain of the binding protein, a second vector encoding the second polypeptide chain of the binding protein, a third vector encoding the third polypeptide chain of the binding protein, and a fourth vector encoding the fourth polypeptide chain of the binding protein, *e.g.*, as shown in the polynucleotides of Table 5. In some embodiments, the vector system comprises a first vector encoding the first and second

polypeptide chains of the binding protein, and a second vector encoding the third and fourth polypeptide chains of the binding protein. In some embodiments, the vector system comprises a first vector encoding the first and third polypeptide chains of the binding protein, and a second vector encoding the second and fourth polypeptide chains of the binding protein. In some embodiments, the vector system comprises a first vector encoding the first and fourth polypeptide chains of the binding protein, and a second vector encoding the second and third polypeptide chains of the binding protein. In some embodiments, the vector system comprises a first vector encoding the first, second, third, and fourth polypeptide chains of the binding protein. The one or more vectors of the vector system may be any of the vectors described herein. In some embodiments, the one or more vectors are expression vectors. In some embodiments, the first, second, third, and fourth polynucleotides are present on one or more expression vectors, *e.g.*, one, two, three, or four expression vectors.

[0178] Standard recombinant DNA methodologies are used to construct the polynucleotides that encode the polypeptides which form the binding proteins, incorporate these polynucleotides into recombinant expression vectors, and introduce such vectors into host cells. *See e.g.*, Sambrook *et al.*, 2001, MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring Harbor Laboratory Press, 3rd ed.). Enzymatic reactions and purification techniques may be performed according to manufacturer's specifications, as commonly accomplished in the art, or as described herein. Unless specific definitions are provided, the nomenclature utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Similarly, conventional techniques may be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, delivery, and treatment of patients.

[0179] In some embodiments, the isolated nucleic acid is operably linked to a heterologous promoter to direct transcription of the binding protein-coding nucleic acid sequence. A promoter may refer to nucleic acid control sequences which direct transcription of a nucleic acid. A first nucleic acid sequence is operably linked to a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence of a binding protein if the promoter affects the transcription or expression of the coding sequence. Examples of promoters may include, but are not limited to, promoters obtained from the genomes of viruses (such as polyoma virus, fowlpox virus, adenovirus

(such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus, Simian Virus 40 (SV40), and the like), from heterologous eukaryotic promoters (such as the actin promoter, an immunoglobulin promoter, from heat-shock promoters, and the like), the CAG-promoter (Niwa et al., Gene 108(2):193-9, 1991), the phosphoglycerate kinase (PGK)-promoter, a tetracycline-inducible promoter (Masui et al., Nucleic Acids Res. 33:e43, 2005), the lac system, the trp system, the tac system, the trc system, major operator and promoter regions of phage lambda, the promoter for 3-phosphoglycerate kinase, the promoters of yeast acid phosphatase, and the promoter of the yeast alpha-mating factors. Polynucleotides encoding binding proteins of the present disclosure may be under the control of a constitutive promoter, an inducible promoter, or any other suitable promoter described herein or other suitable promoter that will be readily recognized by one skilled in the art.

[0180] In some embodiments, the isolated nucleic acid is incorporated into a vector. In some embodiments, the vector is an expression vector. Expression vectors may include one or more regulatory sequences operatively linked to the polynucleotide to be expressed. The term "regulatory sequence" includes promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Examples of suitable enhancers may include, but are not limited to, enhancer sequences from mammalian genes (such as globin, elastase, albumin, α-fetoprotein, insulin and the like), and enhancer sequences from a eukaryotic cell virus (such as SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, adenovirus enhancers, and the like). Examples of suitable vectors may include, for example, plasmids, cosmids, episomes, transposons, and viral vectors (e.g., adenoviral, vaccinia viral, Sindbis-viral, measles, herpes viral, lentiviral, retroviral, adeno-associated viral vectors, etc.). Expression vectors can be used to transfect host cells, such as, for example, bacterial cells, yeast cells, insect cells, and mammalian cells. Biologically functional viral and plasmid DNA vectors capable of expression and replication in a host are known in the art, and can be used to transfect any cell of interest.

Host cells

[0181] Other aspects of the present disclosure relate to a host cell (*e.g.,* an isolated host cell) comprising one or more isolated polynucleotides, vectors, and/or vector systems described herein. In some embodiments, an isolated host cell of the present disclosure is

cultured *in vitro*. In some embodiments, the host cell is a bacterial cell (*e.g.*, an *E. coli* cell). In some embodiments, the host cell is a yeast cell (*e.g.*, an *S. cerevisiae* cell). In some embodiments, the host cell is an insect cell. Examples of insect host cells may include, for example, *Drosophila* cells (*e.g.*, S2 cells), *Trichoplusia ni* cells (*e.g.*, High Five™ cells), and *Spodoptera frugiperda* cells (*e.g.*, Sf21 or Sf9 cells). In some embodiments, the host cell is a mammalian cell. Examples of mammalian host cells may include, for example, human embryonic kidney cells (*e.g.*, 293 or 293 cells subcloned for growth in suspension culture), Expi293™ cells, CHO cells, baby hamster kidney cells (*e.g.*, BHK, ATCC CCL 10), mouse sertoli cells (*e.g.*, TM4 cells), monkey kidney cells (*e.g.*, CV1 ATCC CCL 70), African green monkey kidney cells (*e.g.*, VERO-76, ATCC CRL-1587), human cervical carcinoma cells (*e.g.*, HELA, ATCC CCL 2), canine kidney cells (*e.g.*, MDCK, ATCC CCL 34), buffalo rat liver cells (*e.g.*, BRL 3A, ATCC CRL 1442), human lung cells (*e.g.*, W138, ATCC CCL 75), human liver cells (*e.g.*, Hep G2, HB 8065), mouse mammary tumor cells (*e.g.*, MMT 060562, ATCC CCL51), TRI cells, MRC 5 cells, FS4 cells, a human hepatoma line (*e.g.*, Hep G2), and myeloma cells (*e.g.*, NS0 and Sp2/0 cells).

[0182] Other aspects of the present disclosure relate to a method of producing any of the binding proteins described herein. In some embodiments, the method includes a) culturing a host cell (*e.g.*, any of the host cells described herein) comprising an isolated nucleic acid, vector, and/or vector system (*e.g.*, any of the isolated nucleic acids, vectors, and/or vector systems described herein) under conditions such that the host cell expresses the binding protein; and b) isolating the binding protein from the host cell. Methods of culturing host cells under conditions to express a protein are well known to one of ordinary skill in the art. Methods of isolating proteins from cultured host cells are well known to one of ordinary skill in the art, including, for example, by affinity chromatography (*e.g.*, two step affinity chromatography comprising protein A affinity chromatography followed by size exclusion chromatography).

Pharmaceutical Compositions

[0183] Therapeutic or pharmaceutical compositions comprising binding proteins are within the scope of the disclosure. Such therapeutic or pharmaceutical compositions can comprise a therapeutically effective amount of a binding protein, or binding protein-drug conjugate, in admixture with a pharmaceutically or physiologically acceptable formulation agent selected for suitability with the mode of administration.

[0184] Acceptable formulation materials are nontoxic to recipients at the dosages and concentrations employed.

[0185] The pharmaceutical composition can contain formulation materials for modifying, maintaining, or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption, or penetration of the composition. Suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine, or lysine), antimicrobials, antioxidants (such as ascorbic acid, sodium sulfite, or sodium hydrogen-sulfite), buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates, or other organic acids), bulking agents (such as mannitol or glycine), chelating agents (such as ethylenediamine tetraacetic acid (EDTA)), complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin, or hydroxypropyl-beta-cyclodextrin), fillers, monosaccharides, disaccharides, and other carbohydrates (such as glucose, mannose, or dextrins), proteins (such as serum albumin, gelatin, or immunoglobulins), coloring, flavoring and diluting agents, emulsifying agents, hydrophilic polymers (such as polyvinylpyrrolidone), low molecular weight polypeptides, salt-forming counterions (such as sodium), preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid, or hydrogen peroxide), solvents (such as glycerin, propylene glycol, or polyethylene glycol), sugar alcohols (such as mannitol or sorbitol), suspending agents, surfactants or wetting agents (such as pluronics; PEG; sorbitan esters; polysorbates such as polysorbate 20 or polysorbate 80; triton; tromethamine; lecithin; cholesterol or tyloxapal), stability enhancing agents (such as sucrose or sorbitol), tonicity enhancing agents (such as alkali metal halides – *e.g.*, sodium or potassium chloride – or mannitol sorbitol), delivery vehicles, diluents, excipients and/or pharmaceutical adjuvants (*see, e.g.,* REMINGTON'S PHARMACEUTICAL SCIENCES (18th Ed., A.R. Gennaro, ed., Mack Publishing Company 1990), and subsequent editions of the same, incorporated herein by reference for any purpose).

[0186] The optimal pharmaceutical composition will be determined by a skilled artisan depending upon, for example, the intended route of administration, delivery format, and desired dosage. Such compositions can influence the physical state, stability, rate of *in vivo* release, and rate of *in vivo* clearance of the binding protein.

[0187] The primary vehicle or carrier in a pharmaceutical composition can be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier for injection can

be water, physiological saline solution, or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. Other exemplary pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, which can further include sorbitol or a suitable substitute. In one embodiment of the disclosure, binding protein compositions can be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents in the form of a lyophilized cake or an aqueous solution. Further, the binding protein can be formulated as a lyophilizate using appropriate excipients such as sucrose.

[0188] The pharmaceutical compositions of the disclosure can be selected for parenteral delivery or subcutaneous. Alternatively, the compositions can be selected for inhalation or for delivery through the digestive tract, such as orally. The preparation of such pharmaceutically acceptable compositions is within the skill of the art.

[0189] The formulation components are present in concentrations that are acceptable to the site of administration. For example, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

[0190] When parenteral administration is contemplated, the therapeutic compositions for use can be in the form of a pyrogen-free, parenterally acceptable, aqueous solution comprising the desired binding protein in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which a binding protein is formulated as a sterile, isotonic solution, properly preserved. Yet another preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads, or liposomes, that provides for the controlled or sustained release of the product which can then be delivered via a depot injection. Hyaluronic acid can also be used, and this can have the effect of promoting sustained duration in the circulation. Other suitable means for the introduction of the desired molecule include implantable drug delivery devices.

[0191] In one embodiment, a pharmaceutical composition can be formulated for inhalation. For example, a binding protein can be formulated as a dry powder for inhalation.

Binding protein inhalation solutions can also be formulated with a propellant for aerosol delivery. In yet another embodiment, solutions can be nebulized.

[0192] It is also contemplated that certain formulations can be administered orally. In one embodiment of the disclosure, binding proteins that are administered in this fashion can be formulated with or without those carriers customarily used in the compounding of solid dosage forms such as tablets and capsules. For example, a capsule can be designed to release the active portion of the formulation at the point in the gastrointestinal tract where bioavailability is maximized and pre-systemic degradation is minimized. Additional agents can be included to facilitate absorption of the binding protein. Diluents, flavorings, low melting point waxes, vegetable oils, lubricants, suspending agents, tablet disintegrating agents, and binders can also be employed.

[0193] Another pharmaceutical composition can involve an effective quantity of binding proteins in a mixture with non-toxic excipients that are suitable for the manufacture of tablets. By dissolving the tablets in sterile water, or another appropriate vehicle, solutions can be prepared in unit-dose form. Suitable excipients include, but are not limited to, inert diluents, such as calcium carbonate, sodium carbonate or bicarbonate, lactose, or calcium phosphate; or binding agents, such as starch, gelatin, or acacia; or lubricating agents such as magnesium stearate, stearic acid, or talc.

[0194] Additional pharmaceutical compositions of the disclosure will be evident to those skilled in the art, including formulations involving binding proteins in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. Additional examples of sustained-release preparations include semipermeable polymer matrices in the form of shaped articles, *e.g.* films, or microcapsules. Sustained release matrices can include polyesters, hydrogels, polylactides, copolymers of L-glutamic acid and gamma ethyl-L-glutamate, poly(2-hydroxyethyl-methacrylate), ethylene vinyl acetate, or poly-D(-)-3-hydroxybutyric acid. Sustained-release compositions can also include liposomes, which can be prepared by any of several methods known in the art.

[0195] Pharmaceutical compositions to be used for *in vivo* administration typically must be sterile. This can be accomplished by filtration through sterile filtration membranes. Where the composition is lyophilized, sterilization using this method can be conducted either prior to, or following, lyophilization and reconstitution. The composition for parenteral

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

[0196] Once the pharmaceutical composition has been formulated, it can be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or as a dehydrated or lyophilized powder. Such formulations can be stored either in a ready-to-use form or in a form (*e.g.*, lyophilized) requiring reconstitution prior to administration.

[0197] The disclosure also encompasses kits for producing a single-dose administration unit. The kits can each contain both a first container having a dried protein and a second container having an aqueous formulation. Also included within the scope of this disclosure are kits containing single and multi-chambered pre-filled syringes (*e.g.*, liquid syringes and lyosyringes).

[0198] The effective amount of a binding protein pharmaceutical composition to be employed therapeutically will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will thus vary depending, in part, upon the molecule delivered, the indication for which the binding protein is being used, the route of administration, and the size (body weight, body surface, or organ size) and condition (the age and general health) of the patient. Accordingly, the clinician can titer the dosage and modify the route of administration to obtain the optimal therapeutic effect.

[0199] Dosing frequency will depend upon the pharmacokinetic parameters of the binding protein in the formulation being used. Typically, a clinician will administer the composition until a dosage is reached that achieves the desired effect. The composition can therefore be administered as a single dose, as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion via an implantation device or catheter. Further refinement of the appropriate dosage is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. Appropriate dosages can be ascertained through use of appropriate dose-response data.

[0200] The route of administration of the pharmaceutical composition is in accord with known methods, *e.g.*, orally; through injection by intravenous, intraperitoneal, intracerebral (intraparenchymal), intracerebroventricular, intramuscular, intraocular, intraarterial,

intraportal, or intralesional routes; by sustained release systems; or by implantation devices. Where desired, the compositions can be administered by bolus injection or continuously by infusion, or by implantation device.

[0201] The composition can also be administered locally via implantation of a membrane, sponge, or other appropriate material onto which the desired molecule has been absorbed or encapsulated. Where an implantation device is used, the device can be implanted into any suitable tissue or organ, and delivery of the desired molecule can be via diffusion, timed-release bolus, or continuous administration.

[0202] The pharmaceutical compositions can be used to prevent and/or treat HIV infection. The pharmaceutical compositions can be used as a standalone therapy or in combination with standard anti-retroviral therapy.

[0203] The disclosure also relates to a kit comprising a binding protein and other reagents useful for detecting target antigen levels in biological samples. Such reagents can include a detectable label, blocking serum, positive and negative control samples, and detection reagents. In some embodiments, the kit comprises a composition comprising any binding protein, polynucleotide, vector, vector system, and/or host cell described herein. In some embodiments, the kit comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, IV solution bags, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds a composition which is by itself or combined with another composition effective for treating, preventing and/or diagnosing a condition (*e.g.,* HIV infection) and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). In some embodiments, the label or package insert indicates that the composition is used for preventing, diagnosing, and/or treating the condition of choice. Alternatively, or additionally, the article of manufacture or kit may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

Methods and Uses for Binding Proteins

[0204] Certain aspects of the present disclosure relate to methods of preventing HIV infection in a patient, treating HIV infection in a patient, preventing AIDS in a patient, and

treating AIDS in a patient, using any of the binding proteins or pharmaceutical compositions disclosed herein. Any of the binding proteins or pharmaceutical compositions disclosed herein may find use in a method of the present disclosure, *e.g.*, methods for preventing HIV infection in a patient, treating HIV infection in a patient, preventing AIDS in a patient, and treating AIDS in a patient.

[0205] **FIG. 1** illustrates an exemplary and non-limiting format for a trispecific binding protein that may be employed in the methods and uses described herein. As shown in **FIG. 2**, a proposed mechanism by which the binding protein shown in **FIG. 1** may result in elimination of the HIV reservoir cells in a patient involves: (1) activation of latently infected CD4+ T cells via the anti-CD28 and anti-CD3 arms of the trispecific binding protein; (2) recruitment of CD8+ T cells to activated, latently infected CD4+ T cells via anti-Env and anti-CD3 arms; (3) activation of engaged CD8+ T cells via the anti-CD28 and anti-CD3 arms; and (4) killing of latently infected CD4+ T cells through a Perforin/Granzyme mechanism. Advantageously, this mechanism is thought to activate and subsequently kill HIV-1 reservoir cells, providing a novel strategy for attacking the HIV-1 reservoir in a patient.

[0206] In some embodiments, the methods of the present disclosure comprise administering to the patient a therapeutically effective amount of at least one of the binding proteins or pharmaceutical compositions described herein.

[0207] In some embodiments, the at least one binding protein is administered in combination with an anti-retroviral therapy (*e.g.*, an anti-HIV therepy). In some embodiments, the at least one binding protein is administered before the anti-retroviral therapy. In some embodiments, the at least one binding protein is administered concurrently with the anti-retroviral therapy. In some embodiments, the at least one binding protein is administered after the anti-retroviral therapy. In some embodiments, the at least one binding protein is co-administered with any standard anti-retroviral therapy known in the art.

[0208] In some embodiments, administration of the at least one binding protein or pharmaceutical composition results in elimination of one or more latently and/or chronically HIV-infected cells in the patient. In some embodiments, administration of the at least one binding protein results in neutralization of one or more HIV virions and results in elimination of one or more latently and/or chronically HIV-infected cells in the patient. In some embodiments, the patient is a human.

Table 4. Trispecific binding protein polypeptide sequences

Molecule	*Polypeptide Number (acc. to formula)*	*SEQ ID NO*	*Sequence*
Trispecific 1 VRC07_523 / CD28sup x CD3mid IgG1 LALA/P329A	1	61	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNANTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	2	62	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREP QVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPG
	3	63	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRDMYSET AFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALAAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	64	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 2 VRC07_523 / CD28sup x CD3mid IgG1 NNAS	1	65	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNANTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	2	66	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG

			QGTLVTVSSRTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPG
	3	67	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRDMYSET AFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	68	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 3 VRC07_523 / CD28sup x CD3mid IgG4 FALA/409K	1	69	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNANTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	2	70	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTL PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSLG
	3	71	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRDMYSET AFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	72	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Trispecific 4 VRC07_523 / CD28sup x CD3mid_QQ IgG4 FALA/409K	1	73	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	2	74	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTL PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSLG
	3	75	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRDMYSET AFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	76	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 6 VRC07_523 / CD28sup x CD3mid_QQ IgG4 FALA/409K_ DKTHT linker	1	77	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
	2	78	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTL

			PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSLG
	3	79	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRDMYSET AFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEA AGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	80	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 8 VRC07_523 / CD28sup x CD3mid_QQ IgG1_NNAS/409K_DKTHT linker	1	81	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
	2	82	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	83	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRDMYSET AFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQ DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNY KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	84	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 9	1	85	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK

VRC07_523_F R3-03 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker			LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	86	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTL PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSLG
	3	87	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRQLSQDP DDPDWGTAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	88	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 10 VRC07_523_F R3-03 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	89	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	90	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE

			VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTL PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSLG
	3	91	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRQLSQDP DDPDWGTAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPCSRSTSESTAALG CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCP PCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	92	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 11 VRC07_523_FR3-03 / CD28sup x CD3mid_ENLQ IgG1_NNAS_DKTHT linker	1	93	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	94	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	95	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRQLSQDP DDPDWGTAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	96	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Trispecific 12 VRC07_523_F R3-03 / CD28sup x CD3mid_ENL F IgG1_NNAS_ DKTHT linker	1	97	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	98	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	99	QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHGAVSYARQLQGRVTMTRQLSQDP DDPDWGTAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWDFEHWGQGTPVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVV SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWES NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	100	SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 13 N6 / CD28sup x CD3mid IgG4	1	101	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNANTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	2	102	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEV QFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTLP

			PSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEAL HNHYTQKSLSLSLG
	3	103	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPPVAGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	104	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 14 N6 / CD28sup x CD3mid IgG4	1	105	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNANTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC
	2	106	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVCTL PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA LHNHYTQKSLSLSLG
	3	107	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	108	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 15 N6 / CD28sup x CD3mid_QQ	1	109	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKGQPKAAPDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGK APKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKTKGPSRTVAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQG LSSPVTKSFNRGEC

IgG4 FALA/409K	2	110	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSQVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMH WVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDYWG QGTLVTVSSRTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV PSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR PPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFSCSVMHEA EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS LHNHYTQKSLSLSLG CSVMHEALHNHYTQKSLSLSLG	
	3	111	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	112	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 16 N6 / CD28sup x CD3mid_QQ IgG4 FALA/409K_ DKTHT linker	1	113	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
	2	114	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG	
	3	115	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN

			GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	116	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 17 N6 / CD28sup x CD3mid IgG4 FALA/409K_ DKTHT linker	1	117	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHNNANTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
	2	118	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	119	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	120	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 19 N6 / CD28sup x CD3mid_QQ IgG1_NNAS_ DKTHT linker	1	121	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
	2	122	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD

			YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	123	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	124	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 21 N6 / CD28sup x CD3mid_DNA Q IgG4 FALA/409K_ DKTHT linker	1	125	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHDNAQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISR VEAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAP KLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
	2	126	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	127	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

	4	128	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 22 N6 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	129	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	130	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	131	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	132	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 23 N6 / CD28sup x CD3mid_ENL R IgG4 FALA/409K_ DKTHT linker	1	133	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLRTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	134	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA

			WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	135	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	136	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 24 N6 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	137	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	138	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	139	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

	4	140	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 25 N6_rw52 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	141	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	142	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	143	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGATNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	144	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSSEEGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 26 N6_rw52 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	145	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	146	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA

			WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	147	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGATNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	148	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSSEEGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 27 N6_rw52 / CD28sup x CD3mid_ENL F IgG1_NNAS_ DKTHT linker	1	149	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	150	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	151	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGATNFGGGFRDRVTLTRDVYREIA YMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

	4	152	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSSEEGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 28 N6_FR3-03 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	153	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	154	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	155	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRQLSQDP DDPDWGIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	156	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 29 N6_FR3-03 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	157	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	158	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA

			WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	159	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRQLSQDP DDPDWGIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPCSRSTSESTAALGCL VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVL HQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	160	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 30 N6_FR3-03/ CD28sup x CD3mid_ENL QIgG1_NNAS _DKTHT linker	1	161	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	162	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	163	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRQLSQDP DDPDWGIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

	4	164	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 31 N6_FR3-03 / CD28sup x CD3mid_ENL F IgG1_NNAS_ DKTHT linker	1	165	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	166	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVCTLPPSRDELTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQG NVFSCSVMHEALHNHYTQKSLSLSPG
	3	167	RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQYGAVNFGGGFRDRVTLTRQLSQDP DDPDWGIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALDAWGQGTTVVVSAASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNNASRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPCRDELTKNQVSLWCLVKGFYPSDIAVEWESNG QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
	4	168	YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGVPSRFSGSGFHTSFNLTISDLQADDI ATYYCQVLQFFGRGSRLHIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 34 VRC01.23 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	169	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	170	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA

			WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	171	QVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGKRPEWMGWLKPRWGAVNYARPLQGRVTMTRQLSQDP DDPDWGTAFLELRSLTVDDTAVYFCTRGKNCDYNWDFEHWGRGTPVIVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
	4	172	LTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
Trispecific 35 VRC01.23 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	173	DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRV EAEDVGVYYCGQGTQYPFTFGSGTKVEIKDKTHTDIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPK LLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIKDKTHTRTVAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLS SPVTKSFNRGEC
	2	174	QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTA YMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSSDKTHTQVQLVESGGGVVQPGRSLRLSCAASGFTFTKA WMHWVRQAPGKQLEWVAQIKDKSNSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFD YWGQGTLVTVSSDKTHTASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPR EPQVCTLPPSQEEMTKNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLSLG
	3	175	QVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGKRPEWMGWLKPRWGAVNYARPLQGRVTMTRQLSQDP DDPDWGTAFLELRSLTVDDTAVYFCTRGKNCDYNWDFEHWGRGTPVIVSSASTKGPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPA PEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPCQEEMTKNQVSLWCLVKGFYPSDIAVEWESNGQPENN YKTTPPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

	4	176	LTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSGSRWGPDYNLTISNLESGDFGVYY CQQYEFFGQGTKVQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Table 5. Trispecific binding protein polynucleotide sequences

Molecule	*Polypeptide Number (acc. to formula)*	*SEQ ID NO*	*Sequence*
Trispecific 1 VRC07_523 / CD28sup x CD3mid IgG1 LALA/P329A	1	177	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCGACATCCAGATGACCCAGAGCCCCA GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAAC TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC TACTACTGCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGACCAAGGGCC CCAGCCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG AGCTTCAACCGGGGCGAGTGT
	2	178	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCAGCCAGGTGCAGCTGGTGGAATCT GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTCACCAAGGCCT GGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAAGAGCAACAGCTA CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCTGAGCCCCTTCGA TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTCGGACCGCCAGCACAAAGGGCCCCAGCGTGTTCCCTCTGG CCCCTAGCAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG ACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTGCTGCAGTCCAGCGGCCTGTAC AGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACATCTGCAACGTGAACCACAAGCC

			CAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAGACCCACACCTGTCCCCCTTGTCCTGCC CCCGAAGCCGCCGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCC CGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGAAGTTCAATTGGTACGTGGACGGCGTGG AAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGT GCTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGGCCGCCCCCATCGAG AAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGCCCCCAAGCAGGGACGAGCTGA CCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAAC GGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCT GACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCAC TACACCCAGAAGTCCCTGAGCCTGAGCCCCGGCTAGTGA
	3	179	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAAACCCGGCGACAGCATGCGGATCAGCTGCAGAGCCAGCG GCTACGAGTTCATCAACTGCCCCCATCAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGATG AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGGACATGTACAGCG AGACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTCTGCACCCGGGGCAAGTACTGC ACCGCCAGAGACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTGTGACAGTGTCTAGCGCTTCGAC CAAGGGCCCCAGCGTGTTCCCTCTGGCCCCTAGCAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCG TGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCA GCTGTGCTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGAC CTACATCTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAG ACCCACACCTGTCCCCCTTGTCCTGCCCCCGAAGCCGCCGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAG GACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGA AGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAGCAC GTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCC AACAAGGCCCTGGCCGCCCCCATCGAGAAAACCATCAGCAAAGGCCAGCCCCGCGAACCCCAGGTGTACA CACTGCCCCCATGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGTGGTGTCTGGTGAAAGGCTTCTACCCCTCC GATATCGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCG ACGGCTCATTCTTCCTGTACTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCC GTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC
	4	180	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACACAAGAGC CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT

Trispecific 2 VRC07_523 / CD28sup x CD3mid IgG1 NNAS	1	181	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCGACATCCAGATGACCCAGAGCCCCA GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCGAGAACATCTACGTGTGGCTGAAC TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC TACTACTGCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGACCAAGGGCC CCAGCCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG AGCTTCAACCGGGGCGAGTGT
	2	182	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCACTCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGCCAGGTGCAGCTGGTGGAATCT GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGTCTGCCGCCAGCGGCTTCACCTTCACCAACTACGCCT GGATGCACTGGGTGCGCCAGGCCCCTGGAAAGGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAAGAGCAACAGCTA CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCGGGGCGTGTACTATGCCCTGAGCCCCTTCGA TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGGACCGCCAGCACAAAGGGCCCCAGCGTGTTCCCTCTGG CCCCTAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG ACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTGCTGCAGTCCAGCGGCCTGTAC AGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACATCTGCAACGTGAACCACAAGCC CAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAGACCCACACCTGTCCCCCTTGTCCTGCC CCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCC CGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTTCAATTGGTACGTGGACGGCGTGG AAGTGCACAACGCCAAGACCAAGAGAGGAACAGTACAACAATGCCTCCCGGGTGGTGTCCGTGCTGACCGT GCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGCCCTGCCTCCCCCATCGAG AAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGCCCCCAAGCAGGGACGAGCTGA CCAAGAACCAGGTGTCCCTGAGCTGTGCGTGAAAGGCTTCTACCCCTCCGATATCGCCGTGGAATGGGAGAGCAAC GGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCT GACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCAC TACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC

	3	183	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAAACCCGGCGACAGCATGCGGATCAGCTGCAGAGCCAGCG GCTACGAGTTCATCAACTGCCCCATCAACTGGATCAGACTGGCCCCCTGGCAAGCCGGCCTGAGTGGATGGGATGGATG AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGGACATGTACAGCG AGACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTCTGCACCCGGGGCAAGTACTGC ACCGCCAGAGACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTGTGACAGTGTCTAGCGCTTCGAC CAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGAC CTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAA ACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAA GGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA AGTTCAACTGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG CTCCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCA ACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACAC CCTGCCCCCATGCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGGTAAAAGGCTTCTATCCCAGCG ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGA CGGCTCCTTCTTCCTCTATTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGT GCTGCATGAGGCTCTGCACAGCCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
	4	184	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGC CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
Trispecific 3 VRC07_523 / CD28sup x CD3mid IgG4 FALA/409K	1	185	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCGACATCCAGATGACCCAGAGCCCCA GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAAC TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC TACTACTGCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGACCAAGGGCC CCAGCCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG

			GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG
			CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG
			AGCTTCAACCGGGGCGAGTGT
	2	186	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACAACCAGCATCAG
			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCAGCCAGGTGCAGCTGGTGGAATCT
			GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTCACCAAGGCCT
			GGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAAGAGCAACAGCTA
			CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG
			CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCTGAGCCCCTTCGA
			TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTCGGACCGCCACACAAAGGGCCCATCGGTGTTCCCTCTGG
			CCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG
			ACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTA
			CTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGC
			CCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTGAAGCT
			GCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGAC
			CTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACA
			ACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCA
			GGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATC
			AGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCAGGAAGAGATGACCAAGAACC
			AGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCC
			GAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCTGACCGTGGA
			CAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAG
			AAGTCCCTGTCTCTGTCCCCTGGGC
	3	187	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAAACCCGGCGACAGCATGCGGATCAGCTGCAGAGCCAGCG
			GCTACGAGTTCATCAACTGCCCCCATCAACTGGATCAGACTGGCCCCCTGGCAAGCGGCCTGAGTGGATGGGATGG
			AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGGACACATGTACAGCG
			AGACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTCTGCACCCGGGGCAAGTACTGC
			ACCGCCAGAGACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTGTGACAGTGTCTAGCGCTTCGAC
			CAAGGGCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCG
			TGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCA
			GCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGAC
			CTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCC
			TGCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTG
			ATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTG
			GTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTG

			GTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCC
			TGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCT
			TGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGT
			GGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTC
			TTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGA
			GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	188	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT
			ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGC
			CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC
			GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG
			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCTCTGTCGTGT
			GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG
			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC
			GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA
			ACCGGGGCGAGTGT
Trispecific 4 VRC07_523 / CD28sup x CD3mid_QQ IgG4 FALA/409K	1	189	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA
			GCCAGAGCCTGGTGCACCAGAACGCCCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC
			CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA
			CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC
			TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCGACATCCAGATGACCCAGAGCCCCA
			GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAAC
			TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA
			GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC
			TACTACTGCCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGACCACGGGCC
			CCAGCCGTACGGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT
			GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG
			GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG
			CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG
			AGCTTCAACCGGGGCGAGTGT
	2	190	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG
			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCAGCCAGGTGCAGCTGGTGGAATCT
			GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTCACCAAGGCCT
			GGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAAGAGCAACAGCTA
			CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG
			CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCTGAGCCCCTTCGA

			TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTCGGACCGCCAGCACAAAGGGCCCATCGGTGTTCCCTCTGG
			CCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG
			ACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTA
			CTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGC
			CCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCAGCCCCTGAAGCT
			GCCGGCGGACCCTCCGTGTTCCTGTTCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGAC
			CTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACA
			ACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCA
			GGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATC
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			AGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCC
			GAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCTGACCGTGGA
			CAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAG
			AAGTCCCTGTCTCTGTCCCTGGGC
		191	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAACCCGGCGACAGCATGCGGATCAGCTGCAGAGCCAGCG
			GCTACGAGTTCATCAACTGCCCCATCAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGATG
			AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGGACATGTACAGCG
			AGACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTCTGCACCCGGGGCAAGTACTGC
			ACCGCCAGAGACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTGTGACAGTGTCTAGCGCTTCGAC
			CAAGGGCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCG
			TGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCA
			GCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGAC
			CTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCC
			TGCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAGGACACCCTG
			ATGATCAGCCGGACCCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTG
			GTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTG
			GTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCC
			TGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCT
			TGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGT
			GGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTC
			TTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGA
			GGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
		192	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT
			ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGC
			CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC
			GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG
			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
			GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG

			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
Trispecific 6 VRC07_523 / CD28sup x CD3mid_QQ lgG4 FALA/409K_ DKTHT linker	1	193	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACCAGAACGCCCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	194	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTGTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGAGTGGTGCAGCCTGGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT

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	4	196	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACACAAGAGC CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG GGCGACTTTCGGCGTGTATCTACTGCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
Trispecific 8 VRC07_523 / CD28sup x CD3mid_QQ IgG1_NNAS/4 09K_DKTHT linker	1	197	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACCAGAACGCCCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG

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			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
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			ACCGGGGGCGAGTGT
Trispecific 9 VRC07_523_FR3-03 / CD28sup x CD3mid_ENLQ IgG4 FALA/409K_ DKTHT linker	1	201	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA
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			ACCGGGGGCGAGTGT
	2	202	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
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			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACGCTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
Trispecific 10 VRC07_523_F R3-03 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	205	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCCT GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTATC AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT TTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACGCTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	206	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCAGAAAACCCATACCGAC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTGTCTAGTGATAAGACCCACACCGCGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA

			GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA
			TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT
			GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC
			CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	207	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAAACCCGGCGACAGCATGCGGATCAGCTGCAGAGCCAGCG
			GCTACGAGTTCATCAACTGCCCCATCAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGATG
			AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGCAGCTGAGCCAGG
			ACCCTGATGATCCGGATTGGGGCACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTC
			TGCACCCGGGGCAAGTACTGCACCGCCAGAGACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTG
			TGACAGTGTCTAGCGCTTCGACCAAGGGCCCATCGGTGTTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCT
			ACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGAC
			AAGCGGCGTGCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCA
			GCAGCAGCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGT
			GGAATCTAAGTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCC
			CCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAA
			GATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAAC
			AGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAA
			GTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAG
			CCTCAAGTGTATACCCTGCCCCCTTGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGG
			CTTCTACCCCAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCT
			GTGCTGGACAGCGACGGCTCATTCTTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGT
			GTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	208	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT
			ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGC
			CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC
			GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG
			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
			GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG
			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC
			GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA
			ACCGGGGCGAGTGT
Trispecific 11 VRC07_523_F R3-03 / CD28sup x CD3mid_ENLQ	1	209	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA
			GCCAGAGCCTGGTGCACGAGAACCTGCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC
			CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA
			CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC
			TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC
			TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT
			CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT

			TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT
			GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG
			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
			GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG
			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC
			GACTACGAGAAGCACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA
			ACCGGGGCGAGTGT
	2	210	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG
			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA
			GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT
			TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA
			GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC
			ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCT
			GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
			GCCCCAGCGTGTTCCCTCTGGCCCCTAGCAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAG
			GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG
			CTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACAT
			CTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAGACCCA
			CACCTGTCCCCCTTGTCCTGCCCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACAC
			CCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGAAGTTCA
			ATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAATGCCTCCCG
			GGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAG
			GCCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGC
			CCCCAAGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATC
			GCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCT
			CATTCTTCCTGGTGTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATG
			CACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC
	3	211	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAAACCCGGCGACAGCATGCGGATCAGCTGCAGAGCCAGCG
			GCTACGAGTTCATCAACTGCCCCATCAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGATG
			AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGCAGCTGAGCCAGG
			ACCCTGATGATCCGGATTGGGGCACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTC
			TGCACCCGGGGCAAGTACTGCACCGCCAGAGAACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTG
			TGACAGTGTCTAGCGCTTCGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGC
			ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC
			CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTC

			CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTT GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT CCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG GGAGGAGCAGTACAACAATGCCTCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC CCGAGAACCACAGGTGTACACCCTGCCCCCATGCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGG TAAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGT
	4	212	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACACAAGAGC CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
Trispecific 12 VRC07_523_F R3-03 / CD28sup x CD3mid_ENL F IgG1_NNAS_ DKTHT linker	1	213	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCCT GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTATC AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT TTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	214	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC

TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCCAGCGTGTTCCCCTCTGGCCCCTAGCAGCAAGAGCACATCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG CTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACAT CTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAAGACCCA CACCTGTCCCCCTTGTCCTGCCCCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACAC CCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGAAGTTCA ATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAATGCCTCCCG GGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAG GCCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGC CCCCAAGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATC GCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCT CATTCTTCCTGGTGTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATG CACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC		
	215	CAAGTGCGGCTGTCTCAGTCTGGCGGCCAGATGAAGAAACCCGGCGACAGCATGCGGATCAGCTGCAGAGGCCAGCG GCTACGAGTTCATCAACTGCCCCATCAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGATG AAGCCCAGACACGGGGCCGTGTCCTACGCCAGACAGCTGCAGGGCAGAGTGACCATGACCCGGCAGCTGAGCCAGG ACCCTGATGATCCGGATTGGGGCACAGCCTTCCTGGAACTGCGGAGCCTGACCAGCGACGATACCGCCGTGTACTTC TGCACCCGGGGCAAGTACTGCACCGCCAGAGACTACTACAACTGGGACTTCGAGCACTGGGGCCAGGGCACACCTG TGACAGTGTCTAGCGCTTCGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGAC CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTC CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTT GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT CCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGA GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCG GGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGG AGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCC CCGAGAACCACAGGTGTACACCCTGCCCCCATGCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGG TAAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGG GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCG GGT
	3	

	4	216	AGCCTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGT ACGGCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGC CGCCGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGC GGCGACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCGTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	Trispecific 13 N6 / CD28sup x CD3mid IgG4	1	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCGACATCCAGATGACCCAGAGCCCCA GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCGAACATCTACGTGTGGCTGAAC TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC TACTACTGCCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGACCAAGGGCCC CCAGCCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG AGCTTCAACCGGGGCGAGTGT
		2	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCACGCCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGCCAGCGGTGCAGCTGGTGGAATCT GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTCACCAAGGCCT GGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAAGAGCAACAGCTA CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGCACAAAGGGCCCATCGGTGTTCCCTCTGG TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTCGGACCGCCAGCACAAAGGGCCCATCGGTGTTCCCTCTGG CCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG ACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTA CTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGC CCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTCCTGTG GCTGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTG

			CGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAAC GCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGG ACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATCAG CAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCAGGAAGAGATGACCAAGAACCAG GTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCCGA GAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCTGACCGTGGACA AGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAA GTCCCTGTCTCTGTCCCTGGGC
	3	219	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG GCTACACCTTCACCGCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGGATGGATC AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAAGCTA CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGAC TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT GCCCAGCCCCTCCTGTGGCTGGACCCTCCGTGTTCCTGTTCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGG ACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGG CGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTG ACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCA TCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCAGGAAGA GATGACCAAGAACCAGGTGTCCCTGTGGTGTCTGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGGAGA GCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTACTCC AAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACA ACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	220	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 14	1	221	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA

			CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC
			TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCGACATCCAGATGACCCAGAGCCCCA
			GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGAACATCTACGTGTGGCTGAAC
			TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA
			GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC
			TACTACTGCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGACCAAGGGCC
			CCAGCCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT
			GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG
			GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG
			CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG
			AGCTTCAACCGGGGCGAGTGT
N6 / CD28sup x CD3mid IgG4		222	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG
			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGCCAGCGGTGCAGCTGGTGGAATCT
			GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGTGTCCGCCAGCGGCTTCACCTTCACCTACCAAGGCCT
			GGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAAGAGCAACAGCTA
			CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG
			CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGTCGGGGCGTGTACTATGCCCTGAGCCCCTTCGA
			TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGGACCGCCAGCACAAAGGGCCCATCGGTGTTCCCTCTGG
			CCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG
			ACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTA
			CTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGC
			CCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCAGCCCCTGAAGCT
			GCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGAC
			CTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACA
			ACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCA
			GGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATC
			AGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCAGGAAGAGATGACCAAGAACC
			AGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCC
			GAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCTGACCGTGGA
			CAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAG
			AAGTCCCTGTCTCTGTCCCTGGGC
	3	223	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
			GCTACACCTTCACCGCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC
			AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG
			AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA

			CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCNTGGGCTGCCTCGTGAAGGAC TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT GCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCAGGA AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	224	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 15 N6 / CD28sup x CD3mid_QQ IgG4 FALA/409K	1	225	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGGCCAGCCCAAGGCCGCCCCCCGACATCCAGATGACCCAGAGCCCCA GCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAAC TGGTATCAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCA GCAGATTTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACC TACTACTGCCAGGGCCAGACCTACCCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGACCAAGGGCC CCAGCCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCT GTCGTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCG GCAACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAG CAAGGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAG AGCTTCAACCGGGGCGAGTGT

2	226	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACAAGCCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCGCCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGCCAGGTGCAGCTGGTGGAATCT GGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCTTCACCAAGGCCT GGATGCACTGGGTGCGGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAAGAGCAACAGCTA CGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAACACCCTGTACCTG CAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCTGAGCCCCTTCGA TTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGGACCGCCAGCACAAAGGGCCCATCGGTGTTCCCTCTGG CCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTG ACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTA CTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGC CCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTGAAGCT GCCGGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGAC CTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACA ACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCA GGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATC AGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCAGGAAGAGATGACCAAGAACC AGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCC GAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGGTGTCCAAGCTGACCGTGGA CAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAG AAGTCCCTGTCTCTGTCCCCTGGGC
3	227	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGGATGGATC AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA CGGCGACAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCNTGGGCTGCCTCGTGAAGGAC TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT GCCCAGCCCCTGAAGCTGCCGGCGGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCAGGA AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG

			AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	228	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 16 N6 / CD28sup x CD3mid_QQ IgG4 FALA/409K_ DKTHT linker	1	229	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACCCAGAACGCCCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	230	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCCTGGAAAGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGGGGCGTGCACACCTTTCCAGCCGTG

			CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC
			CTGTAACGTGGACCACACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT
			CCTTGCCCAGCCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC
			AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT
			GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC
			GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA
			GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA
			GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA
			TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT
			GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC
			CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
		231	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
			GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGGATGGATC
			AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG
			AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA
			CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC
			CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCNTGGGCTGCCTCGTGAAGGAC
			TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC
			CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG
			TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT
			GCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC
			CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA
			CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG
			CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT
			CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCAGGA
			AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG
			AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC
			TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC
			ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
		232	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC
			TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA
			AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA
			TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA
			AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC
			GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA
			ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA
			GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC
			TTCAACCGGGGCGAGTGT

Trispecific 17 N6 / CD28sup x CD3mid IgG4 FALA/409K_ DKTHT linker	1	233	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACAACAACGCCAACACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCAG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCGAGTGAGGAGCTTCAAGCCAACAAGGCCACACTGG TGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGG AGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAG CAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTA CAGAATGT
	2	234	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCAGAGGCCGACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC

	3	235	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCNTGGGCTGCCTCGTGAAGGAC TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT GCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCAGGA AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	236	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 19 N6 / CD28sup x CD3mid_QQ IgG1_NNAS_ DKTHT linker	1	237	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACCAGAACGCCCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG

			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC
			GACTACGAGAAGCACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA
			ACCGGGGCGAGTGT
	2	238	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACAAGCCATCAG
			CACCGCCTACATGGAACTGAGCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTGAGCTCTAGTGTCTAGCGACAAAAACCCATACCCAGGTGCA
			GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT
			TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA
			GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC
			ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCT
			GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
			GCCCCAGCGTGTTCCCTCTGGCCCCTAGCAGCAAGAGCACACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAG
			GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG
			CTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACAT
			CTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAGACCCA
			CACCTGTCCCCCCTTGTCCTGCCCCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCCAAGGACAC
			CCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGAAGTTCA
			ATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAATGCCTCCCG
			GGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAG
			GCCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGC
			CCCCAAGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATC
			GCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCT
			CATTCTTCCTGGTGTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATG
			CACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC
	3	239	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
			GCTACACCTTCACCGCCTACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGATGGGGTGGGATGGATC
			AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG
			AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA
			CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTCTCTGCCGCCTCTACAAAGGGCC
			CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
			TACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT
			ACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
			GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACAC
			ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC
			TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
			TGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAATGCCTCCCGTG

			TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC CATGCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGGTAAAAGGCTTCTATCCCAGCGACATCGCC GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT TCTTCCTCTACTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
	4	240	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 21 N6 / CD28sup x CD3mid_DNA Q IgG4 FALA/409K_ DKTHT linker	1	241	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGACAACGCCCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCAG TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCGCCCTCGAGTGAGGAGCTTCAAGCCAACAAGGCCACACTGG TGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGG AGTGGAGACCACACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGAGCCTGACGCCTGAG CAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTA CAGAATGT
	2	242	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACAAGAGCACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCAGAGACAAAACCCATACCGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGCCAGCACCAAGGGCCCCAGCGTG GCTGGTGGAATCTGGCGCGGAGTGGTGCAGCCTGGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGGCGTGTACTATGCCCT

			GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
			GCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG
			GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG
			CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC
			CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT
			CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC
			AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT
			GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC
			GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA
			GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA
			GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA
			TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT
			GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC
			CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	243	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
			GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC
			AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG
			AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA
			CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC
			CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCNTGGGCTGCCTCGTGAAGGAC
			TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC
			CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCAGCCTGGGCACCAAGACCTACACCTG
			TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT
			GCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC
			CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA
			CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG
			CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT
			CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCCAGGA
			AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG
			AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC
			TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC
			ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	244	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC
			TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCTACCACCACA
			AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA
			TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA
			AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC
			GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA

			ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 22 N6 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	245	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	246	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCAGAGACAAGCTACC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTGTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT

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			CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG
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			TTCAACCGGGGCGAGTGT
	Trispecific 23 N6 / CD28sup x CD3mid_ENL R IgG4 FALA/409K_ DKTHT linker	1	249 GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA
			GCCAGAGCCTGGTGCACGAGAACCTGCGTACCTACCTGAGCTGGTATCTGCAGAAGCCCCGGCCAGAGCCCCCAGTCC
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			TTCAACCGGGGCGAGTGT
Trispecific 24 N6 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	253	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA
			GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC
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			AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 25 N6_rw52 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	257	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGGCGAGTGT
	2	258	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACAACCAGCATCAG CACCGCCTACATGGAACTGAGCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCCTCTGGCCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTACCCTGCCCCCTAGCCA

			GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	259	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG GCTACACCTTCACCGCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC AAGCCCCAGTATGGCGCCACCAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG AGATCGCCTACATGGACATCCGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTCTGCCGCCTCTACAAAGGGCC CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAGGAC TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT GCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCTTGCCAGGA AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	260	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCTCCGAAGAGGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 26 N6_rw52 / CD28sup x CD3mid_ENL F IgG4	1	261	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCCT GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTATC AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT

			TTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT
			GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG
			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
			GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG
			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC
			GACTACGAGAAGCACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA
			ACCGGGGCGAGTGT
FALA/409K_ DKTHT linker	2	262	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG
			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA
			GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT
			TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA
			GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC
			ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCT
			GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
			GCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCTGGGCTGCCTCGTGAAG
			GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG
			CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACCGTGCCCAGCAGCCTGGGCACCAAGACCTACAC
			CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT
			CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC
			AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT
			GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC
			GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA
			GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA
			GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA
			TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT
			GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC
			CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	263	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
			GCTACACCTTCACCGCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC
			AAGCCCCAGTATGGCGCCACCAACTTCGGCGGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG
			AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA
			CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC
			CATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCTGGGCTGCCTCGTGAAGGAC
			TACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTGCTC
			CAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACACCTG

			TAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCTCCTT GCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATCAGC CGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGTGGA CGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCCGTG CTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCAGCT CCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATACCCTGCCCCCCTTGCCAGGA AGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAATGGG AGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCTGTAC TCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCCCTGC ACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	264	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCTCCGAAGAGGGCGTGCCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 27 N6_rw52 / CD28sup x CD3mid_ENL F IgG1_NNAS_ DKTHT linker	1	265	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCCT GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTATC AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT TTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	266	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCATCTT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCGCCAGAAAACCCATACCGACGG TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAAACCCATACCCAGGTGCA

		GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT
		TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCCTGGAAAGCAGCTGGAATGGGTGGGCCCAGATCAAGGACAA
		GAGCAACACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC
		ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGGCGTGTACTATGCCCT
		GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
		GCCCCAGCGTGTTCCCTCTGGCCCCTAGCAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAG
		GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG
		CTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACAT
		CTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAAGACCCA
		CACCTGTCCCCCTTGTCCTGCCCCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACAC
		CCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGAAGTTCA
		ATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAATGCCTCCCG
		GGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAG
		GCCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGC
		CCCCAAGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATC
		GCCGTGGAATGGGAGAGCAACGGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCT
		CATTCTTCCTGGTGTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATG
		CACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC
	267	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
		GCTACACCTTTACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC
		AAGCCCCAGTATGGCGCCACCAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGGACGTGTACCGCG
		AGATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTACTGCGCCAGAGACAGAAGCTA
		CGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGTCTGCCGCCTCTACAAAGGGCC
		CATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGAC
		TACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCT
		ACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
		GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACAC
		ATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCC
		TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAAC
		TGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
		TGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
		CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCC
		CATGCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGGTCAAAAGGCTTCTATCCCAGCGACATCGCC
		GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTT
		TCTTCCTCTACTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
		GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
	268	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC
		TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA

			AGCAGCTCCGAAGAGGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACCCTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 28 N6_FR3-03 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker	1	269	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	270	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGTGCCAGCACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTCGGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC

			GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	271	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGCAGCTGAGCCAGG ACCCTGATGATCCGGATTGGGGCATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTAC TGCGCCAGAGACAGAAGCTACGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGT CTGCCGCCTCTACAAAGGGCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCC NTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGT GCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCC TGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAA GTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCAAAGCC CAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAG GTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACA GCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGT GTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTG TATACCCTGCCCCCTTGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCC CAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGAC AGCGACGGCTCATTCTTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTG CTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	272	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCGTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 29 N6_FR3-03 / CD28sup x CD3mid_ENL	1	273	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCCT

			GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGAACATCTACGTGTGGCTGAACTGGTATC
			AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT
			TTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT
			GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG
			TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT
			GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG
			CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC
			GACTACGAGAAGCACAAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA
			ACCGGGGCGAGTGT
	2	274	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG
			CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT
			ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG
			CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
			TGGATTTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA
			GCTGGTGGAATCTGGCGGCGGAGTGGTCAGCCTGGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT
			TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA
			GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC
			ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCT
			GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
			GCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCTGGGCTGCCTCGTGAAG
			GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG
			CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC
			CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT
			CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC
			AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT
			GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC
			GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA
			GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA
			GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA
			TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT
			GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC
			CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	275	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
			GCTACACCTTCACCGCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC
			AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGCAGCTGAGCCAGG
			ACCCTGATGATCCGGATTGGGGCATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTAC
			TGCGCCAGAGACAGAAGCTACGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGT
			CTGCCGCCTCTACAAAGGGCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCC

			NTGGGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGT GCACACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCC TGGGCACCAAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAA GTACGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCC CAAGGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAG GTGCAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACA GCACCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGT GTCCAACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTG TATACCCTGCCCCCCTTGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCC CAGCGACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGAC AGCGACGGCTCATTCTTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTG CTCCGTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	276	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 30 N6_FR3-03/ CD28sup x CD3mid_ENL QIgG1_NNAS _DKTHT linker	1	277	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGAGCCCCAGCAGCCTGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	278	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCATCTT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG

		CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC
		TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA
		GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT
		TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA
		GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC
		ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCT
		GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG
		GCCCCAGCGTGTTCCCTCTGGCCCCTAGCAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAG
		GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG
		CTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCCAGCAGCTCTCTGGGCACCCAGACCTACAT
		CTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAGACCCA
		CACCTGTCCCCCCTTGTCCTGCCCCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACAC
		CCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTGAAGTTCA
		ATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAATGCCTCCCG
		GGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAG
		GCCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGC
		CCCCAAGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATC
		GCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCT
		CATTCTTCCTGGTGTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATG
		CACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC
	279	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG
		GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC
		AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGCAGCTGAGCCAGG
		ACCCTGATGATCCGGATTGGGGCATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTAC
		TGCGCCAGAGACAGAAGCTACGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGT
		CTGCCGCCTCTACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
		CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT
		GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTT
		GGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA
		TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCC
		CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG
		ACCCTGAGGTCAAGTTCAACTGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA
		GTACAACAATGCCTCCCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
		GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACC
		ACAGGTGTACACCCTGCCCCCATGCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGGTAAAAGGCT
		TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT
		GCTGGACTCCGACGGCTCCTTCTTCCTCTACTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT
		TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

	4	280	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
	Trispecific 31 N6_FR3-03 / CD28sup x CD3mid_ENL F IgG1_NNAS_ DKTHT linker	1	281	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCCAGGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCCT GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCGAGAACATCTACGTGTGGCTGAACTGGTATC AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT TTCTGGCAGCGGCTCCGGCACCGAGTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
		2	282	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCCAGCGTGTTCCCTCTGGCCCCTAGCAGCAAGAGCACATCTGGCGGAACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAATTCTGGCGCCCTGACCAGCGGCGTGCACACCTTTCCAGCTGTG CTGCAGTCCAGCGGCCTGTACAGCCTGAGCAGCGTCGTGACAGTGCCCAGCAGCTCTCTGGGCACCCAGACCTACAT CTGCAACGTGAACCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTGGAACCCAAGAGCTGCGACAAAGACCCA CACCTGTCCCCCTTGTCCTGCCCCCGAACTGCTGGGAGGCCCTTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACAC

			CCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCACGAGGACCCTGAAGTTCA ATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCAAGAGAGGAACAGTACAACAATGCCTCCCG GGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAG GCCCTGCCTGCCCCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAACCCCAGGTGTGCACACTGC CCCCAAGCAGGGACGAGCTGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCTCCGATATC GCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCT CATTCTTCCTGGTGTCCAAGCTGACAGTGGACAAGTCCCGGTGGCAGCAGGGCAACGTGTTCAGCTGCTCCGTGATG CACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGAGCCTGAGCCCCGGC
	3	283	AGAGCCCACCTGGTGCAGTCTGGCACCGCCATGAAGAAACCAGGCGCCTCTGTGCGGGTGTCCTGTCAGACAAGCG GCTACACCTTCACCGCCCACATCCTGTTCTGGTTCCGGCAGGCCCCTGGCAGAGGACTGGAATGGGTGGGATGGATC AAGCCCCAGTATGGCGCCGTGAACTTCGGCGGAGGCTTCCGGGATAGAGTGACCCTGACCCGGCAGCTGAGCCAGG ACCCTGATGATCCGGAATTGGGGCATCGCCTACATGGACATCCGGGGCCTGAAGCCCGATGACACCGCCGTGTACTAC TGCGCCAGAGACAGAAGCTACGGCGACAGCAGCTGGGCTCTGGATGCTTGGGGCCAGGGCACAACCGTGGTGGTGT CTGCCGCCTCTACAAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTT GGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAA TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCC CCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAG ACCCTGAGGTCAAGTTCAACTGGTATGTTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT GCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACC ACAGGTGTACACCCTGCCCCCATCCGGGATGAGCTGACCAAGAATCAAGTCAGCCTGTGGTGCCTGGTCAAAGGCT TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGT GCTGGACTCCGACGGCTCCTTCTTCCTCTACTCAAAACTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT
	4	284	TACATCCACGTGACCCAGAGCCCCAGCAGCCTGTCCGTGTCCATCGGCGACAGAGTGACCATCAACTGCCAGACCTC TCAGGGCGTGGGCAGCGACCTGCACTGGTATCAGCACAAGCCTGGCAGAGCCCCCAAGCTGCTGATCCACCACACA AGCAGCGTGGAAGATGGCGTGCCCAGCAGATTTTCCGGCAGCGGCTTCCACACCAGCTTCAACCTGACCATCAGCGA TCTGCAGGCCGACATTGCCACCTACTATTGTCAGGTGCTGCAGTTCTTCGGCAGAGGCAGCAGACTGCACATCA AGCGTACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGTTGAAGTCCGGCACAGCCTCTGTC GTGTGCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCA ACAGCCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAA GGCCGACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGC TTCAACCGGGGCGAGTGT
Trispecific 34	1	285	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGCAGACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTC CCTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCA

VRC01.23 / CD28sup x CD3mid_ENL Q IgG4 FALA/409K_ DKTHT linker			CCCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTATTGTGGCCAGGGCACCCAGTACCCCTTCACC TTTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCAGCC TGTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTAT CAGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGAT TTTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAAGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT
	2	286	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACAGTGTCTAGCGACAAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTGTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	287	CAGGTGCAGCTGGTGCAGTCTGGCGGCCAGATGAAGAAACCCGGCGAGAGCATGCGGATCAGCTGCAGAGCCAGCG GCTACGAGTTCATCGACTGCACCCTGAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGCTG AAGCCTAGATGGGGAGCCGTGAACTACGCCAGACCTCTGCAGGGCAGAGTGACCATGACCCGGCAGCTGAGCCAGG ACCCTGATGATCCGGATTGGGGCACCGCCTTCCTGGAACTGCGGAAGCCTGACCGTGGATGATACCGCCGTGTACTTC

			TGCACCCGGGGCAAGAACTGCGACTACAACTGGGACTTCGAGCACTGGGCAGAGGCACCCCTGTGATCGTGTCAA GCGCGTCGACCAAGGGCCCATCGGTGTTCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCNTG GGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGNTNTGACAAGCGGCGTGCA CACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCAGCCTGG GCACCAAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGAGCGGGTGGAATCTAAGTA CGGCCCTCCCTGCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAA GGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTG CAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCA CCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCC AACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATA CCCTGCCCCCTTGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGC GACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCG ACGGCTCATTCTTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCC GTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	288	CTGACACAGAGCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGTACG GCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGCCGC CGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGCGGC GACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCGTAC GGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGTGCCT GCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAG GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCCGACT ACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCG GGGCGAGTGT
Trispecific 35 VRC01.23 / CD28sup x CD3mid_ENL F IgG4 FALA/409K_ DKTHT linker	1	289	GACATCGTGATGACCCAGACCCCCCTGAGCCTGAGCGTGACACCTGGACAGCCTGCCAGCATCAGCTGCAAGAGCA GCCAGAGCCTGGTGCACGAGAACCTGTTCACCTACCTGAGCTGGTATCTGCAGAAGCCCGGCCAGAGCCCCCAGTCC CTGATCTACAAGGTGTCCAACAGATTCAGCGGCGTGCCCGACAGATTCTCCGGCAGCGGCTCTGGCACCGACTTCAC CCTGAAGATCAGCCGGGTGGAAGCCGAGGACGTGGGCGTGTACTACTTGTGGCCAGGGCACCCAGTACCCCTTCACCT TTGGCAGCGGCACCAAGGTGGAAATCAAGGACAAAACCCATACCGACATCCAGATGACCCAGAGCCCCAGCGCCT GTCTGCCAGCGTGGGCGACAGAGTGACCATCACCTGTCAGGCCAGCCAGAACATCTACGTGTGGCTGAACTGGTATC AGCAGAAGCCCGGCAAGGCCCCCAAGCTGCTGATCTACAAGGCCAGCAACCTGCACACCGGCGTGCCCAGCAGATT TTCTGGCAGCGGCTCCGGCACCGACTTCACCCTGACAATCAGCTCCCTGCAGCCCGAGGACATTGCCACCTACTACT GCCAGCAGGGCCAGACCTACCCCTACACCTTTGGCCAGGGCACCAAGCTGGAAATCAAGGATAAGACCCACACCCG TACGGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGT GCCTGCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAG CCAGGAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCC GACTACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCA ACCGGGGCGAGTGT

	2	290
		CAGGTGCAGCTGGTGCAGTCTGGCGCCGAGGTCGTGAAACCTGGCGCCTCTGTGAAGGTGTCCTGCAAGGCCAGCGG CTACACCTTTACCAGCTACTACATCCACTGGGTGCGCCAGGCCCCTGGACAGGGACTGGAATGGATCGGCAGCATCT ACCCCGGCAACGTGAACACCAACTACGCCCAGAAGTTCCAGGGCAGAGCCACCCTGACCGTGGACAACCAGCATCAG CACCGCCTACATGGAACTGAGCCGGCTGAGAAGCGACACCGCCGTGTACTACTGCACCCGGTCCCACTACGGCC TGGATTGGAACTTCGACGTGTGGGGCAAGGGCACCACCGTGACCGTCTCTAGCGACAAAACCCATACCCAGGTGCA GCTGGTGGAATCTGGCGGCGGAGTGGTGCAGCCTGGCAGAAGCCTGAGACTGAGCTGTGCCGCCAGCGGCTTCACCT TCACCAAGGCCTGGATGCACTGGGTGCGCCAGGCCCCTGGAAAGCAGCTGGAATGGGTGGCCCAGATCAAGGACAA GAGCAACAGCTACGCCACCTACTACGCCGACAGCGTGAAGGGCCGGTTCACCATCAGCCGGGACGACAGCAAGAAC ACCCTGTACCTGCAGATGAACAGCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCGGGCGTGTACTATGCCCT GAGCCCCTTCGATTACTGGGGCCAGGGAACCCTCGTGACCGTCTCTAGTGATAAGACCCACACCGCCAGCACAAAGG GCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGAATCTACAGCCGCCCTGGGCTGCCTCGTGAAG GACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGCTCTGACAAGCGGCGTGCACACCTTTCCAGCCGTG CTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCAGCCTGGGCACCAAGACCTACAC CTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTACGGCCCTCCCTGCCCT CCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAAGGACACCCTGATGATC AGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTGCAGTTCAATTGGTACGT GGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCACCTACCGGGTGGTGTCC GTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCCAACAAGGGCCTGCCCA GCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTGTACCCTGCCCCCTAGCCA GGAAGAGATGACCAAGAACCAGGTGTCCCTGAGCTGTGCCGTGAAAGGCTTCTACCCCAGCGACATTGCCGTGGAA TGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCGACGGCTCATTCTTCCT GGTGTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCCGTGATGCACGAGGCC CTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	3	291
		CAGGTGCAGCTGGTGCAGTCTGGCGGCCAGATGAAGAAACCCGGCGAGAGCATGCGGATCAGCTGCAGAGCCAGCG GCTACGAGTTCATCGACTGCACCCTGAACTGGATCAGACTGGCCCCTGGCAAGCGGCCTGAGTGGATGGGATGGCTG AAGCCTAGATGGGGAGCCGTGAACTACGCCAGACCTCTGCAGGGCAGAGTGACCATGACCCGGCAGCTGAGCCAGG ACCCTGATGATCCGGATTGGGGCACCGCCTTCCTGGAACTGCGGAGCCTGACCGTGGATGATACCGCCGTGTACTTC TGCACCCGGGGCAAGAACTGCGACTACAACTGGGACTTCGAGCACTGGGGCAGAGGCACCCCTGTGATCGTGTCAA GCGCGTCGACCAAGGGCCCATCGGTGTTCCCCTCTGGCCCCTTGCAGCAGAAGCACCAGCGCGAATCTACAGCCGCCNTG GGCTGCCTCGTGAAGGACTACTTTCCCGAGCCCGTGACCGTGTCCTGGAACTCTGGCGNTNTGACAAGCGGCGTGCA CACCTTTCCAGCCGTGCTCCAGAGCAGCGGCCTGTACTCTCTGAGCAGCGTCGTGACAGTGCCCAGCAGCCTGG GCACCAAGACCTACACCTGTAACGTGGACCACAAGCCCAGCAACACCAAGGTGGACAAGCGGGTGGAATCTAAGTA CGGCCCTCCCTGCCCCTCCTTGCCCAGCCCCTGAAGCTGCCGGCGGACCCTCCGTGTTCCTGTTCCCCCCAAAGCCCAA GGACACCCTGATGATCAGCCGGACCCCCGAAGTGACCTGCGTGGTGGTGGATGTGTCCCAGGAAGATCCCGAGGTG CAGTTCAATTGGTACGTGGACGGCGTGGAAGTGCACAACGCCAAGACCAAGCCCAGAGAGGAACAGTTCAACAGCA CCTACCGGGTGGTGTCCGTGCTGACCGTGCTGCACCAGGACTGGCTGAACGGCAAAGAGTACAAGTGCAAGGTGTCC AACAAGGGCCTGCCCAGCTCCATCGAGAAAACCATCAGCAAGGCCAAGGGCCAGCCCCGCGAGCCTCAAGTGTATA CCCTGCCCCCTTGCCAGGAAGAGATGACCAAGAACCAGGTGTCCCTGTGGTGTCTCGTGAAAGGCTTCTACCCCAGC

			GACATTGCCGTGGAATGGGAGAGCAACGGCCAGCCCGAGAACAACTACAAGACCACCCCCCCTGTGCTGGACAGCG ACGGCTCATTCTTCCTGTACTCCAAGCTGACCGTGGACAAGAGCCGGTGGCAGGAAGGCAACGTGTTCAGCTGCTCC GTGATGCACGAGGCCCTGCACAACCACTACACCCAGAAGTCCCTGTCTCTGTCCCTGGGC
	4	292	CTGACACAGAGCCCCTGGCACCCTGTCACTGAGCCCAGGCGAGACAGCCATCATCAGCTGCCGGACAAGCCAGTACG GCAGCCTGGCCTGGTATCAGCAGAGGCCTGGACAGGCCCCCAGACTCGTGATCTACAGCGGCAGCACAAGAGCCGC CGGAATCCCCGATAGATTCAGCGGCTCCAGATGGGGACCCGACTACAACCTGACCATCAGCAACCTGGAAAGCGGC GACTTCGGCGTGTACTACTGCCAGCAGTACGAGTTCTTCGGCCAGGGCACCAAGGTGCAGGTGGACATCAAGCGTAC GGTGGCCGCTCCCAGCGTGTTCATCTTCCCACCTAGCGACGAGCAGCTGAAGTCCGGCACAGCCTCTGTCGTGTGCCT GCTGAACAACTTCTACCCCCGCGAGGCCAAAGTGCAGTGGAAGGTGGACAACGCCCTGCAGAGCGGCAACAGCCAG GAAAGCGTGACCGAGCAGGACAGCAAGGACTCCACCTACAGCCTGAGCAGCACCCTGACACTGAGCAAGGCCGACT ACGAGAAGCACAAGGTGTACGCCTGCGAAGTGACCCACCAGGGCCTGTCTAGCCCCGTGACCAAGAGCTTCAACCG GGGCGAGTGT

CLAIMS

What is claimed is:

1. A binding protein comprising four polypeptide chains that form three antigen binding sites that specifically bind one or more HIV target proteins, wherein a first polypeptide chain comprises a structure represented by the formula:

$$V_{L2}\text{-}L_1\text{-}V_{L1}\text{-}L_2\text{-}C_L \quad [I]$$

and a second polypeptide chain comprises a structure represented by the formula:

$$V_{H1}\text{-}L_3\text{-}V_{H2}\text{-}L_4\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \quad [II]$$

and a third polypeptide chain comprises a structure represented by the formula:

$$V_{H3}\text{-}C_{H1}\text{-hinge-}C_{H2}\text{-}C_{H3} \quad [III]$$

and a fourth polypeptide chain comprises a structure represented by the formula:

$$V_{L3}\text{-}C_L \quad [IV]$$

wherein:

V_{L1} is a first immunoglobulin light chain variable domain;

V_{L2} is a second immunoglobulin light chain variable domain;

V_{L3} is a third immunoglobulin light chain variable domain;

V_{H1} is a first immunoglobulin heavy chain variable domain;

V_{H2} is a second immunoglobulin heavy chain variable domain;

V_{H3} is a third immunoglobulin heavy chain variable domain;

C_L is an immunoglobulin light chain constant domain;

C_{H1} is an immunoglobulin C_{H1} heavy chain constant domain;

C_{H2} is an immunoglobulin C_{H2} heavy chain constant domain;

C_{H3} is an immunoglobulin C_{H3} heavy chain constant domain;

hinge is an immunoglobulin hinge region connecting the C_{H1} and C_{H2} domains; and

L_1, L_2, L_3 and L_4 are amino acid linkers;

wherein the polypeptide of formula I and the polypeptide of formula II form a cross-over light chain-heavy chain pair; and

wherein V_{H1} and V_{L1} form a first antigen binding site;

wherein V_{H2} and V_{L2} form a second antigen binding site that binds a CD3 polypeptide, wherein the V_{H2} domain comprises a CDR-H1 sequence comprising the amino acid sequence of GFTFTKAW (SEQ ID NO:20), a CDR-H2 sequence comprising the amino acid sequence of

IKDKSNSYAT (SEQ ID NO:21), and a CDR-H3 sequence comprising the amino acid sequence of RGVYYALSPFDY (SEQ ID NO:22), and the V_{L2} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QSLVHX$_1$NX$_2$X$_3$TY, wherein X$_1$ is E or Q, X$_2$ is A or L, and X$_3$ is Q, R, or F (SEQ ID NO:293), a CDR-L2 sequence comprising the amino acid sequence of KVS (SEQ ID NO:29), and a CDR-L3 sequence comprising the amino acid sequence of GQGTQYPFT (SEQ ID NO:30); and

wherein V_{H3} and V_{L3} form a third antigen binding site that binds an HIV target protein.

2. The binding protein of claim 1, wherein the first binding site binds a CD28 polypeptide.

3. The binding protein of claim 2, wherein the V_{H1} domain comprises a CDR-H1 sequence comprising the amino acid sequence of GYTFTSYY (SEQ ID NO:31), a CDR-H2 sequence comprising the amino acid sequence of IYPGNVNT (SEQ ID NO:32), and a CDR-H3 sequence comprising the amino acid sequence of TRSHYGLDWNFDV (SEQ ID NO:33), and the V_{L1} domain comprises a CDR-L1 sequence comprising the amino acid sequence of QNIYVW (SEQ ID NO:34), a CDR-L2 sequence comprising the amino acid sequence of KAS (SEQ ID NO:35), and a CDR-L3 sequence comprising the amino acid sequence of QQGQTYPY (SEQ ID NO:36).

4. The binding protein of claim 3, wherein the V_{H1} domain comprises the amino acid sequence of QVQLVQSGAEVVKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWIGSIYPGNVNTNYAQKFQGRATLTVDTSISTAYMELSRLRSDDTAVYYCTRSHYGLDWNFDVWGKGTTVTVSS (SEQ ID NO:59), and/or the V_{L1} domain comprises the amino acid sequence of DIQMTQSPSSLSASVGDRVTITCQASQNIYVWLNWYQQKPGKAPKLLIYKASNLHTGVPSRFSGSGSGTDFTLTISSLQPEDIATYYCQQGQTYPYTFGQGTKLEIK (SEQ ID NO:60).

5. The binding protein of any one of claims 1-4, wherein the CDR-L1 sequence of the V_{L2} domain comprises an amino acid sequence selected from the group consisting of QSLVHQNAQTY (SEQ ID NO:24), QSLVHENLQTY (SEQ ID NO:25), QSLVHENLFTY (SEQ ID NO:26), and QSLVHENLRTY (SEQ ID NO:27).

6. The binding protein of claim 5, wherein the V_{H2} domain comprises the amino acid sequence of

QVQLVESGGGVVQPGRSLRLSCAASGFTFTKAWMHWVRQAPGKQLEWVAQIKDKS NSYATYYADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCRGVYYALSPFDY WGQGTLVTVSS (SEQ ID NO:52), and/or the V_{L2} domain comprises an amino acid sequence selected from the group consisting of DIVMTQTPLSLSVTPGQPASISCKSSQSLVHQNAQTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:54), DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLQTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:55), DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLFTYLSWYLQKPGQSPQSLIYKVSNR FSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:56), and DIVMTQTPLSLSVTPGQPASISCKSSQSLVHENLRTYLSWYLQKPGQSPQSLIYKVSN RFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCGQGTQYPFTFGSGTKVEIK (SEQ ID NO:57).

7. The binding protein of any one of claims 1-6, wherein the third antigen binding site binds an HIV target protein selected from the group consisting of glycoprotein 120, glycoprotein 41 and glycoprotein 160.

8. The binding protein of claim 7, wherein:

(a) the V_{H3} domain comprises a CDR-H1 sequence comprising the amino acid sequence of NCPIN (SEQ ID NO:1) a CDR-H2 sequence comprising the amino acid sequence of WMKPRHGAVSYARQLQG (SEQ ID NO:2), and a CDR-H3 sequence comprising the amino acid sequence of GKYCTARDYYNWDFEH (SEQ ID NO:3), and the V_{L3} domain comprises a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:4), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID NO:5), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:6);

(b) the V_{H3} domain comprises a CDR-H1 sequence comprising the amino acid sequence of GYTFTAHI (SEQ ID NO:7) a CDR-H2 sequence comprising the amino acid sequence of IKPQYGAV (SEQ ID NO:8) or IKPQYGAT (SEQ ID NO:9), and a CDR-H3 sequence comprising the amino acid sequence of DRSYGDSSWALDA (SEQ ID NO:10), and the V_{L3}

domain comprises a CDR-L1 sequence comprising the amino acid sequence of QGVGSD (SEQ ID NO:11), a CDR-L2 sequence comprising the amino acid sequence of HTS (SEQ ID NO:12), and a CDR-L3 sequence comprising the amino acid sequence of CQVLQF (SEQ ID NO:13); or

(c) the V_{H3} domain comprises a CDR-H1 sequence comprising the amino acid sequence of DCTLN (SEQ ID NO:14) a CDR-H2 sequence comprising the amino acid sequence of WLKPRWGAVNYARPLQG (SEQ ID NO:15), and a CDR-H3 sequence comprising the amino acid sequence of GKNCDYNWDFEH (SEQ ID NO:16), and the V_{L3} domain comprises a CDR-L1 sequence comprising the amino acid sequence of RTSQYGSLA (SEQ ID NO:17), a CDR-L2 sequence comprising the amino acid sequence of SGSTRAA (SEQ ID NO:18), and a CDR-L3 sequence comprising the amino acid sequence of QQYEF (SEQ ID NO:19).

9. The binding protein of claim 8, wherein:

(a) the V_{H3} domain comprises the amino acid sequence of QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHG AVSYARQLQGRVTMTRDMYSETAFLELRSLTSDDTAVYFCTRGKYCTARDYYNWD FEHWGQGTPVTVSS (SEQ ID NO:43), and/or the V_{L3} domain comprises the amino acid sequence of SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFS GSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:45);

(b) the V_{H3} domain comprises the amino acid sequence of QVRLSQSGGQMKKPGDSMRISCRASGYEFINCPINWIRLAPGKRPEWMGWMKPRHG AVSYARQLQGRVTMTRQLSQDPDDPDWGTAFLELRSLTSDDTAVYFCTRGKYCTA RDYYNWDFEHWGQGTPVTVSS (SEQ ID NO:44), and/or the V_{L3} domain comprises the amino acid sequence of SLTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFS GSRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:45);

(c) the V_{H3} domain comprises the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQY GAVNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALD AWGQGTTVVVSA (SEQ ID NO:46), and/or the V_{L3} domain comprises the amino acid

sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGV PSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49);

(d) the V_{H3} domain comprises the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQY GATNFGGGFRDRVTLTRDVYREIAYMDIRGLKPDDTAVYYCARDRSYGDSSWALD AWGQGTTVVVSA (SEQ ID NO:47), and/or the V_{L3} domain comprises the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGV PSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49);

(e) the V_{H3} domain comprises the amino acid sequence of RAHLVQSGTAMKKPGASVRVSCQTSGYTFTAHILFWFRQAPGRGLEWVGWIKPQY GAVNFGGGFRDRVTLTRQLSQDPDDPDWGIAYMDIRGLKPDDTAVYYCARDRSYG DSSWALDAWGQGTTVVVSA (SEQ ID NO:48), and/or the V_{L3} domain comprises the amino acid sequence of YIHVTQSPSSLSVSIGDRVTINCQTSQGVGSDLHWYQHKPGRAPKLLIHHTSSVEDGV PSRFSGSGFHTSFNLTISDLQADDIATYYCQVLQFFGRGSRLHIK (SEQ ID NO:49); or

(f) the V_{H3} domain comprises the amino acid sequence of QVQLVQSGGQMKKPGESMRISCRASGYEFIDCTLNWIRLAPGKRPEWMGWLKPRW GAVNYARPLQGRVTMTRQLSQDPDDPDWGTAFLELRSLTVDDTAVYFCTRGKNCD YNWDFEHWGRGTPVIVSS (SEQ ID NO:50), and/or the V_{L3} domain comprises the amino acid sequence of LTQSPGTLSLSPGETAIISCRTSQYGSLAWYQQRPGQAPRLVIYSGSTRAAGIPDRFSG SRWGPDYNLTISNLESGDFGVYYCQQYEFFGQGTKVQVDIK (SEQ ID NO:51).

10. The binding protein of any one of claims 1-9, wherein at least one of L_1, L_2, L_3 or L_4 is independently 0 amino acids in length.

11. The binding protein of any one of claims 1-9, wherein (a) L_1, L_2, L_3 and L_4 each independently are zero amino acids in length or comprise a sequence selected from the group consisting of GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO: 41), S, RT, TKGPS (SEQ ID NO: 39), GQPKAAP (SEQ ID NO: 38), and GGSGSSGSGG (SEQ

ID NO: 42); or (b) L_1, L_2, L_3 and L_4 each independently comprise a sequence selected from the group consisting of GGGGSGGGGS (SEQ ID NO:40), GGGGSGGGGSGGGGS (SEQ ID NO:41), S, RT, TKGPS (SEQ ID NO:39), GQPKAAP (SEQ ID NO: 38), and GGSGSSGSGG (SEQ ID NO:42).

12. The binding protein of any one of claims 1-9, wherein L_1 comprises the sequence GQPKAAP (SEQ ID NO: 38), L_2 comprises the sequence TKGPS (SEQ ID NO:39), L_3 comprises the sequence S, and L_4 comprises the sequence RT.

13. The binding protein of any one of claims 1-9, wherein at least one of L_1, L_2, L_3 or L_4 comprises the sequence DKTHT (SEQ ID NO:37).

14. The binding protein of claim 13, wherein L_1, L_2, L_3 and L_4 comprise the sequence DKTHT (SEQ ID NO:37).

15. The binding protein of any one of claims 1-14, wherein the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG4 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 234 and 235 of human IgG4 according to EU Index, wherein the amino acid substitutions are F234A and L235A.

16. The binding protein of any one of claims 1-14, wherein the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG4 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 233-236 of human IgG4 according to EU Index, wherein the amino acid substitutions are E233P, F234V, L235A, and a deletion at 236.

17. The binding protein of any one of claims 1-16, wherein the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG4 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 228 and 409 of human IgG4 according to EU Index, wherein the amino acid substitutions are S228P and R409K.

18. The binding protein of any one of claims 1-14, wherein the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG1 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions

corresponding to positions 234, 235, and 329 of human IgG1 according to EU Index, wherein the amino acid substitutions are L234A, L235A, and P329A.

19. The binding protein of any one of claims 1-14, wherein the hinge-C_{H2}-C_{H3} domains of the second and the third polypeptide chains are human IgG1 hinge-C_{H2}-C_{H3} domains, and wherein the hinge-C_{H2}-C_{H3} domains each comprise amino acid substitutions at positions corresponding to positions 298, 299, and 300 of human IgG1 according to EU Index, wherein the amino acid substitutions are S298N, T299A, and Y300S.

20. The binding protein of any one of claims 1-19, wherein the hinge-C_{H2}-C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V; and wherein the hinge-C_{H2}-C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are S354C and T366W.

21. The binding protein of any one of claims 1-19, wherein the hinge-C_{H2}-C_{H3} domain of the second polypeptide chain comprises amino acid substitutions at positions corresponding to positions 354 and 366 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are S354C and T366W; and wherein the hinge-C_{H2}-C_{H3} domain of the third polypeptide chain comprises amino acid substitutions at positions corresponding to positions 349, 366, 368, and 407 of human IgG1 or IgG4 according to EU Index, wherein the amino acid substitutions are Y349C, T366S, L368A, and Y407V.

22. The binding protein of claim 1, wherein:

(a) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:61 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:61; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:62 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:62; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:63 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:63; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:64

or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:64;

(b) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:65 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:65; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:66 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:66; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:67 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:67; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:68 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:68;

(c) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:69 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:69; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:70 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:70; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:71 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:71; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:72 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:72;

(d) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:73 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:73; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:74 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:74; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:75 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:75; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:76 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:76;

(e) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:77 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID

NO:77; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:78 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:78; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:79 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:79; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:80 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:80;

(f) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:81 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:81; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:82 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:82; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:83 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:83; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:84 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:84;

(g) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:85 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:85; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:86 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:86; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:87 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:87; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:88 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:88;

(h) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:89 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:89; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:90 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:90; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:91 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID

NO:91; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:92 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:92;

(i) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:93 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:93; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:94 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:94; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:95 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:95; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:96 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:96;

(j) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:97 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:97; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:98 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:98; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:99 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:99; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:100 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:100;

(k) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:101 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:101; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:102 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:102; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:103 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:103; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:104 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:104;

(l) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:105 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:105; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:106 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:106; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:107 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:107; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:108 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:108;

(m) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:109 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:109; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:110 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:110; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:111 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:111; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:112 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:112;

(n) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:113 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:113; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:114 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:114; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:115 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:115; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:116 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:116;

(o) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:117 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:117; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:118 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID

NO:118; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:119 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:119; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:120 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:120;

(p) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:121 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:121; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:122 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:122; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:123 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:123; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:124 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:124;

(q) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:129 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:129; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:130 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:130; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:131 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:131; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:132 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:132;

(r) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:133 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:133; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:134 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:134; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:135 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:135; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID

NO:136 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:136;

(s) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:137 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:137; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:138 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:138; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:139 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:139; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:140 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:140;

(t) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:141 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:141; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:142 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:142; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:143 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:143; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:144 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:144;

(u) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:145 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:145; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:146 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:146; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:147 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:147; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:148 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:148;

(v) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:149 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID

NO:149; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:150 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:150; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:151 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:151; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:152 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:152;

(x) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:153 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:153; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:154 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:154; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:155 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:155; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:156 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:156;

(y) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:157 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:157; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:158 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:158; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:159 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:159; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:160 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:160;

(z) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:161 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:161; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:162 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:162; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:163 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID

NO:163; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:164 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:164;

(aa) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:165 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:165; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:166 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:166; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:167 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:167; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:168 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:168;

(bb) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:169 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:169; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:170 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:170; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:171 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:171; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:172 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:172; or

(cc) the first polypeptide chain comprises the amino acid sequence of SEQ ID NO:173 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:173; the second polypeptide chain comprises the amino acid sequence of SEQ ID NO:174 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:174; the third polypeptide chain comprises the amino acid sequence of SEQ ID NO:175 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:175; and the fourth polypeptide chain comprises the amino acid sequence of SEQ ID NO:176 or an amino acid sequence that is at least 95% identical to the amino acid sequence of SEQ ID NO:176.

23. An isolated nucleic acid molecule comprising a nucleotide sequence encoding the binding protein of any one of claims 1-22.

24. An expression vector comprising the nucleic acid molecule of claim 23.

25. An isolated host cell comprising the nucleic acid molecule of claim 23 or the expression vector of claim 24.

26. The isolated host cell of claim 25, wherein the host cell is a mammalian or insect cell.

27. A pharmaceutical composition comprising the binding protein of any one of claims 1-22 and a pharmaceutically acceptable carrier.

28. A method of preventing and/or treating HIV infection in a patient comprising administering to the patient a therapeutically effective amount of at least one binding protein of any one of claims 1-22 or the pharmaceutical composition of claim 27.

29. The method of claim 28, wherein the binding protein is co-administered with standard anti-retroviral therapy.

30. The method of claim 28 or claim 29, wherein administration of the at least one binding protein results in the elimination of one or more latently and/or chronically HIV-infected cells in the patient.

31. The method of any one of claims 28-30, wherein the patient is a human.

32. The binding protein of any one of claims 1-22 or the pharmaceutical composition of claim 27 for the prevention and/or treatment of HIV infection in a patient.

33. The binding protein for use of claim 32, wherein the binding protein is to be co-administered with standard anti-retroviral therapy.

34. The binding protein for use of claim 32 or claim 33, wherein the binding protein causes the elimination of one or more latently and/or chronically HIV-infected cells in the patient.

35. The binding protein for use of any one of claims 32-34, wherein the patient is a human.

36. A vector system comprising one or more vectors encoding a first, second, third, and fourth polypeptide chain of a binding protein of any one of claims 1-22.

37. The vector system of claim 36, wherein the vector system comprises a first vector encoding the first polypeptide chain of the binding protein, a second vector encoding the second polypeptide chain of the binding protein, a third vector encoding the third polypeptide chain of the binding protein, and a fourth vector encoding the fourth polypeptide chain of the binding protein.

38. A kit of polynucleotides, comprising:

(a) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:177, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:178, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:179, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:180;

(b) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:181, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:182, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:183, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:184;

(c) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:185, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:186, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:187, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:188;

(d) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:189, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:190, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:191, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:192;

(e) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:193, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:194, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:195, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:196;

(f) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:197, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:198, a third

polynucleotide comprising the polynucleotide sequence of SEQ ID NO:199, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:200;

(g) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:201, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:202, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:203, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:204;

(h) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:205, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:206, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:207, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:208;

(i) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:209, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:210, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:211, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:212;

(j) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:213, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:214, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:215, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:216;

(k) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:217, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:218, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:219, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:220;

(l) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:221, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:222, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:223, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:224;

(m) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:225, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:226, a third

polynucleotide comprising the polynucleotide sequence of SEQ ID NO:227, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:228;

(n) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:229, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:230, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:231, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:232;

(o) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:233, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:234, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:235, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:236;

(p) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:237, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:238, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:239, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:240;

(q) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:241, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:242, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:243, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:244;

(r) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:245, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:246, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:247, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:248;

(s) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:249, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:250, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:251, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:252;

(t) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:253, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:254, a third

polynucleotide comprising the polynucleotide sequence of SEQ ID NO:255, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:256;

(u) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:257, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:258, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:259, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:260;

(v) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:261, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:262, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:263, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:264;

(w) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:265, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:266, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:267, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:268;

(x) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:269, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:270, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:271, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:272;

(y) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:273, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:274, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:275, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:276;

(z) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:277, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:278, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:279, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:280;

(aa) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:281, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:282, a third

polynucleotide comprising the polynucleotide sequence of SEQ ID NO:283, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:284;

(bb) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:285, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:286, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:287, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:288; or

(cc) a first polynucleotide comprising the polynucleotide sequence of SEQ ID NO:289, a second polynucleotide comprising the polynucleotide sequence of SEQ ID NO:290, a third polynucleotide comprising the polynucleotide sequence of SEQ ID NO:291, and a fourth polynucleotide comprising the polynucleotide sequence of SEQ ID NO:292.

39. The kit of claim 38, wherein the first, second, third, and fourth polynucleotides are present on one or more expression vectors.